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Total number of hits satisfying chosen parameters:
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                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                             ac06c04.sl Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:855654 3' similar to contains element MSR1 MSR1 repetitive
                                                                                                                                                                                                                           element ;, mRNA sequence. AA664125
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Copyright (c) 1993 - 2000 Compugen Ltd:
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                                        908 ca 909
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Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S., Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B., White,Y., Wylle,T., Waterston,R. and Wilson,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 425.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
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/db_xref="taxon:9606"
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Pred. No. 8.9e-70;
0; Mismatches 1; Indels 0;
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Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

em\_estfun:\*

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em\_htc:\* em\_estro:\* em\_estpl:\* em\_estom:\* em\_estin:\* em\_esthum:\*

gb\_est1:\*

em\_estov:\* em\_estba:\*

DEFINITION

AA664125/c RESULT

AA664125

482 bp

em\_gss\_pro:\*
em\_gss\_rod:\* em\_gss\_pln:\* em\_gss\_hum:\* em\_gss\_fun:\* gb\_gss:\* gb\_htc:\* gb\_est2:\*

em\_gss\_inv:\*

em\_gss\_other: \*

em\_gss\_vrt:\*

KEYWORDS VERSION

EST.

AA664125.1 GI:2618116

ORGANISM

Homo sapiens

ACCESSION

Scoring table: Sequence: Perfect score:

IDENTITY\_NUC

US-09-668-119-1

OM nucleic -

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Makimum DB seq length: 2000000000
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Copyright (c) 1993 - 2000 Compugen Ltd.
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REFERENCE
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Query Match 59.5
Best Local Similarity 99.7
Matches 1037; Conservative
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Submitted (02-DEC-1996) Psychiatry, Johns Hopkins Univ. Sch. of
Med., 600 N. Wolfe Street, Meyer 2-181, Baltlmore, MD 21205, USA
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/rpt_unit=CAG
388 c 251
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/db_xref="taxon:9606"
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                                   59.5%;
99.7%;
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                                       Score 1035.8; DB 9; Pred. No. 1.2e-148;
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                                                                        agatgaagagccttctggac 1515
                                                AGATGAAGAGCCTTCTGGAC 1041
                             ccctycyccgcatgatcaacaagatcgacaagaacgaagacagaaaaaaaggacctgagta 1495
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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
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OM nucleic - nucleic search, using sw model

February 28, 2002, 17:49:47; Search time 86.87 Seconds (without alignments)
4536.338 Million cell updates/sec

US-09-668-119-1

Perfect score: 1 atgaggaaagctggtgtggc.....cacattcgttccagccatga 1740

Scoring table: IDENTITY\_NUC
Gapop 10.0 , Gapext 1.0

351203 seqs, 113238999 residues

Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100%

Listing first 45 summaries

Database :

Issued\_Patents\_NA: \* /cgn2\_6/ptodata/2/ina/5A\_COMB.seq:\*
/cgn2\_6/ptodata/2/ina/5B\_COMB.seq:\*
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/cgn2\_6/ptodata/2/ina/PCTUS\_COMB.seq:\*
/cgn2\_6/ptodata/2/ina/Packfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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sequence /, Appli		Sequence 1, Sequence 15 Sequence 15 Sequence 15 Sequence 15 Sequence 15	Sequence 1, Sequence 2, Sequence 1, Sequence 1,	sequence 1, sequence 1, sequence 1, sequence 1,		Sequence 1, Appli Sequence 20, Appl Sequence 20, Appl	Description

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; Sequence 3, Application US/08469802B; Patent No. 5741645
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APPLICANT: Ranum, Laura P.W.
APPLICANT: Chung, Ming-yi
APPLICANT: Zoghbi, Huda Y.
TITLE OF INVENTION: Gene Sequence for Spinocerebellar Ataxia
Patent No. 5741645
                                                                                                                                                                                                                                                                                                          Query Match 7.5%; Score 130.8; DB 1; Best Local Similarity 75.7%; Pred. No. 2.8e-20; Matches 162; Conservative 0; Mismatches 52;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 612-305-1225
INFORMATION FOR SEQ ID NO:
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NAME: Mueting, Ann M.
REGISTRATION NUMBER: 33,
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: 11
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 234 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 11
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-305-1217
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Type 1 and Method for Diagnosis NUMBER OF SEQUENCES: 47
                                                                                                                                                                             430 cagcagcagcagcaggcggcgctacagcagcagcagcagcagcagcagcagcagcagttc 489
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Bole
                  550 ctccagcagcagcagcagcagcagcatctaa 583
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181 CAGCAGCAGCAGCAGCAGCAGCACCTCA 214
                                                                         TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Minneapolis STATE: MN
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                                                                                                                                                        TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE:
                                                                                                                                                                                                                                 INFORMATION:
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Database sequences: 522463
Database length: 74073290
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/SIDS2/gcgdata/geneseq/geneseqp/AA2001.DAT:AAM42082
/SIDS2/gcgdata/geneseq/geneseqp/AA2001.DAT:AAM4282
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/SIDS2/gcgdata/geneseq/geneseqp/AA2001.DAT:AAM61998
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/SIDS2/gcgdata/geneseq/geneseqp/AA2001.DAT:AAM52830
/SIDS2/gcgdata/geneseq/geneseqp/AA2001.DAT:AAM52830
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/SIDS2/gcgdata/geneseq/geneseqp/AA2001.DAT:AAB69614
/SIDS2/gcgdata/geneseq/geneseqp/AA2001.DAT:AAB49614
/SIDS2/gcgdata/geneseq/geneseqp/AA2001.DAT:AAB4941
/SIDS2/gcgdata/geneseq/geneseqp/AA2001.DAT:AAY74791
/SIDS2/gcgdata/geneseq/geneseqp/AA2001.DAT:AAB95124
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-Q-/cgn2_1/USPTO_spool/spoil-frasta_1.1824
-Q-/cgn2_1/USPTO_spool/spoil-frasta -SUFFIX=rag -GAPOP=12.000
-DB=A_Gencseq_1101 -QEMT=fastan -SUFFIX=rag -GAPOP=12.000
-GAPEXT=4.000 -MINMATCH=0.100 -LOOPCL-0.000 -LOOPEXT=0.000
-QGAPEXT=4.000 -QGAPEXT=0.050 -XGAPOP=10.000 -XGAPEXT=0.500
-FGAPOP=6.000 -GAPEXT=7.000 -YGAPDP=10.000 -YGAPEXT=0.500
-DELOP-6.000 -DELEXT=7.000 -YGAPDP=10.000 -YGAPEXT=0.500
-DELOP-6.000 -DELEXT=7.000 -START=1 -MATRIX=blosum62
-TRANS-human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE-PCt
-THR_MAX=100 -THR_NIN=0 -ALIGN=15 -MODE-LOCAL -OUTFMT-pfs
-NORM-ext -MINLEN=0 -MAXLEN=200000000
-USER=US09568119_@CGN1_1_87 -NCPU=6 -ICPU=3 -LONGLOG -NO_XLPXY
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The invention relates to human nucleic acids (AAI57798-AAI61369) and CC the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful CC in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous CC system, such as peripheral nervous injuries, peripheral neuropathy and Clocalised neuropathies and central nervous system diseases, such as C localised neuropathies and central nervous system diseases, such as C lateral sclerosis, and Shy-Drager Syndrome. Other uses include the C lateral sclerosis, and Shy-Drager Syndrome. Other uses include the C utilisation of the activities such as: Immune system suppression, C and thrombolytic activity, chemotactic/chemokinetic activity, haemostatic and thrapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and C C.N.S disorders.

Sequence specification.

Note: The sequence data

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thromboluvic, drug commandiatic;
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Zhao QA,
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N-PSDB; AAI59455.
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Wang Z,
, Zhou P,
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2000US-0620312.
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2000US-0662191.
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Wehrman T,
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Xu C, Xue AJ,
R, Drmanac RT;
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76 699	aleroThreroProProProProValeroProThrLysGlnGlnTy TGCCAGCCGCTCCTGGATGCCGTCCTGGCCAACATCCGCTCACCTG
6	CCACCGCCCCGGTGCCACCGACCAAACAGCAGTAC
.599	1551 GACCTTGCAAAAGTGTGAGATCGCCCTGGAGAAACTCAAGAATGACATGC 1 
155C	1501 AAGAGCCTTCTGGACATTCTGACAGACCCCTCGAAGCGGTGTCCCCTGAA 1 
L500 526	1451 TCAACAAGATCGACAAGAACGAAGAAGAAAAAAGGACCTGAGTAAGATG 1 
1450 510	1401 GGACAAGCTGAAGCAGCTGTCGAAGTACATCGAGCCCCTGCGCCCGCATGA 1 
140C 493	1351 TCTGTCATGAGCCCAGCTGGCTCCAGCCAGGCTGAGGAGCAGCAGCAGTACCT 1
135 <b>47</b> 6	1301 ACTTCAGTGTCCCCTCACCTGGACCTTTAAACACACCTGTGAACCCCAGC
130 460	1251 CCCCTCACCGCAGCCCTCCCCAGAGCCCCAGTGACGGCGCGGGGGCCCACAGA [ - - - - - - - - - - - - - - - - - - -
125 443	1201 TCCAACGTCAGCCTCTGGGCCCTGCCCCATCTCCCAGTAGCTTCCTGCCCAGIIIIIIIIII
120 426	1151 CTCCCCCCAGCCGTCCCCGCAGCCCGGCCAGCCCAGCCC
115 410	1101 GTCCTCGCCGTCACCGGGCCAGCAGGTGCAGACCCCGCAGTCGATGCCCC
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AC AAM42085;
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AC AAM42085;
XX
DT 22-OCT-2001 (first 6
XX
Human; nootropic; imm
KW Human; nootropic; imm
KW Alzheimer's; Parkinss
RW Alzheimer's; Parkinss
PT Stample 2; Sequence 780 AA;
Sequence 780 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; neuropathy; central nervous system; CNS; plathelmer's; parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
                                                                                                      system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, ampotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, activinyinhibin activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and
                                                                                                                                                                                                                                                                              The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polypucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous
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                                                                     Note: The sequence data
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, Xu C, Xue AJ,
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lnLeuGlnGlnGlnGlnGlnGlnHisLeuIleLysLeuHisHis
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                                                                                                                                                                                                                                                                  ArgTyrSerSerSerSerSerSerAsnSerLysGlnPheGlnAlaGl
                                                                                                                                                                                                                                                                                                                        laAlaAlaAlaAlaThrAlaArgSerSerSerSerSerArgArg
                                                                                                                                                                                                                                                                                                                                                                            CGTGTCTACGGCAACTCCACAGACCCAGCTGCAGCTCCAGCAGGTGGC.G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   euGlyGlyMetGlySerLeuGlyAlaMetGlyGlnProMetSerLeuSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TGCGGGAGCCGCTGGAATTGGCATGCCTCCTCGGGGCCCCGGGACAGTCTC 250
                                                                               ACAGCTGCAGCTCCAACAACAGCAACAGCAGCAGCAGCAGCAGCAGCAGC
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Gaps: 0
Percent Identity: 98.967
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CAGCAGCCACAGCCTCCGCCCTCCCAGGCTCTGCCCCAGCAGCTGCAGCA 797

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1548
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    391 alGlnProGlnValGlnGlnGlnGlnThrAlaValGlnThrAlaGlnAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    374 nProProLeuLysPheValArgAlaProMetValValGlnGlnProProV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    948
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            848 CAGTTGCTCAGAACCAACCATCACAACTCCCGCCACAGTCGCAGACCCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          324 nMetHisHisThrGlnHisHisGlnProProProGlnProGlnGlnProP
                   TACCTATGCCAGCCGCTCCTGGATGCCGTCCTGGCCAACATCCGCTCACC
                                                           GAAGACCTTGCAAAAGTGTGAGATCGCCCTGGAGAAACTCAAGAATGACA 1597
                                                                                                                                                                                                                                                          ATGAAGAGCCTTCTGGACATTCTGACAGACCCCTCGAAGCGGTGTCCCCT 1547
                                                                                                                                                                                                                                                                                                                    etIleAsnLysIleAspLysAsnGluAspArgLysLysAspLeuSerLys 557
                                                                                                                                                  uLysThrLeuGlnLysCysGluIleAlaLeuGluLysLeuLysAsnAspM 591
                                                                                                                                                                                                                                    MetLysSerLeuLeuAspIleLeuThrAspProSerLysArgCysProLe
                                                                                                                                                                                                                                                                                                                                                                                                    CCTGGACAAGCTGAAGCAGCTGTCGAAGTACATCGAGCCCCTGCGCCCCA 1447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AGCTCTGTCATGAGCCCAGCTGGCCTCCAGCCAGGCTGAGGAGCAGCAGTA 1397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CCCCTCCCCCCAGCCGTCCCCGCAGCCCGGCCAGCCCAGCCTCACAGCCC 1197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GCTGTCCTCGCCGTCACCGGGCCAGCCAGGTGCAGACCCCGCAGTCGATGC 1147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GCCCAGATGGTGGCTCCCGGAGTCCAGGTCAGCCAGAGCAGCCTCCCCAT 1097
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AGAACTTCAGTGTCCCCTCACCTGGACCTTTAAACACACCTGTGAACCCC 1347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       oSerProSerProGlnProPheGlnSerProValThrAlaArgThrProG 491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CAGCCCCTCACCGCAGCCCTCCCAGAGCCCAGTGACGGCGCGGACCCCAC 1297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AACTCCAACGTCAGCTCTGGCCCTGCCCCATCTCCCAGTAGCTTCCTGCC 1247
SerSerValMetSerProAlaGlySerSerGlnAlaGluGluGlnGlnTy 524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        lnAsnPheSerValProSerProGlyProLeuAsnThrProValAsnPro 507
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              roProProGlnProSerProGlnProGlyGlnProSerSerGlnPro 457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                tLeuSerSerProSerProGlyGlnGlnValGlnThrProGlnSerMetP 441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AlaGlnMetValAlaProGlyValGlnValSerGlnSerSerLeuProMe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACCACCACTGAAATTTGTCCGAGCTCCGATGGTGGTGCAGCAGCCCCCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CCTTTGGTGTCACAGGCGCAAGCTCTCCCTGGACAAATGTTGTATACCCA 947
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          roValAlaGlnAsnGlnProSerGlnLeuProProGlnSerGlnThrGln
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                        1696
                                                              607
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alignment_block:
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ID AAM14262 standard.
   Align seg 1/1 to: AAM14262
                                  US-09-668-119-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          seq_name:
                                                                               Percent Similarity:
                                                                                                                                                                                                                                                              The present invention relates to human single exon nucleic acid probes (SENP: see AAI10068-AAI28459). The present sequence is a peptide encoded by one such probe. The SENPs are derived from human HeLa cells. The SENPs can be used to produce a single exon microarray, which can be used for measuring human gene expression in a sample derived from human cervical epithelial cells. By measuring gene expression, the probes are therefore useful in grading and/or staging of diseases of the cervix, notably
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1697 TGTCTTCAACCATTCCCTGTACCGCACATTCGTTCCAGCCATG 1739
                                                                                                                                                                              Sequence
                                                                                                                                                                                                                     Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                analyzing
                                                                                                                                                                                                           at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                           cervical cancer.
                                                                                                                                                                                                                                                                                                                                                                                             Claim 27; SEQ ID No 19088; 487pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                             Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human cervical epithelial cells -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30-JUN-2000;
03-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-488901/53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            04-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21-SEP-2000;
27-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       04-FEB-2000;
26-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-JAN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     09-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cervical cancer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Probe; human; microarray; gene expression; cervical epithelial cell;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Peptide #696 encoded by probe for measuring cervical gene expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12-OCT-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      624 oValPheAsnHisSerLeuTyrArgThrPheValProAlaMet 638
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    608 TyrLeuCysGlnProLeuLeuAspAlaValLeuAlaAsnIleArgSerPr 624
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /SIDS2/gcgdata/geneseq/geneseqp/AA2001.DAT:AAM14262
                                                                                                               Quality:
                                                                                                Ratio:
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                                                                                                                                                                             79 AA;
                                 x AAM14262
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; 2000US-0236359.
; 2000GB-0024263.
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2000US-0632366.
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                                                                              390.00
4.937
100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chen W, Rank DR;
from: 1
                                                                               Percent Identity:
 to: 79
                                                                                                             Length:
                                                                                             Gaps:
                                                                               100.000
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376 CAGCTGCAGCTCCAGCAGGTGGCGCTGCAGCAGCAGCAGCAACAGCAGCA 425

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seq_name: /SIDS2/gcgdata/geneseq/geneseqp/AA2001.DAT:AAM26672
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    _documentation_block:
                                                                                                                                                                                                                                                                                                                                              03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    576 GCATCTAATTAAATTGCATCATCAAAATCAGCAACAG 612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                426
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      526 GCAGTAGTGCAGCAGCAGCAGCTCCAGCAGCAGCAGCAGCAGCAGCA
                                                                                                   The present invention relates to single exon nucleic acid probes (SENP: see AAI31315-AAI57546). The present sequence is a peptide encoded by one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   genetic disorder
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Probe; microarray; human; placenta; antenatal diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Peptide #709 encoded by probe for measuring placental gene expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                      26-MAY-2000;
30-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200157272-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17 nPheGlnGlnGlnGlnAlaAlaLeuGlnGlnGlnGlnGlnGlnGlnG
                                                                                                                                                                                     Claim 27; SEQ ID No 26941; 654pp; English.
                                                                                                                                                                                                             analyzing gene expression in human placenta
                                                                                                                                                                                                                            Human genome-derived single exon nucleic acid probes useful
                                                                                                                                                                                                                                                                               Penn SG,
                                                                                                                                                                                                                                                                                                                                   04-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                               04-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                          30-JAN-2001; 2001WO-US00663.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      09-AUG-2001.
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                                                                                        human genetic disorders.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 \verb|lnGlnGlnPheGlnAlaGlnGlnSerAlaMetGlnGlnPheGln|\\
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AACAGCAGCAGTTCCAGGCTCAGCAGAGTGCCATGCAGCAGCAGTTCCAA 525
           Quality:
                                                                                                                                                                                                                                                                                                        MOLECULAR DYNAMICS INC
Ratio:
                                                                                                                                                                                                                                                                               Hanzel DK,
                                                                79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                             2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-0236359.
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                                                                                                                                                                                                                                                                                                                                   2000GB-0024263.
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                                                                AA;
390.00
4.937
                                                                                                                                                                                                                                                                                 Chen W, Rank DR;
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              Length:
Gaps:
  79
0
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alignment_block:
seq_documentation_block:
ID AAM01992 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      seq_name: /SIDS2/gcgdata/geneseq/geneseqp/AA2001.DAT:AAM01992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Align seg 1/1 to: AAM26672
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Percent Similarity: 100.000
                                                                                                                                                                                             04-FEB-2000; 2000US-0180312.
26-MAY-2000; 2000US-0060408.
30-JUN_2000; 2000US-0632366.
03-AUG-2000; 2000US-0632366.
21-SEP-2000; 2000US-0234687.
27-SEP-2000; 2000US-0234635.
04-OCT-2000; 2000GB-0024263.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          376 CAGCTGCAGCTCCAGCAGGTGGCGCTGCAGCAGCAGCAGCAGCAGCAGCA 425
                                                                                                                                                                                                                                                                                                                                                                                                                  Peptide #674 encoded by probe for measuring human breast gene expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAM01992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAM01992 standard; Protein; 79
                                                                                                                                                                                                                                                                                                                09-AUG-2001
                                                                                                                                                                                                                                                                                                                                      WO200157270-A2
                                                                                                                                                                                                                                                                                                                                                                                              Probe; human;
                                                                                                                                                                                                                                                                                                                                                                                                                                            09-OCT-2001
                                                                                                                                                                                                                                                                                        29-JAN-2001; 2001WO-US00661.
                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                   inflammatory disease;
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                                                                                                                                                   Penn
                                                                                                                                                                        (MOLE-)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    nHisLeuIleLysLeuHisHisGlnAsnGlnGlnGln 79
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GCAGTAGTGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          \verb|lnGlnGlnPheGlnAlaGlnGlnSerAlaMetGlnGlnPheGln|
                                                                                                                                                   SG,
                                                                                                                             2001-476286/51.
                                                                                                                                                                         MOLECULAR DYNAMICS INC.
                                                                                                                                                   Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                              breast disease; breast cancer; development disorder;
                                                                                                                                                    Chen W,
                                                                                                                                                                                                                                                                                                                                                                                   proliferative breast disease; non-carcinoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Percent Identity: 100.000
                                                                                                                                                    Rank DR;
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The present invention relates to novel single exon nucleic acid probes (see AAI00010-AAI10067). The present sequence is a peptide encoded by one such probe. The probes are useful for measuring human gene expression in a human breast sample, where the probe hybridises at high stringency to a nucleic acid expressed in the human breast. The probes are useful for

Claim 27; SEQ ID No 10732; 322pp; English

Novel single exon nucleic acid in a human breast -

probe used to measuring

gene expression

breast disease and non-carcinoma tumours.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO

at ftp.wipo.int/pub/published\_pct\_sequences.

79

predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human breast, particularly those diseases with polygenic aetiology. The diseases include: breast cancer, disorders of development, inflammatory diseases of the breast, fibrocystic changes, proliferative

N-PSDB; AAV29009.

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seq_documentation_block:
ID AAW37856 standard; Protein; 1004 AA.
XX
AC AAW37856;
XX
DT 28-AUG-1998 (first entry)
XX
DE Human polyhomeotic 1 (hph1) protein.
XX
KW Polyhomeotic 1; hph1 gene; oncogene; h
KW dysplasia; hyperplasia; diagnosis; tum
XX
FN WO9807860-A1.
XX
PN WO9807860-A1.
XX
PPN 26-FEB-1998.
XX
PPN 26-FEB-1997; 97WO-US14886.
XX
PPF 22-AUG-1996; 96US-0036939.
PR 04-DEC-1996; 96US-0031569.
XX
PR 04-DEC-1996; 96US-0031569.
XX
PR 04-DEC-1996; 96US-0031569.
XX
PR (CHIR ) CHIRON CORP.
XX
PA (CHIR ) CHIRON CORP.
XX
PA Randazzo F;
XX
PR Randazzo F;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  seq_name:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             09-668-119-1 x AAM01992
                                                                                                                                                                                                                                                                                                                                                                               Polyhomeotic 1; hph1 gene; oncogene; human; neopiasia; dysplasia; hyperplasia; diagnosis; tumour; metastasis; therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        576 GCATCTAATTAAATTGCATCAAAATCAGCAACAG 612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            476 AACAGCAGCAGTTCCAGGCTCAGCAGAGTGCCATGCAGCAGCAGTTCCAA 525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   376 CAGCTGCAGCTCCAGCAGGTGGCGCTGCAGCAGCAGCAGCAACAGCAGCA 425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            526 GCAGTAGTGCAGCAGCAGCAGCAGCTCCAGCAGCAGCAGCAGCAGCAGCA 575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            426 GTTCCAGCAGCAGCAGCAGCGGCGCGCTACAGCAGCAGCAGCAGCAGCAGC 475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17 nPheGlnGlnGlnGlnAlaAlaLeuGlnGlnGlnGlnGlnGlnGlnG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 GlnLeuGlnLeuGlnGlnValAlaLeuGlnGlnGlnGlnGlnGlnGlnGl 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      nHisLeuIleLysLeuHisHisGlnAsnGlnGlnGln 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      lnGlnGlnPheGlnAlaGlnGlnSerAlaMetGlnGlnPheGln
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /SIDS2/gcgdata/geneseq/geneseqp/AA1998.DAT:AAW37856
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CC encoded by the hphl oncogene that is implicated in neoplastic CC disorders. Also claimed are: (1) an hphl polypeptide consisting of CC at least 22 contiguous amino acids; (2) an hphl fusion protein; (3) CC antibodies which specifically bind to a hphl protein; (4) an expression construct for expressing all or a portion of hphl CC expression construct for expressing all or a portion of hphl CC identifying neoplastic tissue of a human, where over-expression of CC the hphl gene identifies the tissue as being neoplastia; (7) a cC method to aid in the diagnosis or prognosis of neoplasia; where a CC difference in the hphl gene, mRNA, or protein between a first and CC second tissues indicates neoplasia in the first tissue; (8) a method of CC to aid in detecting a genetic predisposition to neoplasia; (9) a cC method of identifying a human chromosome 12; and (10) a method of CC inducing a cell to de-differentiate by contact with a hphl gene or CC expression product. The products can also be used to inhibit hphl CC expression to suppress neoplasia, dysplasia, or hyperplastic cell CC growth. They can be used to treat e.g. tumours, anhydric hereditary CC dysplasia, endometrial, adrenal, breast, prostate, or thyroid CC dysplasia, endometrial, adrenal, breast, prostate, or thyroid CC dysplasia, endometrial, adrenal, breast, prostate, or thyroid CC down-regulation or inhibition of hphl expression can help contaction. In these disorders, decreasing hphl expression can help contaction. In these disorders, decreasing hphl expression is contacters, effecting hphl down-regulation can suppress metastases.
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Isolated human polyhomeotic 1 oncogene - used to develop products for diagnosis and therapy of proliferative and developmental disorders, e.g. neoplasia, dysplasia or hyperplasia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Page 28-30; 39pp; English.
1004 AA;
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alignment_block:
US-09-668-119-1 x AAW37856
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341 laAspGlySerGlyGlnGlnAsnValGlyMetAsnLeuThrArgThrAla 357
                                               416 AACAGCAGCAGTTCCAGCAGCAGCAGCAGCGGCGCGCTACAGCAGCAGCAG
                                                                                                                                                                                                                                               316 GGGACCTCGGGGATGGCCCCTCACAGCATGGCTGTCGTGTCTACGGCAAC
                                                                                                                                                                                                                                                                                               293 lnLeuProSerSerGly.....MetGlyGlyGlySerCysProArgLys 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    178 CAGAGCCTGACTGGCGGACCTGCTGCGGGAGCCGCTGGAATTGGCATGCC 227
                                                                                                                                                                                                308 GlyThrGlyValValGlnProLeuProAlaAlaGlnThrValThrValSe
                                                                                                                                                                                                                                                                                                                                                                                                                                                   228 T.....CCTCGGGGCCCGGGACAGTCTCTGGGCGGGATGGGTA 265
                                                                                                                                                                                                                                                                                                                                                    266 GCTTTGGTGCCATGGGACAGCCAATGTCTCTCTCAGGGCAGCCGCCTCCT 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     260 GlnSerLeuAsnLeuSerGlnAlaGlyGlyGlySerGlyAsnSerIlePr 276
                                                                                                 rGlnGlySerGlnThrGluAlaGluSerAlaAlaAlaLysLysAlaGluA
                                                                                                                                                 TCCACAGACCCAGCTGCAGCTCCAGCAGGTGGCGCTGCAGCAGCAGCAGC 415
                                                                                                                                                                                                                                                                                                                                                                                                      oGlySerMetGlyProGlyGlyGlyGlyGlnAlaHisGlyGlyLeuGlyG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Quality:
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1.379
54.023
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20
28.544
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1024 ACAGCAGTACAGACAGCTCAGGCTGCCCAGATGGTGGCTCCCGGAGTCCA 1073
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 657
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           610 CAGATACAGCAGCAGCAGCAGCTGCAGCGAATAGCA...CAGCTGCA 656
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    374 eGlnProHisSerLeuIleGlnGlnGlnGlnGlnIleHisLeuGlnGlnL 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 466 CAGCAGCAGCAGCAGCAGTTCCAGGCTCAGCAGAGTGCCATGCAGCA 515
                                                                                                                         1273 .....AGCCCAGTGACG 1284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1074 GGTCAGCCAGAGCAGCCTCCCCATGCTGTCCTCGCCGTCACCGGGCCAGC 1123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      745 ATGCAGCAGCCACAGCCTCCGCCCTCCCAGGCTCTGCCCCAGCAGCTGCA 794
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    358 ThrProAlaProSerGlnThrLeuIleSerSerAlaThrTyrThrGlnIl 374
1285 GCGCGGACCCCACAGAACTTCAGTGTCCCCTCACCTGGACCTTTAAACAC 1334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           491 LysProProIlePro......1leGlnSe 498
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  845 CTCCAGTTGCTCAGAACCAACCATCACAACTCCCGCCACAGTCGCAGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           465 nGlnGlnAlaGlnThrLeuValValGln.....
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                                                                                                                                                                                         583 nGluCysProThrLeuAlaProGlyMetThrLeuAlaProValGlnG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               530 ValGlyThrArgGlnProGlyThrAlaGlnAlaGlnAlaLeuGlyLeuAl 546
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         498 rLysProProValAlaProIleLysProProGlnLeuGlyAlaAlaLysM 515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         945 CCAACCACCACTGAAATTTGTCCGAGCTCCGATGGTG........ 981
                                                            600 lyThrAlaHisValValLysGlyGlyAlaThrThrSerSerProValVal 616
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     etSerAlaAlaGlnGlnProPro.....ProHisIleProValGlnVal 529
                                                                                                                                                                                                                                                            CCCATCTCCCAGTAGCTTCCTGCCCAGCCCCTCACCGCAGCCCTCCCAG. 1272
                                                                                                                                                                                                                                                                                                                      AlaHisLeuAlaSerSerProProSerSerGlnAlaProGlyAlaLeuGl 583
                                                                                                                                                                                                                                                                                                                                                                                         CCCGGCCAGCCCAGCTCACAGCCCAACTCCAACGTCAGCTCTGGCCCTGC 1223
                                                                                                                                                                                                                                                                                                                                                                                                                                                         .....ThrSerArgGlyMetProGlyThrValGln...SerGlyGln
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AGGTGCAGACCCCGCAGTCGATGCCCCCCCCCCCCCAGCCGTCCCCCAG 1173
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seq_name: /SIDS2/gcgdata/geneseq/geneseqp/AA1998.DAT:AAW52830
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1385 AGGAGCAGCAGTACCTGGACAAGCTGAAGCAGCTGTCGAAGTACATCGAG 1434
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23-AUG-1996;
04-DEC-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1549 AAGACCTTGCAAAAGTGTGAGATCGCCCTGGAGAAACTCAAGAATGACAT 1598
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           661 AlaLysAlaSerProValAlaGluSerProLysValMetAspGluLysSe 677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           644 spSerGluGluArgAspAspValSerThrLeuGlySerMetLeuPro 660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              630 uProGlyLysProGlnThrLeu......AlaValLysArgLysAlaA 644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          694 roSerSerGluLeuValAlaLeuThr ..ProAlaProSerValProProP 710
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          677 rSerLeuGlyGluLysAlaGluSerValAlaAsnValAsnAlaAsnThrP 694
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     727 AlaIleValLysPro 731
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 neoplasia; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tumour suppressor gene; polyhomeotic 1; hph1; human chromosome 12p13; identification; neoplastic tissue; cellular differentiation; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A tumour suppressor gene called polyhomeotic 1 (hph1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   09-JUL-1998 (first entry)
                                                                                 Isolated human poly:homeotic 1 oncogene - used to develop products for diagnosis and therapy of proliferative and developmental disorders, e.g. neoplasia, dysplasia or hyperplasia
                                                                                                                                                       WPI; 1998-169162/15.
N-PSDB; AAV21060.
                                                                                                                                                                                                                                                                                                                                                                                                               WO9807858-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW52830 standard; Protein; 1004 AA
                                                   Claim 1; Pages 28-30; 40pp; English.
                                                                                                                                                                                                           Randazzo F;
                                                                                                                                                                                                                                                                                                                                              22-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                                               26-FEB-1998
The present sequence encodes a novel human tumour suppressor gene termed polyhomeotic 1 (hph1). The hph1 gene maps to human chromosome
                                                                                                                                                                                                                                         (CHIR ) CHIRON CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       roThrLeuAlaMetValSerArgGlnMetGlyAspSerLysProProGln 726
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CCCCTGCGCCCCATGATCAACAAGATCGACAAGAACGAAGACAGAAAAAA 1484
                                                                                                                                                                                                                                                                                                             97US-0036939
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alignment\_block: alignment\_scores: Align seg 1/1 to: AAW52830 from: 1 to: 1004 US-09-668-119-1 x AAW52830 Percent Similarity: 610 CAGATACAGCAGCAGCAGCAGCTGCAGCGAATAGCA...CAGCTGCA 656 391 ysGlnValValIleGlnGlnGlnIleAlaIleHisHis.....GlnGln 566 AGCAGCAG.....CAGCATCTAATTAAATTGCATCATCAAAATCAGCAA 609 707 422 406 374 eGlnProHisSerLeuileGlnGlnGlnGlnGlnIleHisLeuGlnGlnL 391 358 ThrProAlaProSerGlnThrLeuIleSerSerAlaThrTyrThrGlnIl 374 466 CAGCAGCAGCAGCAGCAGTTCCAGGCTCAGCAGAGTGCCATGCAGCA 515 416 AACAGCAGCAGTTCCAGCAGCAGCAGCAGGCGGCGCTACAGCAGCAGCAG 465 12p13, a region which is frequently lost in non-small cell lung cancer and breast cancer. A method of identifying neoplastic tissue of a human comprises comparing the expression of a hph1 gene in a tissue of a human suspected of being neoplastic with the expression of a hph1 gene in a tissue of the human which is normal Under-expression of the hph1 gene identifies the subject as having neoplastic tissue. The hph1 concogene functions to suppress neoplastia and dysplastic or hyperplastic cell growth as well as to induce cellular differentiation. The cDNA, protein and vectors can be used as diagnostic and therapeutic tools for proliferative and developmental disorders and to identify a pl3 region of a human chromosome 12. They can be used for the detection, diagnosis or prognosis of neoplasia or for detecting a genetic predisposition to 341 laaspGlySerGlyGlnGlnAsnValGlyMetAsnLeuThrArgThrAla 357 324 rGlnGlySerGlnThrGluAlaGluSerAlaAlaAlaLysLysAlaGluA 341 366 TCCACAGACCCAGCTGCAGCTCCAGCAGGTGGCGCTGCAGCAGCAGCAGC 415 308 GlyThrGlyValValGlnProLeuProAlaAlaGlnThrValThrValSe 324 178 CAGAGCCTGACTGGCGGACCTGCTGCGGGAGCCGCTGGAATTGGCATGCC 316 GGGACCTCGGGGATGGCCCCTCACAGCATGGCTGTCGTGTCTACGGCAAC 365 293 lnLeuProSerSerGly.....MetGlyGlySerCysProArgLys 307 266 GCTTTGGTGCCATGGGACAGCCAATGTCTCTCTCAGGGCCAGCCGCCTCCT 315 276 oGlySerMetGlyProGlyGlyGlyGlyGlnAlaHisGlyGlyLeuGlyG 293 228 T.....CCTCGGGGCCCGGGACAGTCTCTGGGCGGGATGGGTA 265 Sequence neoplasia. They can also be used to treat tumours. AG......GCTTTGGAGGCCCAGCCAATTCAGCAGCCACCG 744 GlnPheGlnHisArgGlnSerGlnLeuLeuHisThrAlaThrHisLeuGl 422 GCAGTTCCAAGCAGTAGTGCAGCAGCAGCAGCAGCTCCAGCAGCAGCAGC 565 Quality: Ratio: 1004 AA; 389.00 1.379 54.023 Length: 522
Gaps: 20
Percent Identity: 28.544 405

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1518 594	GGACCTGAGTAAGATGAAGAGCCTTCTGGACATT	1485 677
1484 677	GACAGAAAAAA     :::   :: AspGluLysSe	1435 661
1434 660	GCAGCAGTACCTGGACAAGCTGAAGCAGCTGTCGAAGTACATCGAG :::::::	64
1384 644	GAGCCCAGCTGGCTCCAGCCAGGCTG       ::: ::     :AlaValLysArgLysAlaA	1335 630
133 <b>4</b> 630	TCACCTGGACCTTTAAACAC       SerValHisLe	1285 617
616	rAlaHisValValLysGlyGlyAlaThrThrSerSerProValVal	600
200	ysProProThrLeuAlaProGlyMetThrLeuAlaProValGlnG	583
1272	CAGTAGCTTCCTGCCCAGCCCCTCACCGCAGCCCTCCCAG.	1224
		567
1000	CAGCCCAGCTCACACACACACACACACACACACACACACA	1174
, i	GGTGCAGACCCCGCAGTCGATGCCCCCCCCCCCCAGCCCGTCCCCCGCAG	1124
553		546
1123	CAGCCTCCCCATGCTGTCCTCGCCGTCACCGGGCCAGC	1074
1073 546	ACAGCAGTACAGACAGCTCAGGCTGCCCAGATGGTGGCTCCCGGAGTCCA :::::::::::::::::::::::::::::::::::	102 <b>4</b> 530
1023 529	:::	982 515
515	rLysProProValAlaProIleLysProProGlnLeuGlyAlaA	498
981	CCAACCACTGAAATTTGTCCGAGCTCCGATGGTG	945
944 498	CAGCCTTTGGTGTCACAGGCGCAAGCTCTCCCTGGACA:::    :: :::   :: LysProProIlePro	895 491
490	ProMetLeuGlnSerSerProLeuSerLeuProProAspAlaAla	475
	CTCCAGTTGCTCAGAACCAACCATCACAACTCCCGCCACAGTCGCAGAC	845
474		6
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794 465	ATGCAGCAGAGCCACAGCCTCCGAGGCTCTGCCCAGGCI	745 456
455	_	Ü

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seq_documentation_block:
ID AAB72673 standard; Pr
XX

AC AAB72673;

XX

DT

DE

POlyglutamine tract #
XX

Animal model; polyglu
KW Animal model; polyglu
KW Manimal model; polyglu
KW Manimal model; polyglu
KW Myeloid leukaemia fac
Leukaemia fac
KW Myeloid leukaemia fac
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KW Myeloid leukaemia fac
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RW Leukaemia fac
Leukaemia fac
Leukaemia fac
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Leukaemia fac
KW Myeloid leukaemia fac
Leukaemia fac
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Leukaemia fac
Leukaemia fac
RW WPI; 2001-147537/15.
XX
Identifying genes or
Losidentifying genes or
Losidentifying genes or
Losidentifying treat
CC modulate polyglutamia
CC The present invention
CC modulate polyglutamia
CC Corsophila heat shock
CC (TPR2) and myeloid la
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alignment_block:
US-09-668-119-1 x AAB72673
                                                                                                    Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Animal model; polyglutamine tract; neurodegenerative disorder; HDJ1; heat shock protein 40; tetratricopeptide repeat protein 2; TPR2; stroke myeloid leukaemia factor 1; MLF; human; fruit fly; Alzheimer's disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                09-MAY-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention describes a method of screening for genes which modulate polyglutamine toxicity using animal models with polyglutamine sequences that cause toxicity in the animal. The model is preferably prosophila, and toxic polyglutamine sequences include the human and prosophila heat shock protein 40/HDJ1, tetratricopeptide repeat protein (TPR2) and myeloid leukaemia factor 1 (MLF) genes. The model is useful for identifying treatments for neurodegenerative and proliferative disorders, including Alzheimer's disease, Parkinson's disease,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14-AUG-2000; 2000WO-US22496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB72673 standard; Protein; 149
                                                                                                                                                                                                                                                                                                                                                                                                                           Creutzfeldt-Jacob's disease (CJD), bovine spongiform encephalopathy (BSE), Huntington's disease, Machado-Joseph disease, spinocerebellar ataxias, dentatorubropallidoluysian atrophy, Kennedy's disease, stro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Identifying genes or other compounds that modulate polyglutamine toxicity, useful for treating Alzheimer's disease, Parkinson's disease and Creutzfeldt-Jakob disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Parkinson's disease; CJD; BSE; Huntington's disease; head trauma; cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-147537/15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (CALY ) CALIFORNIA INST OF TECHNOLOGY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 2; Fig 1B; 275pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GCGGTGCCCACTCCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 roThrLeuAlaMetValSerArgGlnMetGlyAspSerLysProProGln 726
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAGACCTTGCAAAAGTGTGAGATCGCCCTGGAGAAACTCAAGAATGACAT 1598
                                                                                                                                                                                                                                                                                                                                                                                             trauma and cancer.
                                                                                                                                                                        Quality:
                                                                                                                                      Ratio:
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99US-0148934.
2000US-0177047.
2000US-0205720.
                                                                                                    376.50
3.620
63.804
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                                                                                                        Percent
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                                                                                                        Identity: 55.828
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seq_documentation_block:
ID AAB69612 standard:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              445
                                                                                                                                                                                                               Neurological disorder; Huntington's disease; Alzheimer's disease; Parkknson's disease; prion disease; frontotemporal dementia; amyotrophic lateral sclerosis; spinal and bulbar muscular atrophy; dentatorubal-pallidoluysian atrophy; spinocerebellar ataxia type 1; SCA2; SCA3; SCA4; SCA5; SCA6; SCA7; protein accumulation; intrabody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          395 TGGCGCTGCAGCAGCAGCAGCAGCAGCAGCAGTTCCAGCAGCAGCAGCAG 444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      345 GGCTGTCGTGTCTACGGCAACTCCACAGACCCAGCTGCAGCTCCAGCAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      130 GlnGlnGlnGlnGlnGlnThrSerArgThrTyrPro 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 745 ATGCAGCAGCCACAGCCTCCGCCCTCCCAGGCTCTGCCC 783
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       595 CATCAAAATCAGCAACAGATACAGCAGCAGCAACAGCAGCTGCAGCGAAT
                                           27-JUL-1999;
21-JUL-2000;
                                                                                                                       01-FEB-2001
                                                                                                                                                      WO200106989-A2
                                                                                                                                                                                  Synthetic
                                                                                                                                                                                                                                                                                                           Huntingtin accumulation inhibitor peptide HD-Q104-Myc-HIS6
                                                                                                                                                                                                                                                                                                                                            30-APR-2001
                                                                                                                                                                                                                                                                                                                                                                            AAB69612;
(MESS/) MESSER A.
                                                                                         24-JUL-2000; 2000WO-US20131
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AGCAGCTCCAGCAGCAGCAGCAGCAGCAGCATCTAATTAAATTGCAT 594
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    /SIDS2/gcgdata/geneseq/geneseqp/AA2001.DAT:AAB69612
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                                                                                                                                                                                                                                                                                                                                            (first entry)
                                             2000US-0620955
                                                             99US-0146047
                                                                                                                                                                                                                                                                                                                                                                                                         Protein; 155 AA
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alignment_scores
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Percent Similarity:
                                                                                                                                                      111
                                                                                                                                                                                                                                                                                                                                      597
                                                                                                                                                                                                                                                                                                                                                                                                          547 CAGCTCCAGCAGCAGCAGCAGCAGCAGCATCTAATTAAATTGCATCA 596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                497 AGCAGAGTGCCATGCAGCAGCAGTTCCAAGCAGTAGTGCAGCAGCAGCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      used in the prevention of diseases such as Alzheimer's, Parkinson's and Huntington's diseases, prion disease, frontotemporal dementia, amyotrophic lateral sclerosis, spinal and bulbar muscular atrophy, dentatorubal-pallidoluysian atrophy, spinocerebellar ataxia type 1 (SCA1), SCA2, SCA3, SCA4, SCA5, SCA6 and SCA7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               aggregates of certain proteins, involving contacting the protein with binding molecule known as an intrabody. Proteins to be bound include those associated with neurological disorders, and so the method can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Inhibiting intracellular polypeptide accumulation, useful for treating neurological disorders, e.g. Alzheimer's disease, comprises contacting the polypeptide with a specific intrabody -
                                                                                                                                                                                                                            94
                                                                                                                                                                                                                                                                                                                                                                           66
                                                                                                                                                                                                                                                                                                                                                                                                                                                   49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention describes a method for inhibiting the formation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Huston JS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (LECE/) LECERF J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    euAsnMetHisThrGluHisHisHis.HisHisHis 155
                                                                                                                                                                                                                      GCAGCAGCCACAGCCTCCGCCCTCCCAGGCTCTGCCCCAGCAGCTGCAGC 796
                                                                                                                                                 GlnGlnGlnGlnGlnGlnGlnGlnLeuGlnProGlyGlySe
                                                                                                                                                                                   CAGCAGCAGCCTTTGGAGGCCCAGCCACCAATTCAGCAGCCACCGAT 746
                                                                                                                                                                                                                                                           CACAGCTGCAGCTCCAACAACAGCAACAGCAGCAGCAGCAGCAGCAGCAG 696
                                                                                                                                                                                                                                                                                                                                TCAAAATCAGCAACAGATACAGCAGCAGCAACAGCAGCTGCAGCGAATAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GGCGCTACAGCAGCAGCAGCAGCAGCAACAGCAGCAGTTCCAGGCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AGATGCATCACACAGCACCACCAGCCGCCACCAC 832
                                                                       rThrMetSerArgGlyProPheGluGlnLysLeuIleSerGluGluAspL 144
                                                                                                                                                                                                                                                                                                Quality:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           155 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Messer A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Page 99; 108pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              353.50
3.432
70.548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   from:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 and so the method can be
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                                                                                                                                                                                                                        alignment_block:
                                                                                                                                                                                                                                                                                                         alignment_scores:
                                                                                                                                                                                                      US-09-668-119-1 x AAB69614
                                                                                                                                                                                                                                                     Percent Similarity:
                                                                                                                                                                      Align seg 1/1 to: AAB69614
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                                                                                                                                                                                                                                                                                       Quality:
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3.416
61.963
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seq\_documentation\_block:
IID AAB69614 standard; Pr
XX AAB69614;
XX AAB69614;
XX AAB69614;
XX DT 30-APR-2001 (first e
XX Huntingtin accumulati
XX Neurological disorder
KW Parkinson's disease;
KW Mozollo6989-A2.
XX Synthetic.
XX WO200106989-A2.
XX WO200106989-A2.
XX Synthetic.
XX Huntingtin 2000WO-U
XX 27-JUL-1999; 99US-C
PR 21-JUL-2000; 2000WO-U
XX 27-JUL-1999; 99US-C
PR 21-JUL-2000; 2000WS-C
XX (HUST/) HUSTON J S.
PA (HUST/) HUSTON J S.
PA (MESS/) MESSER A.
XX (HUST/) LECERF J.
XX PI Huston JS, Messer A,
XX PI Huston JS, Messer A,
XX PI Huston JS, Messer A,
XX DR (MESS/) MESSER A.
DR (MESS/ aggregates of certain proteins, involving contacting the protein with a binding molecule known as an intrabody. Proteins to be bound include those associated with neurological disorders, and so the method can be used in the prevention of diseases such as Alzheimer's, Parkinson's and Huntington's diseases, prion disease, frontotemporal dementia, amyotrophic lateral sclerosis, spinal and bulbar muscular atrophy, dentatorubal-pallidoluysian atrophy, spinocerebellar ataxia type 1 303 GCAGCCGCCTCCTGGGACCTCGGGGATGGCCCCTCACAGC...... 343 344 TGGCTGTCGTGTCTACGGCAACTCCACAGACCCAGCTGCAGCTCCAGCAG Disclosure; Page 100; 108pp; English Parkinson's disease; prion disease; frontotemporal dementia; amyotrophic lateral sclerosis; spinal and bulbar muscular atrophy; dentatorubal-pallidoluysian atrophy; spinocerebellar ataxia type 1; SCA2; SCA3; SCA4; SCA5; SCA6; SCA7; protein accumulation; intrabody. The present invention describes a method for inhibiting the formation 21-JUL-2000; 2000US-0620955 24-JUL-2000; 2000WO-US20131. Neurological disorder; Huntington's disease; Alzheimer's disease; Parkinson's disease; prion disease; frontotemporal dementia; Huntingtin accumulation inhibitor peptide GFP-HD-Q104 30-APR-2001 (first entry) AAB69614 standard; Protein; 145  $\dots. \texttt{ProValThrGlyThrGlySerMetAlaThrLeuGluLysLeuMetL}$ GlyGlyGlyGlyLysGly.... SCA3, SCA4, SCA5, 99US-0146047 Lecerf J; from: 1 Percent Identity: 55.828 SCA6 and SCA7. AA to: 145

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seq_name: /SIDS2/gcgdata/geneseq/geneseqp/AA2001.DAT:AAB84634
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cellular protein; cell proliferation; p300; CBP; Rb protein; immunosuppressant; Ela viral protein; cell differentiation; malignant cell; protein 532.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Amino acid sequence of CBP protein of Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            87
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   The present sequence represents a CBP protein. A probe derived from the CBP protein is used to isolate a Drosophila cellular protein, designated 532. Protein 532 interacts with proteins involved in the control of cell prolliferation, in particular partners of p300/CBP
                                                                                      Disclosure; Fig 10; 147pp; French.
                                                                                                                                   New nucleic acid encoding a protein that interacts with p300/CBP and Rb proteins, useful for identifying specific interaction partners,
                                                                                                                                                                                      WPI; 2001-425633/45.
N-PSDB; AAH28279.
                                                                                                                                                                                                                                                                      (INSR ) INST ROUSSY GUSTAVE. (CNRS ) CENT NAT RECH SCI.
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                                                                                                                      including immunosuppressants
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alignment_scores:
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                                                                                                                                                                                                                                                                                                                                                                                                        1114 laAlaGlyLeuGlyValGlyValGlyValThrAsnAsnMetValThrMet 1130
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1177 GlyMetValValAsnProAlaLeuSerProTyrGlnThrThrAsnValLe 1193
                                                                                                     1160 lySerGlyAlaGlyLysMetLeuValGlyProProGlyProSerProGly 1176
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                                                  445 ......GCGGCGCTACAGCAGCAGCAGCAG.....
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                                                                                                                                                                                                                                                     .....rcrcrgggcgggargggtagctttggtgccatgggacagcc 287
                                                                                                                                                                                                        nGlnGlnGlnArgMetGlnPheProGlnGlnGlnGlnGlnGlnProProG 1160
                                                                                                                                                                                                                                                                                                                                                             TCTACGGCAACTCCACAGACCCAGCTGCAGCTCCAGCAGGTGGCGCTGCA 404
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	AlaGlySerGlyThrProLeuSerSerValSerThrProT CTGTCCTCGCCGTCACCGGCCAGCGAGGTGCAGGACGCCCCACTGC	1093
1092	AGATGGTGGCTCCCGGAGTCCAGGTCAGCCAGAGCAGCCTC	4 (
1435	erGlyAlaThrAlaAlaGlyAlaSerSerThrSerSerSerSerSer	1420
1045	GCCCCAGGTGCAGCAGCAGCAGCAGCAGCAGCAGCAGACAGCTCAGG	996
995 1419	aSerAlaAlaAlaThrCysAlaSerSerGlySerGlySerAsnSerSer	0 '
4.	CAACCACTACTAAA THITE TOO TOO TOO TOO TOO TOO TOO TOO TOO T	946
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7	CCACAGCCCCAGCAGCCTCCAGTTGCTCAGAACCAACCAT 	829 1359
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645 1275	CAGCAGCAGCAACAGC	125
1259	nGlyMetLeuLeuProGlnSerProPheSerAsnSerThrProLeuGln	44
595	GCAGCATCTAATT	7
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522 1225	OCAGGCTCAGCAGAGTGCCATGCAGCAGCAGTTC :::       ::::::::    0 snGlyGlyThrGlyAlaAsnProGlnLeuSerGluIleMetLysGln	121
1210	3 uThrSerProValProGlyGlnGlnGlnGlnGlnGlnPheIleAs	
489	9 ·····CAGCAGCAGCAGCAGCAGCAGTTC	. 4

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seq_documentation_block:
ID AAY74791 standard.
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AAZ53015 to AAZ54536, AAZ54577 to AAZ54615, and AAY74253 to AAY75941 represent novel Neisseria meningitis and N. gonorrheae polynucleotides and polypeptides. AAZ54537 to AAZ54576 and AAZ54616 to AAZ54737 represent PCR primers used in the exemplification of the present invention. The polypeptides, the polynucleotides, antibodies and compositions of the invention can be used as vaccines, as diagnostic reagents, and as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1549 GlyGlyMetAlaSerLysGlyLys.....LeuAspSerIleLysGln 1562
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                                                                                                                     Claim 2; Page 606; 1453pp; English.
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                                                                                                                                                                                                                                                         Petersen J, Pizza M, Tettelin H, Venter JC;
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                                                                                                                                                                                                                                                                                            Fraser C,
                                                                                                                                                                                                                                                                                                                                                                                             09-OCT-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          antibacterial; gene therapy.
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                                                                                                                                                                                                                                                                       Galeotti C, Grandi G,
Pizza M, Rappuoli R,
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98US-0103794.
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Scalato E, 9
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                                                                                                                                                                                                                                                                                                                                                                                                                          611 TGTTGCTGATTTTGATGATGCAATTTAATTAGATGCTGCTGCTGCTGCTG 562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4 GlyCysAlaGlyGlyCysGlyAlaAlaThrThrThrGlyAla...CysGl 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GlyCysAlaAlaCysThrAlaCys.....GlyThrCysAlaAlaCysAl
                                                        AACTGCTGCTGCATGGCACTCTGCTGAGCCTGGAACTGCTGCTGTTGCTG 472
                                                                                                                                                                                                                                                                                                                                                               GlyCys......AlaGlyCysAlaGlyGlyCysAlaGlyThrCy 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      lyalaThrGlyCysGlyGlyGlyCysThrAlaCysAlaAlaCysCysAla 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       aAlaCysThrCysAlaAlaAlaGlyCysAlaThrThrThrThrThrCysG 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GlyThrAlaThrCysCysGlyAlaCysGlyAlaGlyGly......Al 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hrGlyGlyCysGlyAlaAlaAlaAlaAlaGlyGlyCysGlyCysGly 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TGTGTGATGCATCTGCTGC.....AGCTGCTGGGGCAGAGCCTGGG 770
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GTGACACCAAAGGCTGGGTCTGCGACTGTGGCGGGAGTTGTGATGGTTGG 86
                                                                                                                       hrAlaSerTyrCysThrGlyGlyCysAlaAlaCysCysCysThrGlyThr
                                                                                                                                                                                                                                           sGlyAlaAlaGlyThrCysGlyThrGlyAlaThrGlyGlyGlyCysGlyT 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sThrThrCysAlaCysCysCysAlaAlaGlyCysCysGlyThrAlaAlaT 62
                                                                                                                                                                                  .....TGCTGCTGGAGCTGCTGCTGCTGCACTACTGCTTGG 522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .....TGCATCGGTGGCTGCTGAATTGGTGGCTGGGCCTCCAA 712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .....CysCy 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ratio:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    341.00
2.706
49.027
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                                                                                                                       171
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seq_documentation_block:
ID AAB95124 standard.
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complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprising a sequence complementary to a polynucleotide which comprises a 3'-end sequence, where the oligonucleotide comprises at least 15 nucleotides and the combination of the 5'-end sequence/3'-end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs easily without any specialised methods. AAH03166 to AAH13628 and AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to
                                                                                                                                                                                                                                                                                 to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination
                                                                                                                                                                                                                                                                                                                                          The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligonucleotide complementary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11-JAN-2000;
02-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           430
                                                                                                                                                                                                                                                            of an oligonucleotide comprising a sequence complementary to the
                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 8; SEQ ID 17122; 2537pp + CD ROM; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                            full-length cDNAs -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-318749/34.
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27-AUG-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human protein sequence SEQ ID NO:17122.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     471 CTGCTGCTGCTGC.....TGTAGCGCCGCCTGCTGCTGCTGCT 431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (HELI-) HELIX RES INST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AlaGlyGlyCysThrThrAla 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AGCTGGGTCTGTGGAGTTGCC 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  laAlaThrCysAlaAlaCysCysCysGlyAlaAlaThrThrGlyCys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GGAACTGCTGCTGCTGCTGCTGCTGCAGCGCCACCTGCTGGAGCTGC 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  aAlaCysCysThrCysGlyGlyAlaCysAlaAlaAlaCysCysGlyAlaA 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Isogai T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sugiyama T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2000JP-0241899
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2000JP-0183767
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            detection; diagnosis; antisense therapy; gene therapy
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99JP-0300253
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Wakamatsu A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hayashi K, S
A, Nagai K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Saito K,
K, Otsuki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Yamamoto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 detection by the
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alignment_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Align seg 1/1 to: AAB95124 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-668-119-1/rev x AAB95124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1004 GGCTGCACTGGGGGCTGCTGCACCATCGGAGCTCGGACAAATTTCAG 955
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1033 GTACTGCTGTCTGC...........TGCTGCTGCACCTGG 1005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1083 CTGGCTGACCTGGACTCCGGGAGCCACCATCTGGGCAGCCTGAGCTGTCT 1034
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  represent oligonucleotides, all of which are used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                746 ATCGGTGGCTGC...TGAATTGGTGGCTGGGCCTCCAAAGCCTGCTGCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 954 TGGTGGTTGGGTATACAACATTTGTCCAGGGAGAGCTTGCGCCTGTGACA 905
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         32 ysValArgLeuCysGlyCysThrPheValCysValCysAlaCysValCys 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23 u.....CysValTrpValHisIleCysValC 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11 IleCysValCysValPro.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GTCTGCACCTGCTGGCCCGGTGACGGCGAGGACAGCATGGGGAGGCTGCT 1084
GCTGCACTACTGCTTGGAACTGCTGCTGCATGGCACTCTGCTGAGCCTGG
                                                                                                                                                                        PheValCysValCysAlaCysValCysGlyCysThrPhe.....
                                                                                                                                                                                                                                                                                        alTrpGlyCysThrPheValCysValCysAlaCysValTrpGlyCysThr
                                                                                                                                                                                                                                                                                                                                              GTTGGAGCTGCAGCTGTGCTATTCGCTGCAGCTGC.......
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ValCysGlyCysLeuCysValCysGlyAlaHisLeuCysValCysValCy 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CCTGGGAGGCCGAGGCTGTGGCTGC.....TGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TTCTGAGCAACTGGAGGCTGCTGGGGGGCTGGTGGTGCTG 811
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CCAAAGGCTGGGTC.....TGCGACTGTGGCGGGAGTTGTGATGGTTGG 861
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                                                         .ValCysValCysAlaCysValCysGlyCysThrPheValCysValCysL
                                                                                                                  TTTAATTAGATGCTGCTGCTGCTGCTGCTGCTGGAGCTGCTGCT 539
                                                                                                                                                                                                                                                                                                                                                                                                          sLeuCysValGlyAlaHisLeuCysValCysLeuCysValCysAlaCysV 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CTGCTGC.........TGCTGCTGCTGCTGCTGCTGCTGTT 665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .....ValCysGlyCysThrPheValCysValCysAlaCys 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TGTGTGATGC.....ATCTGC...TGCAGCTGCTGGGGGCAGAG
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                                                                                                                                                                                                                               .....TGTTGCTGCTGCTGTATCTGT...TGCTGATTTTGATGATGCAA 589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .....ValProValCysGlyGlyAlaHisLeuCysVa
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2.588
41.009
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27.445
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seq_documentation_block:
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The protein sequences, and fragments of them, are useful as immunogens and/or antigens. The nucleotide sequences can be useful as immunogens and/or antigens. The nucleotide sequences can be used in vaccines and in diagnostic assays. The proteins and nucleotides can be useful for the detection and diagnosis of S. pneumoniae. The protein sequences are also useful for screening an agent capable of antagonising, inhibiting or interfering with the function or expression of the proteins in which the agent is useful for treatment or prophylaxis of S. pneumoniae infection and meningitis. AAA05591 to AAA05614 represent primers used in the
                                                                                                                                                                                           AAY81501 to AAY81679 represent specifically claimed protein sequences isolated from Streptococcus pneumoniae. AAA05407 to AAA05590 represent specifically claimed nucleotide sequences isolated from S. pneumoniae.
                                                                                                                                                                                                                                                                                                                      or inhibiting expression of the protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Streptococcus pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Streptococcus pneumoniae; vaccine; screening; protein antigen; antibacterial; antiinflammatory; meningitis; infection; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           353
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                                                                                                                                                                                                                                                                               Claim 1; Page 83; 108pp; English.
                                                                                                                                                                                                                                                                                                                                        New Streptococcal protein, useful as a vaccine, for diagnosis of pneumococcal diseases and for screening agents capable of antagonizing
                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2000-195300/17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gilbert CFG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10-FEB-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 pneumococcal disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY81609;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          453 TAGCGCCGCCTGCTGCTGCTGCTGCAACTGCTGCTGCTGCTGCTGCT 404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   212 HisIleCysValCysAlaCysValTrpValHisIleCysValCysValPr 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (MICR-) MICROBIAL TECHNICS LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACGACAGCCATGCTGTGAGGGGCCATCCCCGAGGTCCCCAGGAGGCGGCTG 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GCAGCGCCACCTGCTGGAGCTGCAGCTGGGTCTGTGGAGTTGCCGTAGAC 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   oValCysValCysLeuCysValTrpValHisIleCysValCysValCysL 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    euCysValTrpValHisIleCysValCysValCysLeuCysValTrpVal 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  euCysValTrpValHisIleCysValCysValCysAlaCysValCys...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AACTGCTGCTGCTGCTGC.....TGCTGCTGCTGCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hansbro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98GB-0016337.
99US-0125164.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99WO-GB02451.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       454
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SXS
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US-09-668-119-1 x AAY81609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Align seg 1/1 to: AAY81609 from: 1 to: 1237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     225 GCCTCCTCGGGGCCCGGGACAGTCTCTGGGCCGGGATGGGTAGCTTTGGTG 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         525 AGCAGTAGTGCAGCAGCAGCAGCAGCTCCAGCAGCAGCAGCAGCAGCAGC 574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                751, laSerThrSerAlaSerGlySerAlaSerThrSerThrSerAlaSerAla 767
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 708
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            691 aSerAlaSerThrSerAlaSerAlaSerAlaSerThrSerAlaS 708
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    475 CAACAGCAGTTCCAGGCTCAGCAGAGTGCCATGCAGCAGCAGTTCCA 524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        734 rAlaSerThrSerAlaSerAlaSerAlaSerThrSerAlaSerAlaSerA 751
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               425 AGTTCCAGCAGCAGCAGCAGCGGCGCGCTACAGCAGCAGCAGCAGCAGCAG 474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      718 SerAlaSerThrSerAlaSerAlaSerAlaSerThrSerAlaSerGluSe 734
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       375 CCAGCTGCAGCTCCAGCAGGTGGCGCTGCAGCAGCAGCAGCAACAGCAGC 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             275 CCATGGGACAGCCAATGTCTCTCTCAGGGCAGCCGCCTCCTGGGACCTCG 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       675 AlaSerAlaSerAlaSerThrSerAlaSerGluSerAlaSerThrSerAl 691
                                                                                                                                                                                                                                                                                                         851 AsnArgHisGlnProValArgGlnProGlnGlnValLeuValHisGlnLe 867
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        722 AGCCACCAATTCAGCAGCCACCGATGCAGCCAGCAGCCT...... 762
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     818
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   675 GCAGCAGCAGCAGCAGCA...GCAGCAGCAGCAGGCTTTGGAGGCCC 721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        784 rIleSerAlaSerGluSerAlaSerThrSerAlaSerGluSerAlaSerT 801
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              575 AGCATCTAATTAAATTGCATCATCAAAATCAGCAACAGATACAGCAGCAG 624
865 CCATCACAA...CTCCCGCCACAGTCGCAGACCCAGGCCTTTGGTGTCACA 911    ::::|| | | | | | :::::||
                                                                                   884 lnArgGlnProValArgGlnLeuGlnGlnValProValLeuGlnSerGln 900
                                                                                                                                                                                                                                               792 GCAG...CAGATGCATCACACACAGCACCACCAGCGGCGCCACCA...... 831
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                801 hrSerThrSerAlaSerAlaSerThrSerAlaSerGluSerAlaSerThr 817
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        erAlaSerAlaSerThr.....SerAlaSerGlu 717
                                                                                                                                                                                                                                                                                                                                                       ......ccgcccrcccaggcrcrgcccagcagcr 791
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GGGATGGCCCCTCACAGCATGGCTGTCGTGTCTACGGCAACTCCACAGAC 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SerAlaSerAlaSerAlaSerThrSerAlaSerAlaSerAlaSerThrSe 834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CAACAGCAGCTGCAGCGAATAGCACAGCTGCAGCTCCAACAACAGCAACA 674
                                                                                                                                                                                                                                                                                                                                                                                                                    rAlaSerAlaSerAlaArg.GlnValArgArgProGlnProValHisLeu 850
                                                                                                                                    .....cagccccagcagccrccagrrgcrcagaaccaa 864
                                                                                                                                                                                              uGlnHisGlnArgValHisArgLeuGlnHisGlnProValProArgLeuG 884
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1237 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    329.00
1.061
58.271
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Gaps: 21
Percent Identity: 25.376
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	1601 GGTGCCCACTCCCCCACCGCCCCCGGTGCCACCGACCA 1638 ::    :::     :::    ::: ::         1165 InValProValArgGInProGlnArgArgGInValArgArgPro 1179	
1600 1165	1560 AAAGTGTGAGATCGCCCTGGAGAAAACTCAAGAATGACATGC  :::	
1559 1148	1531 TCGAAGCGGTGTCCCCTGAAGACCTTGCA :::	
1530 1131	1504AGCCTTCTGGACATTCTGACAGACCCC :::       ::::: ::: :::    1115 roGlnGlnAlaHisGlnLeuLeuAsnLeuHisGlnProValArgGlnPro	
1503 1115	1458 GATCGACAAGAACGAAGACAGAAAAAAGGACCTGAGTAAGATGAAG :::::::::::::::::::::::::::::::	
1457 1098	1414 CAGCTGTCGAAGTACATCGAGCCCCTGCGCCCGCATGATCAACAA	
1413 1081	1364 CAGCTGGCTCCAGCCAGGCTGAGGAGCAGCAGCAGCTGAACGTGAAGCTGAAGCTGAAGCTGAAGCTGAAGCTGAAGCTGAAGCTGAAGCTGAAGCTGAAGCTGAAGCTGAAGCTGAAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG	
1363 1065	1317 ACCTGGACCTTTAAACACACCTGTGAACCCCAGCTCTGTCATGAGCC :::   :::   ::::   ::::   1052 gHisGlnArgValArgProLeuGlnGlnValLeuAlaP	
1316 1052	1267 TCCCAGAGCCCAGTGACGGCGCGGACCCCACAGAACTTCAGTGTCCCCTC :::::::::::::::::::::::::::::	
1266 1035	1217 GCCCTGCCCCATCTCCCAGTAGCTTCCTGCCCAGCCCCTCACCGCAGCCC	
1216 1025	1167 CCCGCAGCCCGGCCAGCCCAGCTCACAGCCCAACCTCCAACGTCAGCTCTG               :::::     ::: 1008 largGlnProGlnGlnValSerGlnArgLeuAsnArgHisGlnArgValA	
1166 1008	1117 GGCCAGCAGGTGCAGACCCCGCAGTCGATGCCCCCTCCCCCCCAGCCGTC :::::::::   :::	
1116 991	1079 GCCAGAGCAGCCTCCCCCATGCTGTCCTCGCCGTCACCG :::       :::    975 roValArgGlnLeuProHisGlnGlnValProArgLeuGlnGlnAlaPro	
1078 975	1045	
1044 958	1012 CAGCAGCAGCAGACAGCAGTACAGACAGCTCAG	
1011 941	962 TRGTCCGAGCTCCGATGGTGGTGCAGCAGCCCCAGTGCAGCCCCAGGTGC :::     :::::	
926	912 GGGGAAGGTCTCCCTGGACAAATGTTGTATACCCAACCACCACCACCACCACCACCACCACCACCAC	
ر بر م	01 HisGlnGlnValLeuGlnProGlnHisArgGlnValProArgLeuGlnGl	

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seq\_documentation\_block:

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alignment_block:
US-09-668-119-1 x AAB69609
                                                                                                                                                                                                                                                                                                                                                                                             alignment_scores:
                                                                                                                                                                                                      Align seg 1/1 to: AAB69609 from: 1 to: 121
                                                                                                                                                                                                                                                                                         Percent Similarity:
                              476 AACAGCAGCAGTTCCAGGCTCAGCAGAGTGCCATGCAGCAGCAGTTCCAA 525
                                                                                                 426 GTTCCAGCAGCAGCAGCAGCGCGCGCTACAGCAGCAGCAGCAGCAGCAGCAGC 475
                                                                                                                                                                   376 CAGCTGCAGCTCCAGCAGGTGGCGCTGCAGCAGCAGCAGCAGCAGCAGCA 425
                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention describes a method for inhibiting the formation of aggregates of certain proteins, involving contacting the protein with a binding molecule known as an intrabody. Proteins to be bound include those associated with neurological disorders, and so the method can be used in the prevention of diseases such as Alzheimer's, Parkinson's and Huntington's diseases, prion disease, frontotemporal dementia, amyotrophic lateral sclerosis, spinal and bulbar muscular atrophy, dentatorubal pallidoluysian atrophy, spinocerebellar ataxia type 1 (SCA1), SCA2, SCA3, SCA4, SCA5, SCA6 and SCA7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Inhibiting intracellular polypeptide accumulation, useful for treating neurological disorders, e.g. Alzheimer's disease, comprises contacting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Neurological disorder; Huntington's disease; Alzheimer's disease; Prarkinson's disease; prion disease; frontotemporal dementia; amyotrophic lateral sclerosis; spinal and bulbar muscular atrophy; dentatorubal-pallidoluysian atrophy; spinocerebellar ataxia type 1; SCA2; SCA3; SCA4; SCA5; SCA6; SCA7; protein accumulation; intrabody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 98; 108pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-182700/18.
     51
                                                                      34
                                                                                                                                 (MESS/) MESSER A. (LECE/) LECERF J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27-JUL-1999; 99US-0146047.
21-JUL-2000; 2000US-0620955.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24-JUL-2000; 2000WO-US20131.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-FEB-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200106989-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (HUST/) HUSTON J S.
(MESS/) MESSER A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Huntingtin accumulation inhibitor peptide HD-Q104-GFP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAB69609 standard; Protein; 121 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30-APR-2001 (first entry)
                                                                   polypeptide with a specific intrabody -
                                                                                                                                                                                                                                                                                                                           Quality:
                                                                                                                                                                                                                                                                                                           Ratio:
                                                                                                                                                                                                                                                                                                                                                                                             121 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Messer A,
                                                                                                                                                                                                                                                                                        328.50
4.056
72.973
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lecerf J;
                                                                                                                                                                                                                                                                                         Percent Identity: 69.369
 67
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/cgn2_6/ptodata/z/iaa/5A_COMB.pep:US-08-458-310-2 + 292.50 317.1
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/cgn2_6/ptodata/z/iaa/5A_COMB.pep:US-08-089-862-11 - 287.00 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OM of: US-09-668-119-1 to: Issued_Patents_AA:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Database sequences: 212252
Database length: 22503292
Search time (sec): 67.610000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Date: Feb 28, 2002 7:25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query length: 1740
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query: US-09-668-119-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Search information block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Command line parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 About: Results were produced by the GenCore software, version 4.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence Strd Orig ZScore EScore Len ! Docum /cgn2_6/ptodata/2/iaa/5B_COMB.pep:US-08-977-767-3 - 601.00 /cgn2_6/ptodata/2/iaa/5A_COMB.pep:US-07-906-349A-6 - 446.50 /cgn2_6/ptodata/2/iaa/5B_COMB.pep:US-08-916-352-2 + 389.00 /cgn2_6/ptodata/2/iaa/6B_COMB.pep:US-08-916-352-2 + 389.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Database:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   score_list:
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/cgn2_6/ptodata/2/iaa/6B_COMB.pep:US-08-478-029A-41 -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -DELOP-6.000 -DELEXT-7.000 -START-1 -MATRIX-blosum62
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-TRANS=human40.cdi -LIST-45 -DOCELICAL -OUTFMT-Pfs
-THR_MAX-100 -THR_MIN-0 -ALIGN-15 -MODE-LOCAL -OUTFMT-Pfs
-NORM-ext -MINLEN-0 -MAXLEN-20000000
USER-US9668119_@CGN1_1_26 -NCPU-6 -ICPU-3 -LONGLOG -NO_XLPXY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -MODEL=frame+_n2p.model -DEV-xlp
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US-09-668-119-1/rev x US-08-977-767-3
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                                                                                                                                                                                    Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
1592 TTCTTGAGTTTCTCCAGGGGGATCTCACACTTTTGCAAGGTCTTCAGGGG 1543
                                                                   NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Greenwald, Sara
APPLICANT: Corley, Neil C.
TITLE OF INVENTION: CARBONIC ANHYDRASE VIII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION: TELEPHONE: 650-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                   IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                      MEDIAL GENELIBRARY: GENELIBRARY: 1532042
                                  37 CysalaalaalaGlyCysGlyAlaGlyGlyGlyAlaGlyAlaGly..... 51
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322	ThrCysAlaCysAlaThrCysGlyGlyAlaCysCysCysGlyCysAlaCy	0 4
0	yCysalaCysThrG1yG1yG1yAlaG1yCysG1yG1yCysAlaCysG1y	017
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9		
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63	······GlyAlaGlyGlyAlaGlyAlaGlyAlaGlyAlaGlyGlyA	5

369 527	C'IGCTGGAGCTGCAGCTGGGTCTGT	610	
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394	·····························TGTTGCTGCTGCTGCAGCGCAC	19	
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425 577	GCTGCTGCTGTAGCGCCGCCTGCTGCTGCTGCTGCAACT        :::::::	474 560	
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825		825	
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4 0	729 TGGTGGCCTCCAAAGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	
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352	lacyscyscysThr	
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347	46 rCys	
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Ñ	ysThrCysAl	
117	CAGGGCCAGAGCTGACGTTGGAGTTGGGCTGTGAGCTGGGCTGGCCG	
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58	1456 TGTTGATCATGCGGCGCAGGGGCTCGATGTACTTC 1	
4	у 2	
457	CATCTTACTCAGGTCCTTTTTTCTGTCTTCGTTCTTGTCGATCT 1	
2	208 nTyrValThrProValAsnArgAsnValCysAlaAlaAlaAlaGiyAlaA 2	

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2/6 GGCACCAAAGCTACCCATCCCGCCCAGAGACTGTCCCGGGCCCCGAGGAG 227	
UI N	
76 GGGTCTGTGGAGTTGCCGTAGACACGACAGCCATGCT 45      ::: 45AlaCySGlyAla	
N H	******
34	
473TGCTGCTGCTGCTGCTGCTGCTGCGCCGCCTGCTGCTGCT	
516 CTGCTGCATGGCACTCTGCTGAGCCTGGAACTGCTGCTGTTGC 474	
539 TGCTGCACTACTGCTTGGAACTG 517 ::::::	
45 13	_
528 rThrThrAlaCysGlyGlyThrThrThrThrGlyAlaAlaThrGlyG 545	
15ThrThrThrCysAlaAlaCy	
96 TGATGCAATTTAATTAGATGCTGCTGCTGCTGC	
VULL-TOCTGTATCTGTTGCTGATTTTGA 5	
Сy	
624 CTGC	
662GGAGCTGCAGCTGTGCTATTCGCTGCAGCTGCTGTTG 625 :::    :::   468 AlaAlaAlaThrGlyCysCysAlaAlaAlaAlaCysThrThrAlaCy 484	
51 hrcyscyscyscys	
679 GCTGCTGTTGCT 663	

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alignment_scores:
Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          alignment_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; MOLECULE TYPE: protein US-08-916-352-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-668-119-1 \times US-08-916-352-2 ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Align seg 1/1 to: US-08-916-352-2 from: 1 to: 1004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Percent Similarity: 54.023
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 510-653 TELEFAX: 510-653 TELEFAX: 510-653 TELEFAX: 100: 2: SEQUENCE CHARACTERISTICS: FRIGHT: 1004 amino acids
358 ThrProAlaProSerGinThrLeuIleSerSerAlaThrTyrThrGlnIl 374
                                         466 CAGCAGCAGCAACAGCAGCAGTTCCAGGCTCAGCAGAGTGCCATGCAGCA 515
                                                                                                                                         416 AACAGCAGCAGTTCCAGCAGCAGCAGCAGCGGCGCGCTACAGCAGCAGCAG 465
                                                                                          341 laAspGlySerGlyGlnGlnAsnValGlyMetAsnLeuThrArgThrAla 357
                                                                                                                                                                                   324 rGlnGlySerGlnThrGluAlaGluSerAlaAlaAlaLysLysAlaGluA 341
                                                                                                                                                                                                                                                                                   308 GlyThrGlyValValGlnProLeuProAlaAlaGlnThrValThrValSe 324
                                                                                                                                                                                                                                                                                                                            316 GGGACCTCGGGGATGGCCCCTCACAGCATGGCTGTCGTGTCTACGGCAAC 365
                                                                                                                                                                                                                                    366 TCCACAGACCCAGCTGCAGCTCCAGCAGGTGGCGCTGCAGCAGCAGCAGC 415
                                                                                                                                                                                                                                                                                                                                                                         293 lnLeuProSerSerGly.....MetGlyGlyGlySerCysProArgLys 307
                                                                                                                                                                                                                                                                                                                                                                                                                       266 GCTTTGGTGCCATGGGACAGCCAATGTCTCTCTCAGGGCAGCCGCCTCCT 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   276 oGlySerMetGlyProGlyGlyGlyGlyGlyGlnAlaHisGlyGlyLeuGlyG 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  228 T...9.....CCTCGGGGGCCCGGGACAGTCTCTGGGCGGGATGGGTA 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   260 GinSerLeuAsnLeuSerGlnAlaGlyGlyGlySerGlyAsnSerIlePr 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           178 CAGAGCCTGACTGGCGGACCTGCTGCGGGAGCCGCTGGAATTGGCATGCC 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 13:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 510-923-2707
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/916,352
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: POTTER, JANE
REGISTRATION NUMBER: 33,332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 94608
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: TUMOR SUPPRESSOR NUMBER OF SEQUENCES: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
STRANDEDNESS: sir
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: 510-52.
TELEPHONE: 510-655-3542
TELEPHONE: 510-655-3542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: EMERYVILLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             389.00
1.379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Percent Identity: 28.544
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26 59 34 4 51 77 88 60 3 4	alignment_scores: Quality: 316.50 Length: 637 Ratio: 0.995 Gaps: 38	CLASSIFICATION: ATTORNEY/AGENT INFORMATION: NAME: Campbell, Cathryn A. REGISTRATION NUMBER: 31.815 REFERENCE/DOCKET NUMBER: P-LJ 2626 TELECOMMUNICATION INFORMATION: TELEPHONE: (619) 535-9001 TELEPHONE: (619) 535-9001 TELEPHONE: (619) 535-8949 INFORMATION FOR SEQ ID NO: 23: SEQUENCE CHARACTERISTICS: LENGTH: 1185 amino acids TYPE: amino acids TYPE: amino acids TOPOLOGY: linear MOLECULE TYPE: protein US-09-041-886-23		seq_documentation_block:  Sequence 23, Application Us/09041886  Patent No. 6235872  GENERAL INFORMATION: APPLICANT: Bredesen, Dale E. APPLICANT: Bredesen, Dale E. TITLE OF INVENTION: Proapoptotic Peptides, Dependence TITLE OF INVENTION: Proapoptotic Peptides of Use NUMBER OF SEQUENCES: 72  CORRESPONDENCE ADDRESS: ADDRESSE: Campbell & Flores LLP STREET: 4370 La Jolla Village Drive, Suite 700	1599 GCGGTGCCCACTCCC 1613    :::     727 AlaIleValLysPro 731 seq_name: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:US-09-041-886-23	1519	1435 CCCCTGCGCCCATGATCAACAAGATCGACAAGAACGAAGAACAAGAAAAA 1484 :::	630 uProGlyLysProGlnThrLeuAlaValLysArgLysAlaA 644 1385 AGGAGCAGCAGTACCTGGACAAGCTGTAAGCAGTACATCGAG 143 ::::::::::::::::::::::::::::::::::::
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845	rgAlaProValGlu	834
1595	GATCGCCCTGGAGAAACTCAAGAATGA	1546
833		818
7 E 7 E	COURT AND TAXABLE AND TAXABLE AND	1496
1495	GTA	1449 802
801		785
1448	CAGCTGTCGAAGTACATCGAGCCCCTGCGCCCGCAT.	1408
785	yrPheValProLeuGluGlyS	768
1407		1407
1407 768	CCAGCTGGCTCCAGCCAGGCTGAGGAGCAGCAGTACCTGGACAAG    ::: :::         ::: ::::::       ::: ProSerHisAlaSerGlnSerAlaArgPheAsnLysHisLeuAspArgGl	1363 752
136; 751	ACCTGTGAACCCCAGCTCTGTCATGAGC :    :::   ::::: rProSerProProProLysValValAspVal	735
735	SlnIleLysGlnGluProAlaGluGluTyrGluThrProGluSerP	718
131	CCACAGAACTTCAGTGTCCCCTCAC	1290
718		703
128		1240
123 702	CACAGCCCAACTCCAACGTCAGCTCTGGCCCTGCCCCATCTCCCAGTAGC	1190 687
687		671
118	CCCTCCCCCCAGCCGTCCCCGCAGCCCGGCCAGCCCAGC	1149
670	oGlySerPr	654
114	GCARACTARIA COCCOCATA THIS ALL STATEMENT ALL	1122
112	AGAGCAGCCTCCCCATGCTGCTCGCCGTCACCGGGCCA	1082
640	AlaSerProProGlyProProProTyrGlyLysArgAlaProSer	626
108	ACAGACAGCTCAGGCTGCCCAGATGGTGGCTCCC	1032
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103	GIGCAGCAGCCCCAGIGCAGCCCCAGGIGCAGC	982
981	oProValProThrValThrThrSerSerAlaThrLeuSerThrV	597
		0
931 597	<pre></pre>	581
000	TO THE STATE OF TH	
881	CAGCCCCAGCAGCCTCCAGTTGCTCAGAACCAACCATC ::::: :::::::::          ::: ::: erSerAsnSerSerSerSerThrSerGlnGlvSerTvr	566 566
566	н	549

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seq_name: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:US-08-991-300-2
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                                                                                                                                                                                                                                         ; TYPE: amino acid
; STRANDEDNESS: Single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-991-300-2
                                             alignment_block:
US-09-668-119-1 x US-08-991-300-2
                                                                                                                                                      alignment_scores:
    Quality:
Align seg 1/1 to: US-08-991-300-2 from: 1
                                                                                                           Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Patent No. 5973225
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2,
                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 800

PRIOR APPLICATION DATA:
APPLICATION NUMBER: IT MI 96/A 002663
FILING DATE: 19-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,618
REGISTRATION NUMBER: 2264-0201-0X
TELEPAN: 703-413-3000
TELEPAN: 703-413-3220
TELEPAN: 703-413-3220
                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 703-413-2220 INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1684 ACATCCGCTCACCTGTTCCAACCATTCCCTGTACCGCACATTCGTTCC 1732
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1634 GACCAAACAGCAGTACCTATGCCAGCCGCTCCTGGATGCCGTCCTGGCCA 1683
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1596 CATGCGGTGC......CCACTCCCCCACCGCCCCGGTGCCACC 1633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: D'OVIDIO, RENATO
APPLICANT: PORCEDDU, ENRICO
APPLICANT: MERCHITELLI, CINZIA
APPLICANT: MERCHITELLI, CINZIA
APPLICANT: CARDELLI, LUISA ERCOLI
TITLE OF INVENTION: ISOLATION AND CHARACTERIZATION OF A GENE
TITLE OF INVENTION: ENCODING A LOW MOLECULAR WEIGHT GLUTENIN
NUMBER OF SEQUENCES: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             875 rProAlaLeuArgThrLeuSerGluTyrAlaArgProHisValMetSer 891
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 1755 S.
CITY: ARLINGTON
STATE: VA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT ADDRESSEE: P.C. STREET: 1755 S. JEFFERSON DAVIS HIGHWAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: U.
ZIP: 22202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                    LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    , Application US/08991300 5973225
                                                                                                                                                                                                                                                                                                                                                      369 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16-DEC-1997
                                                                                                           311.50
1.639
50.398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US/08/991,300
                                                                                                      Length: 377
Gaps: 16
Percent Identity: 32.095
    to: 369
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1211	SACTORACIONAR ORDENARACIONARAC	116
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1167	CGATGCCCCCCTCCCCCC	114
272	ArgAlaIleValTyrSerIleIleLe	25
1140	G	1140
1139 255	O CTCCCCATGCTGTCCTCGCCGTCACCGGGCCAGCAGGTGCAGACCCCGCA	109 23
1089 238	O CTCAGGCTGCCCAGATGGTGGCTCCCGGAGTCCAGGTCAGCCAGAGCAGC	1040 225
225	GCCCCCAGTGCAGCCCCAGGTGCAGCAGCAGCAGAAAAAAAA	208
23		9
989	TATACCCAACCACCACTGAAATTTGTCCGAGCTCCGATGGTGGTGC	940
939 191	AGACCCAGCCTTTGGTGTCACAGGCGCAAGCTCTCCCTGGACAAATGTTG	890 181
889 180	GCAGCCTCCAGTTGCTCAGAACCAACCATCAC            	840 165
165	CTGCAGCAGATGCATCACACACACACACACACACACACAC	790 156
in α	CGATGCAGCAGCCACGCCCCCCCCCCCCCCCCCCCCCCC	حب سا
- ω - <b>-</b>	GCAGCAGCAGGCTTTGGAGGCCCAGCCACCAATTCAGCAGCCA	699 122
2 9	CTCCAACAACAGCAACAGCAGCAGCAGCAGCAGCAGCAGCAG	658 106
	TAGCACAGC	616 89
9	ATTGCATCATCAAAATCAGCAACAGATA ::: ::: :::         ::: oGlnGlnProSerPheSerGlnGlnGlnLeuPro	573 72
572 72	CAGCAGCAGCAG.	544 56
543 55	in in	494 39
493 39	.CAGCAGCAACAGCAGCAGTTCCAGG         eGlnGlnProHisGlnPheProG	450 22
449 22	GGCGGC :: rLeuSe	400

	; LIBRARY: GenBank	
	SOUT	
	NESS:	
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	EQUENCE CHARACTERISTICS:	
	; INFORMATION FOR SEQ ID NO: 4:	
	AX: 415-8	
	; TELECOMMONICATION INFORMATION:	
	REFERENCE/DOCKET NUMBER: P	
	REGISTRATION NUMBER: 36,749	
	EY/AGENT INFORMATI	
	; FILING DATE:	
	PLICAT	
	ING DATE: Fi	
	T APPLICATION DATA:	
	SOFTWARE: FastSEO for Windows Version 2.0	
	88	
	CA ALC	
	; STREET: 3174 Porter Dr.	
	ADDRESSEE: Incyte Ph	
	$\circ$	
-	TITLE OF INVENTION:	
	APPLICANT: Murry, Lynn E.	
	APPLICANT: Lawton, Mich	
	APPLICANT: Hutchinson, N	
	GENERAL INFORMATION: APPLICANT: Mitchell	
	atent No. 5876963	
	tation	
	<pre>seq_name: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:US-08-918-914-4</pre>	
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118	102 hrCysalaAlaCysGlyAlaThrCysThrThrGlyCysAlaCysAlaThr	
429	478 GTTGCTGCTGCTGCTGCTGTGAGCGCCGCCTGCTGCTGCTGCTGG	
102	СувСувС	
479	528 TGCTTGGAACTGCTGCTGCATGGCACTCTGCTGAGCCTGGAACTGCTGCT :::	
93	GlyAlaCysThrThrThrCysCy	
529	578 TGCTGCTGCTGCTGCTGCTGCTGCAGCTGCTGCTGCTGCTGCACTAC	
80	76 lyThrGlyGlyCys	
579	617TGTATCTGTTGCTGATTTTGATGATGCAATTTAATTAGA	

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; CLONE: 1
US-08-918-914-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-668-119-1 x US-08-918-914-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Align seg 1/1 to: US-08-918-914-4 from: 1 to:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      357 TACGGCAACTCCACAGACCCAGCTGCAGCTCCAGCAGGTGGCGCTGCAGC 406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  307 CCGCCTCCTGGGACCTCGGGGATGGCCCCTCACAGCATGGCTGTCGTGTC 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       557 AGCAGCAGCAGCAGCAGCATCTAATTAAATTGCATCATCAAAATCAG 606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          261 oProGlnProGlnProGlnProGlnProProGlnArgProProG 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                507 CATGCAGCAGCAGTTCCAAGCAGTAGTGCAGCAGCAGCAGCAGCTCCAGC 556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            457 CAGCAGCAGCAGCAGCAACAGCAGCAGTTCCAGGCTCAGCAGAGTGC 506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      407 AGCAGCAGCAACAGCAGCAGCAGCAGCAGCAGCAGCGCGCGCTACAG 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         214 aProGluTyrProSerAlaGlnGlnGlnGlnGlnGln.....ArgG 228
                                                                                                                                                                                                                                                                                                                                                                                                                                     807 CACACAGCACCAGCCGCCACCACCAGCCGCAGCCTCCAGTTGCTC 856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           307 ....GlnGlnGlnArgGlnGlnAsnProGlnGlnGlnProGlnGlnT 322
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              757 CAGCCTCCGCCCTCCCAGGCTCTGCCCCAGCAGCTGCAGCAGATGCATCA 806
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                                                   392 yGlyPheCysAlaProValPro.......GlnAlaProGln. 403
                                                                                                         930 ACAAATGTTGTATACCCAACCACCACTGAAATTTGTCCGAGCTCCGATGG 979
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980 TGGTGCAGCAGCCCCAGTGCAGCCCCAGGTGCAGCAGCAGCAGCAGCA 1029
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hrThrGlnPheGlyGlnSerGlnIleGln.....LeuGlnSerGly 335
                                                                                                                                                                                                                                                                        euAspGlnHisAlaGlnLeuTyrGlnGlnArgMetSerGlnTyrArgGlu 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InGlnProGlnSerPheSerGlyThrHisGluLeuHisLeuGlnArgGln 294
                                                                                                                                                                                                                                                                                                                                                                                  sProGlnGlnGlnProGlnGlnProGluLeuGluArgSerProL 359
                                                                                                                                                                                                                  ....TCGCAGACCCAGCCTTTGGTGTCACAGGCGCAAGCTCTCCCTGG 929
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    300.50
1.990
51.536
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       293
11
33.788
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404 ....GlnGluArgProThrProProProVal...... 412

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seq_name: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:US-08-728-323A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            seq_documentation_block:
                                                                                                                                                                                                                                                                                                ; MOLECULE TYPE: protein US-08-728-323A-2
                                                                                                                        alignment_block:
US-09-668-119-1 x US-08-728-323A-2
                                                                                                                                                                                                                                      alignment_scores:
                                                                              Align seg 1/1 to: US-08-728-323A-2 from: 1 to: 1162
                                                                                                                                                                                Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2, Application US/08728323A Patent No. 5948676
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 212-391-0525
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1080 CCAGAGCAGCCTCCCCATGCTGTCCTCGCCGTCACCGGGCCAGCAGGTGC 1129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1030 GTACAGACAGCTCAGGCTGCCCAGATGGTGGCTCCCGGAGTCCAGGTCAG 1079
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1130 AGACCCCGCAGTCGATGCCCCCCTCCCCCC 1158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  413 .....ValileAs 418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       418 nThrAlaThrGlnProProLeuProGlnProTyrProThrArgTyrArgP 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Bohenzky, Roy A.
APPLICANT: Russo, James J.
APPLICANT: Edelman, Isidore
                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 05
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-278-0400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 1162 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
379 CTGCAGCTCCAGCAGGTGGCGCTGCAGCAGCAGCAGCAACAGCAGCAGTT 428
                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: 212-391-0525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/728,323A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         roAlaPro.....ProProProPro 441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10036
                                                                                                                                                                                                                       Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New York
                                                                                                                                                                                                     Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1185 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Edelman, Isidore S. Moore, Patrick S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chang, Yuan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cooper & Dunham LLP
                                                                                                                                                                                1.394
51.574
                                                                                                                                                                                                                       297.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Immediate Early Protein From Kaposi's Sarcoma-Associated Herpesvirus, DNA
                                                                                                                                                                                  Percent Identity: 26.634
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0575/52268/JPW/MSC/SKS
                                                                                                                                                                                                                         Length:
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304	701 GluGlnGlnAspGluGlnGluGlnGlnAspGluGlnGlnGlnAsp 7
	84 IUGInGInAspGluGlnGlnAspGluGlnGlnAspGluGln
.254	05 ACGTCAGCTCTGGCCCTGCCCCATCTCCCAGTAGCTTCCTGCC
1204 584	1161 GCCGTCCCCGCAGCCCGGCCAGCCCAGCTCACAGCCCAACTCCA 1
567	51 GlnGlnAspGluGlnGlnGlnAspGluGln
1160	CCGGGCCAGCAGGTGCAGACCCCGCAGTCGATGCCCCCCTCCCCCC
50	:::::: :::::::::::::::::::::::::::
1110	61 CTCCCGGAGTCCAGGTCAGCCAGAGCAGCCTCCCCATGCTG
<i>i</i> 6	ATGGTGG
623	12GinAspGluGlnGlnGlnAspGluGlnGlnGlnAs
1010	CGATGGTGGTGCAGCAGCCCCAGTGCAGCCCCAGGT
611	604 luGlnGlnAspGluGlnGln
960	GGCGCAAGCTCTCCCTGGACAAATGTTGTATACCCAACCACCACTGAAA
910 604	861 CCAACCATCACAACTCCCGCCACAGTCGCAGACCCAGCCTTTGGTGTCAC ::::   :::         :::    587 gGluProGlnGlnArgGluProGlnGlnGlnAspGluGlnGlnGlnAspG
587	71 GlnArgGluProGlnGlnArgGluProGlnGlnArgGluProGlnGlnAr
7	oGlnGlnArgGluProGlnGlnArgGluProGlnGlnArgGluProGln
813	67 CCTCCAGGCTCTGCCCCAGCAGCTGCAGCAGATGCATCACACACAG
766 554	720 CCAGCCACCAATTCAGCAGCCACCGATGCAGCCACAGCCTCCGC :::         :::    :::    ::
w	
<b>⊢</b> 1	CAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCTTTTGGAG
669 520	GCAGCTGCAGCGAF
<b>⊢</b> ⊢	
_	CAGCATCTAATTAAATTGCATCATCAAAATCAGCAACAGATACAG
569 502	520 TTCCAAGCAGTAGTGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG
519 485	470 AGCAGCAACAGCAGCAGTTCCAGGCTCAGCAGAGTGCCATGCAGCAGCAGCAG
469 469	23 CHAPCHAGCAGCAGCAGCGGCGCTACA
	O CONCORD CARCAGO CONTRACTOR CONT

	; LOCATION: 1309	
	<pre>; ORGANISM: N. clavipes ; TISSUE TYPE: minor ampullate gland</pre>	
	RCE:	
	OTHETICAL: NO	
	; MOLECULE TYPE: protein	
	NDEDNESS: S	
	amino	
	CHARACTERISTICS:	
	5-8050	
	TELEPHONE: 703-	
	CKET NUMBER: 1	
	REGISTRATION NUMBER: 28,977	
	ION:	
	A: US/08/209,747	
	D +	
	IBM PC compatible	
	; COMPUTER READABLE FORM: ; MEDIUM TYPE: Floppy disk	
	22040-3487	
	Virginia : USA	
	Falls Church	
	~ r	
	R OF SEQUENCES: 56	
der	OF INVENTION: cDNAs Encoding Minor Ampullate Spi	
	ANT: Lewis, Ra ANT: Colgin, M	
	Η.	
	<pre>seq_documentation_block: ; Sequence 2, Application US/08209747 . patent NC 5732771</pre>	
	<pre>seq_name: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:US-08-209-747-2</pre>	
	LeuGluAspGlnGluGlnGluLeuGluG	
	1555 TTGCAAAAGTGTGAGATCGCCCTGGAGAAACTCAAGAA 1592	
773	760 uGlnGluGluGluGlnGluLeuGlu	
1554	CGGTGTCCCCTGAAGA	
σ		
1504	AAGATCGACAAGAACGAAGACAGAAAAAAGGA	
743	728 GluGlnGlnGlnAspGluGlnGlnGlnGlnAspGluGlnGlnGln	
1454	GCTGAAGCAGCTGTCGAAG	
727	  nGln	
1404	AGGCTGAGGAGCAGCAGTACCTGG	
716	716	
1354	1305 CAGTGTCCCCTCACCTGGACCTTTAAACACACCTGTGAACCCCAGCTCTG	

US-08-209-747-2

alignment\_scores:
Quality: 293.00
Ratio: 1.118
Percent Similarity: 52.505 Percent Identification

Percent Similarity: 52.505 Percent Identity: 29.259
alignment\_block:
US-09-668-119-1/rev x US-08-209-747-2 ...

Align seg 1/1 to: US-08-209-747-2 from: 1 to: 832

1719 GGTACAGGGAATGGTTGAAGACAGGTGAGGGGATGTTGGCCAGGACGGCA 1670

> 680 TGCTGCTGTTGCT......GTTGTTGGAGCTGCAG 652 |:::||| ||| ||| 436 aGlyAlaGlyAlaGlyGlyTyrGlyGlyGlnGlyGlyTyrGlyAlaGlyA 453

|||:::|||||||::: 528 yAlaGlyAlaAlaAlaGlyAlaGlyAlaGlyAlaAlaAlaGlyAla 543 seq\_name: /cgn2\_6/ptodata/2/iaa/5A\_COMB.pep:US-08-458-298-2

seq\_documentation\_block:
 Sequence 2, Application US/08458298
 Patent No. 5756677
 GENERAL INFORMATION:
 APPLICANT: Lewis, Randolph V.
 APPLICANT: Coloin Mark

APPLICANT: Lewis, Randolph V.
APPLICANT: Colgin, Mark
APPLICANT: Colgin, Mark
TITLE OF INVENTION: CDNAS Encoding Minor Ampullate Spider
TITLE OF INVENTION: SLIK Proteins
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:

ADDRESSEE: Birch, Stewart, Kolasch & Birch

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alignment_block:
US-09-668-119-1/rev x US-08-458-298-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; NAME/KEY: CDS
; LOCATION: 1..309
US-08-458-298-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Quality: 293.00
Ratio: 1.118
Percent Similarity: 52.505
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1469 TTCTTGTCGATCTTGTTGATCATGCGGCGCAGGGGCTCGATGTACTTCGA 1420
                                                                                                                                                                                          1519 GAATGTCCAGAAGGCTCTTCATCTTACTCAGGTCCTTTTTTCTGTCTTCG 1470
                                                                                                                                                                                                                                                                                                                                                                               1569 CTCACACTTTTGCAAGGTCTTCAGGGGACACCGCTTCGAGGGGTCTGTCA 1520
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1619 CGGTGGGGAGTGGCACCGCATGTCATTCTTGAGTTTTCTCCAGGGCGAT 1570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1669 TCCAGGAGCGGCTGGCATAGGTACTGCTGTTTGGTCGGTGGCACCGGGGG 1620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1719 GGTACAGGGAATGGTTGAAGACAGGTGAGCGGATGTTGGCCAGGACGGCA 1670
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 832 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 703-205-8050
INFORMATION FOR SEQ ID NO: 2:
                                                                                     196 AlaAlaGlyAlaGlyAlaGlyGlyTyrGlyGly...... 206
                                                                                                                                                                                                                                                                               182 laGlyGlyTyrGlyArgGlyAlaGlyAlaGlyAlaGly......Ala 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    :|||:::|||:::|||:::|||::: ::: ::: :::: ||| ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               149 yAlaGiyAlaGiyAlaGiyTyrGlyGly..GlnGlyGlyTyrGlyAl 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         133 GlyTyrGlyArgGlyAlaGlyAlaGlyAlaGlyAlaAlaAlaGlyAlaGl 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: protein HYPOTHETICAL: NO FRAGMENT TYPE: internal ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 1447-104P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-205-8000
TELEPAX: 703-205-8050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/458,298
FILING DATE: 02-UUN-1995
FILING DATE: 02-UUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/209,747
FILING DATE: 14-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: MULTPHY JT., Gerald M.
REGISTRATION NUMBER: 28,977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: N. clavipes
TISSUE TYPE: minor ampullate gland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: USA
ZIP: 22040-3487
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CITY: Falls Church
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Virginia
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767 403	TGATGCATCTGCTGCAGCTGCTGGGGGCAGAGCCTGGGAGG	386
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323	GlyAlaGlyGlyTyrGly	31,
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0	CATCGACTGCGGGGTCTGCACCTGCTGGCCCGGTGACGGCGAGGACAG	114
	************GlyAlaGlyAlaGlyAl	28
1148	·····	115
282	5 aGlyAlaAlaAlaAlaAla***********************	26
1160	9 GGGACGGCT	116
5	0 GlyAlaGlyAl	26
_	9 GGCCAGAGCTGACGTTGGAGTTGGGCTGTGAGCTGGGCTGGCT	121
59	0 lyAlaGlySerTyrGlyGlyGlnGlyT	25
1220	9 GGAGGGCTGCGGTGAGGGGCCTGGGCAGGAAGCTACTGGGGAGATGGG	126
50	5ArgGlyAlaGlyAlaGlyAlaGlyAlaAlaAlaAlaGlyAlaG	23
	9 GGTGAGGGGACACTGAAGTTCTGTGGGGTCCGCGCGCCGTCACTGGGCTCT	131
ũ	2GlyTyrGly	23
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231	<pre>::     :::   1 laAlaAlaGlyAlaGlySerGlyGlyAlaGly</pre>	22
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221	07GlnG1yG1yTyrG1yA1aG1yA1aG1yA1aG1yA1aA1aA1aA	20

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seq_documentation_block:
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                                                                                                                                             ; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-853-310-2
                                                                    alignment_scores:
Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2, Application Patent No. 5948640 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                 TELEPHONE: (510) 923-3888
TELEFAX: (510) 655-3542
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               601 TTTGATGATGCAATTTAATTAGATGCTGCTGCTGCTGCTGCTGCTGC 552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 453
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 451 GCGCCGCCTGCTGCTGCTGCT......GGAACTGCTGCTGT 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    495 lyGlyGlnGlyGlyTyrGlyAlaGlyAlaGlyAlaGlyAlaAlaAlaAla 511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    478 yAlaGlyAlaAlaAlaGlyAlaGlyAlaGlyThrGlyGlyAlaGlyTyrG 495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    551 AGCTGCTGCTGCTGCACTACTGCTTGGAACTGCTGCTGCATGGCACT 502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              512 AlaGlyAlaGlyAlaGlyGlyAlaGlyTyrGlyArgGlyAlaGlyAlaGl 528
                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION.
ATTORNEY/AGENT INFORMATION:
NAME: Guth, Joseph H.
NAME: Guth, JOSEPH H.
ATTORN NUMBER: 31,261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: Mammalian Additional Sex Combs (Asx) Acts as a Tumor Suppress NUMBER OF SEQUENCES: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           528 yAlaGiyAlaAlaAlaGiyAlaGiyAlaGiyAlaAlaAlaGiyAla 543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         416 TGCTGCTGCTGCAGCGCCACCTGCTGGAGCTGCAGCTGGGTCT 371
                                                                                                                                                                                                                                                                                                                                                                                   REGISTRATION NUMBER: 31,261
REFERENCE/DOCKET NUMBER: 12
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Chiron Corporation STREET: 4560 Horton Street CITY: Emeryville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: California
                                                                                                                                                                                                                                        TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CTGCTGAGCCTGGAACTGCTGCTGCTGCTGCTGCTGCTGTA 452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 laGlyAlaGlyAlaAlaAlaAlaAlaThrGlyAlaGlyGlyAla... 468
                                                Quality:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Application US/08853310
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                                                                                                                                                                                   یدی: single
linear
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292.50
1.312
41.068
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US/08/853,310
  Percent Identity: 25.230
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alignment_block:
US-09-668-119-1 x US-08-853-310-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             147 ProMetSerAlaAlaGluMetGluValSerSerThrValIleThrAsnSe 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            473 AGCAACAG.....CAGCAGTTCCAGGCTCAGCAGAGTGCCATGCAG 513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  213 rAsnGlyGlnIleIleGlyAsnPheLeuLeuGlnGlnGlnArgGlnGlnG 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     197 GlnAsnAlaGlnSerAsnAlaGlnGlnGlnArgGlnIleLeuValAspSe 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       180 snSerLeuThrIleAsnGlnMetProHisGlnAlaSerGlnGlnProGln 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     322 ....rcggggaTggccccTcAcAgcaTggcTgTcGTgTCTAcGgcAA 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      277 alAlaLeuArgAsnGlyThrGlnGlnPheLeuSerProAsnLeuIleAla 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 247
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            230 lnGlnGlnLeuLeuGlnGlnPheThrLeuGlnAlaAlaAlaAlaGln 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       365 CTCCACAGACCCAGCTGCAGCTCCAGCAGGTGGCGCTGCAGCAGCAGCAG 414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             163 rSerAsnSerAsnAspSerSerAsnAsnIleSerLeuCysSerSerThrA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                286 CCAATGTCTCTCAGGGCAGCCGCCTCCTGGGACC.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 589 TTGCATCAT.....CAAAATCAGCAACAGATACAGCAGCAGCAACAGCA 632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      260 nGlnGlnGlnAlaThrSerSerAsnSerLeuGlyLysThrLeuProV 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               564 GCAGCAGCAG.....
                                                                                                                                                                                                                                                                                                     360 rGlnAlaLysPheIleAlaLysProLeuAsnIleIleSerMetThrArgP 377
                                                                                                                                                                                                                                                                                                                                                                                                           344 LeuLeuGlnGlnGlnGlnGlnGlnGlnAsnValAlaLeuProThrTh 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                        688 .....CAGCAGCAGCAGCAGCAGCAGGCTTTGGAGGCCCAGCCAAT 731
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                327 lnAlaGlnLeuHisGlnArgGlnLeuLeuAlaGlnAlaAlaAsnAsnAsn 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 665 AACAGCAACAGCAGCAGCAGC..... 687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              310 nAlaThrAlaGlnGlnLysHisGlnGlnIleGlnGlnPheAlaLeuGlnG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   294 GlnGlnHisGlnGlnGlnGlnGlnGlnLeuGluGlnHisGlnGlnGl 310
                        816 CCACCAGCCGCA...CCACAGCCCCCAGCAGCCTCCAGTTGCTCAGAACC 862 :::::::||||||| ||| |||||||||||
                                                                                             394 IleProSerAlaTyrAlaAsnValValAlaValThrGlyAlaGlnGlnGl 410
                                                                                                                                                                                                                                                        767 CCTCCCAGGCTCTGCCCCAGCAGCTGCAGCAGATGCATCACACA..... 810
                                                                                                                                                                                                                                                                                                                                                           roAlaAsnAlaSerProThrThrAlaAlaThrThrAlaAsnThrAlaSer 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ......CAGCGAATAGCACAGCTGCAGCTCCAAC 664
                                                                                                                                                  903
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5643772  NFORWATION: NT: PETERSEN, CAROLYN NT: LEECH, JAMES NT: NELSON, RICHARD, C.	; Patent ; GENER ; APF ; APF
_documentation_block: equence 35, Application US/08415751	. Ō
_name: /cgn2_6/ptodata/2/iaa/5a_COMB.pep:US-08-415-751-35	seq_name
1322 GACCTTTAAACACACCCTGTGAACCCCAGC 1350    ::::::::    :::   ::: 659 alProValGlnAsnProGlnGlnProAla 668	32 65
1287 GCGGACCCCACAGAACTTCAGTGTCCCCTCACCTG 1321	64
626 LeuI	62
60	60
.MetGlyValGlyArgProGlyValTyrLysValIleGlyProArgMetS 609	59
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559 alalaalaalaProProGlnAsnValLeuLysGlnGluGluLeuLeuVal 575	Ú1
1218 1218	21
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1165 TCCCGGCAGCCCGGCCAGCCCAGCTC 1190 :::      :::   526 AlaProAlaProIleAsnProValThrLeuAsnValSerThrValAlaAl 542	52
4 0	14 50
1092 CCCCATGCTGTCCTCGCCGTCACCGGGCCAGCAGGTGCAGACCCCGCAGT 1141 :	09 49
1063 CCCGGAGTCCAGGTCAGCCAGAGCAGCCT 1091       :::    :::    :::    :::    :::    :::     :::	-4
	46
96 45	96 45
444 MetLysThrLeuProProSer	4
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803 AACCATCACAACTCCCGCCACAGTCGCAGACCCAGCCTTTGGTGTCACAG 912	4- 0

632TGCTGTTGCTGCTGCTGTATCTGTTG	676 GCTGTTGCTGTTGGAGCTGCAGCTGTGCTATTCGCTGCAGC	717 CTCCAAAGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGC	Align seg 1/1 to: US-08-415-751-35 from: 1 to: 362	alignment_block: US-09-668-119-1/rev x US-08-415-751-35	Percent S	<ul> <li>NAME/KEY: POSITIONS coded by nonsense codons are</li> <li>NAME/KEY: identified as Xaa.</li> <li>US-08-415-751-35</li> </ul>	ptosporidium parvum	рертисе	GY: linear	cid	; SEQUENCE CHARACTERISTICS; ; LENGTH: 362 amino acids	ORMATION FOR SEQ ID	TELEPHONE: (415) 324-1677	; REFERENCE/DOCKET NUMBER: 480.19-2 (HHD) ; TELECOMMUNICATION INFORMATION:	; NAME: Hana DOLEZALOVA ; REGISTRATION NUMBER: 30,518	ATTORNEY/AGENT INFORMATION:	; APPLICATION NUMBER: 07/891,301	; APPLICATION NUMBER: 08/071,880 ; FILING DATE: June 1, 1993		; CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/415.751	SOFTWARE: Wordperfect 5.1	TYPE: Diskette - 3.5 inch, 1.44 Kb stora	OF PINCE	California	Sherman Avenue, lto	SEE: PHILLIPS, MOORE, LEMPIO	NCES: 50	; TITLE OF INVENTION: METHODS FOR IMMUNOTHERAPY AND	ION: VECTOR AND TRANSFORMED HOS	ION: CRYPTOSPORIDIUM ANTIBOI	ION: POLYPEPTIDES BINDING ANT	-
3 607 1 127	. 633 5 110	F 677																														

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eq_name: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:US-08-415-751-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 6, Application US/08415751 Patent No. 5643772
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    422
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    374 .GTCTGT.....GGAGTTGCCGTAGACACGACA 348
                                                                                                                                                                                                                                                                                                                SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
                                                                                                                     APPLICATION NUMBER: 08/071,880
FILING DATE: June 1, 193
APPLICATION NUMBER: 07/891,301
FILING DATE: May 29, 1992
ATTORNEY/REENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
                  REFERENCE/DOCKET NUMBER: 480.19-2 (HHD) FELECOMMUNICATION INFORMATION: TELEPHONE: (415) 324-1677
                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/415,751 FILING DATE: 03-APR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Palo Alto
STATE: California
                                                                                                                                                                                                                                                     CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
                                                                                     REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CTGCTGCTGCTGTAGCGCCGCCTGCTGCTGCTGCTGGAACTGC....
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   s......CysSerLeuPheTrpCysCysCysCysCysCysLeuA 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AspThrValAsnPheAsnCysTrpAspTrpAsnPheLeuHisGlnIleLe 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       erSerGlyLeuSerValPheHisCysCysCysArgCysTrp***ArgIle 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ...TGCTGCAGCGCCACCTGCTGGAGCTGCAGCTGG.......
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  94306-1840
                                                                                                          Hana Dolezalova
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               385 Sherman Avenue, Suite 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LEECH, JAMES
NELSON, RICHARD, C.
(415) 324-1678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PETERSEN, CAROLYN
                                                                                                                                                                                                                                                                                                                                                                                             PC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PHILLIPS, MOORE, LEMPIO & FINLEY
                                                                                                                                                                                                                                                                                                                                                                                                            Diskette - 3.5 inch, 1.44 Kb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               JIRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POLYPEPTIDES BINDING ANTI-
CRYPTOSPORTDIUM ANTIBODIES, DNA
AND RNA ENCODING THEM, HYBRID
VECTOR AND TRANSFORMED HOST AND
METHODS FOR IMMUNOTHERAPY AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DIAGNOSIS AND KIT
                                                                              30,518
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US-08-415-751-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ratio: 3.789
Percent Similarity: 40.212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Align seg 1/1 to: US-08-415-751-6 from: 1 to: 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-668-119-1/rev x US-08-415-751-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 362 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             891 CTGCGACTGTGGCGGGAGTTGTGATGGTTGGTTCTGAGCAACTGGAGGCT 842
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       671 TGCTGTTGTTGGAGCTGCAGCTGTGCTATTCGCTGCAGCTGCTGTTGCTG 622
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       741 TGGCTGCTGAATTGGTGGCCTGGGCCTCCAAAGCCTGCTGCTGCTGCTGC. 693
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           135 elleArgVal********ThrThrValIleValIleAsnHisSerCysV 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   841 GCTGGGGCTGTGGCGCCTGGTGGTGTGTGTGATGCATCTGCTGC 792
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                621 CTGCTGTATCTGTTGCTGATTTTGATGATGCAATTTAATTAGATGCTGCT 572
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181 ValSerLeuGlySerSerSerCysArgTrpHisCysCysCysCysCysCy 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  164 snPheAsnValThrAspIleArg***TrpCysArgCysCysCysHisPhe 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              156 HisLeuPheAsnTrp.AspTrp.....
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                                                                                                                                                                                                                    474 CTGCTGCTGC.....TGCTGCTGCTGTAGCGCCGCCTGCTGCTGCT 434
                                                                                                                                                                                                                                                                 219 TrpLeu.....ThrTrpAsnLeuCysCysCy 227
                                                                                                                                                                                                                                                                                                                                                         202 ysCysCysAsnTyrTrpLeu***CysCysCysCysGlyTyrTrp 218
                                                                                                                                                                                                                                                                                                                 524 TGGAACTGCTGCATGGCACTCTGCTGAGCCTGGAACTGCTGCTGTTG 475
                                          383 TGCAGCTGGGTCTGT 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY:
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                                                                                                                                                                                                                                                                                                                                                                                   ......rgcrgcrgcrgcrgcrgcrgcrgcrgcr 672
******LeuValCys 259
                                                                                                                               GCTGGAACTGCTGCTGCTGCTGCTGCAGCGCCACCTGCTGGAGC 384
                                                                                                                                                                        sCysCysCysTrpPheLeuSerCysCysCysAsnAsp............ 239
                                                                                  ..TrpIleLysSerCysCysGlyCysCysLeuArg***...Trp*** 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  H: 362 amino acids amino acid
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Percent Identity: 31.217
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alignment_block:
US-09-668-119-1/rev x US-08-089-862-11
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Align seg 1/1 to: US-08-089-862-11 from: 1 to: 1018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 11, Application US/08089862 Patent No. 5723588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 11:
                                         1528 GGTCTG.....TCAGAATGTCCAGAAGGCTCTTCATCTTACTCAGG 1488
                                                                                                                               1578 CAGGGCGATCTCACACTTTTGCAAGGTCTTCAGGGGACACCGCTTCGAGG 1529
                                                                                                                                                                                                                    1628 CACCOGGGGGGGGGGGGGGGGGGGCACCGCATGTCATTCTTGAGTTTCTC 1579
                                                                                                                                                                                                                                                                                                          1669 TCCAGGAGCG......GCTGGCATAGGTACTGCTGTTTGGTCGGTGG 1629
                                                                                                                                                                                                                                                                                                                                                                                                  1719 GGTACAGGGAATGGTTGAAGACAGGTGAGCGGATGTTGGCCCAGGACGGCA 1670
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                                                                                                                                                                           |:::|||:::|||:::|| || |||:::::::: ||| :::::|
| 134 ySerGlyAlaGlyAlaGlyAlaGlyAlaGlyAlaGlyAlaAlaP 151
168 GlyAlaGlyAlaGlySerGlyAlaGlyAlaGlySerGlyAlaGlyAlaGl 184
                                                                                     118 yAlaGlyAlaGlySerGlyAlaGlyAlaGlySerGlyAla.Gly.AlaGl 134
                                                                                                                                                                                                                                                                                                                                                      102 GlyAlaGlySerGlyAlaGlyAlaGlySerGlyAlaGlyAlaGlySerGl 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 1018 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Donofrio, David A
APPLICANT: Stedronsky, Erwin R
TITLE OF INVENTION: PROTEIN-ENRICHED THERMOPLASTICS
NUMBER OF SEQUENCES: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
STRANDEDNESS: sir
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Rowland, Bertram I REGISTRATION NUMBER: 20,015 REFERENCE/DOCKET NUMBER: A-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 4 Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: USA
ZIP: 94111-4187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                09-JUL-1993
N: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          287.00
0.966
55.827
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18	GCTGTGCTATTCGCTGCAGCTGCTGTTGCTGCTGCTGTATCTGTTGCTGA 6 ::: serGlyAlaGlyAlaGlySerGlyAlaGlyAlaGly	407
06	CTGCTGCTGCTGCTGCTGCTGCTGCTGTTGCTGTTGTTGGAGCTGCA 6 ::   :::   :::    :::    :::    :::	ن ف ن
703 190	AA FA	752 375
753 874	GCATCTGCTGCAGCTGCTGGGGCAGAGCCTGGGAGGCGGAGGCTGTGGC 7 :::::::   :::::	802 364
363	AACTGGAGGCTGCTGGGGCTGTGGTGGTGCTGTGTGTGAT 8 :::::       ::::::    ::::::::::::::	852 347
853 347	<pre>SCGGGAGTTGTGATGGTTGGTTCTGAGC      :::  </pre>	ω io
894 330	TACAACATTTGTCCAGGGAGAGCTTGCGCCTGTGACACCAAAGGCTGG    :::     :::	
9 <b>44</b> 319	GGGCTGCTGCACCACCATCGGAGCTCGGACAAATTTCAGTGGTGGTTGGG      :::   1yAlaGlyAla	993 316
994 316	TGAGCTGTCTGTACTGCTGCTGCTGCTGCACCTGGGGCTGCACTGGG	1043 301
1044 300	GGAGGCTGCTCTGGCTGACCTGGACTCCGGGAGCCACCATCTGGGCAGCC:::   :::::	1093 293
109 <b>4</b> 292	CGACTGCGGGGTCTGCACCTGCTGGCCCGGTGACGGCGACGACAGCATGG ::::::::::::   :::   1ySerGlyAlaGlyAlaGlySerGlyAlaGlyAlaGlyAlaGlySerGlyAlaGly	1143 276
1144 276	TGTGAGCTGGGCTGGCCGGGCTGCGGGGGGGGGGGGGGG	1193 261
119 <b>4</b> 260	GGAAGCTACTGGGAGATGGGGCAGGGCCAGAGCTGACGTTGGAGTTGGGC	1243 252
1244 251	CGCGCCGTCACTGGGCTCTGGGAGGGCTGCGG:::::	1290 235
1291 235	ACAGGI	1340 221
1341 221	GCTCCTCAGCCTGGCTGGAGC      AlaGlyAlaGlySerGlyAla	1390 205
1391 204	<b>L</b> -0	1437 188
1438 188	7 TCCTTTTTTCTGTCTTCGTTCTTGTCGATCTTGTTGATCATGCGGCGCAG	1487 184

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seq_documentation_block:
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                                                                                           APPLICATE:
FILING DATE:
CLASSIFICATION: 530
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: ROWLAND, Bertram I
REGISTRATION NUMBER: 20015
REFERENCE/DOCKET NUMBER: a58854-2/bir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 18, Application US/08587333
Patent No. 5808012
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       302 CCTGAG...AGAGACATTGGCTGTCCCATGGCACCAAAGCTACCCCATCCC 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      493 erGlyAlaGlyAlaGlySerGlyAlaGlyAlaGlySerGlyAlaGlyAla 509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           402 CAGCGCCACCTGCTGGAGCTGCAGCTGGGTCTGTGGAGTTGCCGTAGACA 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: PROTEIN-ENRICHED THERMOPLASTICS NUMBER OF SEQUENCES: 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: DONOFRIO, David A. APPLICANT: STEDRONSKY, Erwin R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    543 erGlyAlaGly.AlaGlySerGlyAlaGlyAlaGlySer 555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      526 sValAlaValSerAlaGlyProSerAlaGlyTyrGlyAlaGlyAlaGlyS 543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   205 CCGCAGCAGGTCCGCCAGTCAGGCTCTGGAGTGCATTCA 167
                            SEQUENCE CHARACTERISTICS: LENGTH: 1018 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: Four Embarca
CITY: San Francisco
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: UZIP: 94111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CGACAGCCATGCTGTGAGGGGCCATCCCCGAGGTCCCAGGAGGCGGCTGC 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AGCGCCGCCTGCTGCTGCTGCAACTGCTGCTGTTGCTGCTGCTGCTG 403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        lyAlaGlySerGlyAlaGlyAlaGlySerGly...AlaGlyAlaGlySer 443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .....SerGlyAlaGlyAlaGlySerGlyAlaG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           laGlyAlaGlySerGlyAlaGlyAlaGlySer..GlyAlaGlyAlaGlyS 493
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    E: FLEHR, HOHBACH, TEST, ALBRITTON . Four Embarcadero Center, Suite 3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ALBRITTON & HERBERT
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; STRANDEDNESS: ; TOPOLOGY: line; MOLECULE TYPE: pour US-08-587-333-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             alignment_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Align seg 1/1 to: US-08-587-333-18 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-668-119-1/rev x US-08-587-333-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1669 TCCAGGAGCG......GCTGGCATAGGTACTGCTGTTTGGTCGGTGG 1629
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1628 CACCGGGGGGGGGGGGGGGGCACCGCATGTCATTCTTGAGTTTCTC 1579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1719 GGTACAGGGAATGGTTGAAGACAGGTGAGCGGATGTTGGCCAGGACGGCA 1670
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1578 CAGGGCGATCTCACACTTTTGCAAGGTCTTCAGGGGACACCGCTTCGAGG 1529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1437
                                                                                                      1093 GGAGGCTGCTCTGGCTGACCTGGACTCCGGGAGCCACCATCTGGGCAGCC 1044
                                                                                                                                                                                                               1143 CGACTGCGGGGTCTGCACCTGCTGGCCCGGTGACGGCGAGGACAGCATGG 1094
                                                                                                                                                                                                                                                                                                                                                                                                                                  1243 GGAAGCTACTGGGAGATGGGGCAGGGCCAGAGCTGACGTTGGAGTTGGGC 1194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1340 ACAGGTGTGTTTAAAGGTCCAGGTGAGGGGACACTGAAGTTCTGTGGGGT 1291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  102 GlyAlaGlySerGlyAlaGlyAlaGlySerGlyAlaGlyAlaGlySerGl 118
1043 TGAGCTGTCTGTACTGCTGTCTGCTGCTGCACCTGGGGCTGCACTGG 994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  235 laGlyProSerAlaGlyTyrGlyAlaGlyAlaGlyAlaGlyAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       168 GlyAlaGlyAlaGlySerGlyAlaGlyAlaGlySerGlyAlaGlyAlaGl 184
                                                                                                                                                                                                                                                                                                                                                                            252 GlySerGlyAlaGlyAlaGlySerGly.....
                                                   293 AlaGlySerGlyAlaAlaProGly................................. 300
                                                                                                                                                            276 lySerGlyAlaGlyAlaGlySerGlyAlaGlyAlaGlySerGlyAlaGly 292
                                                                                                                                                                                                                                                             261 ....AlaGlyAlaGlySerGlyAlaGlyAlaGlySerGlyAlaGlyAlaG
                                                                                                                                                                                                                                                                                                                   TCCTTTTTTCTGTCGTTCTTGTCGATCTTGTTGATCATGCGGCGCAG 1438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CCGCGCCGTCACTGGGCTCTGGGAGGGCTGAGGGGC...TGGGCA 1244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         rGlyAlaAlaProGlyAlaSerIleLys.....ValAlaValSerA 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AlaGlyAlaGlySerGlyAlaGlyAlaGlySerGlyAlaGlyAlaGlySe 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GCTCCTCAGCCTGGCTGGAGCCAGCTGGGCTCATGACAGAGCTGGGGTTC 1341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       lyAlaGlySerGlyAlaGlyAlaGlySerGlyAlaGlyAlaGlySerGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GGGCTCGATGTACTTCGACAGCTGCTTCA...GCTTGTCCAGGTACTGCT 1391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          y.....SerGlyAlaG 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GGTCTG.....TCAGAATGTCCAGAAGGCTCTTCATCTTACTCAGG 1488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   roGlyAlaSerIleLysValAlaValSerAlaGlyProSerAlaGlyTyr 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               peptide
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55.827
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                to: 1018
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£	CCGCAGCAGGTCCGCCAGTCAGGCTCTGGAGTGCATTCA 167 :::	
206	GCCCAGAGACTGTCCCGGGCCCCGAGGAGGCATGCCAATTCCAGCGGCTC	526
256 526	CCTGAGAGAGACATTGGCTGTCCCATGGCACCAAAGCTACCCATCCC:::	302
303 509	CGACAGCCATGCTGAGGGGCCATCCCCGAGGTCCCAGGAGGCGGCTGC ::	193
353 493	CAGCGCCACCTGCTGGAGCTGCAGCTGGGTCTGTGGAGTTGCCGTAGACA    :::      ::	102
403 477	AGCGCCGCCTGCTGCTGCTGCTGCAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGC	160
453 460	TCTGCTGAGCCTGGAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGC	144
503 443	GAGCTGCTGCTGCTGCACTACTGCTTGGAACTGCTGCTGCATGGCAC	428
553 428	ATGCAATTTAATTAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	60:
603 418	ATTCGCTGCAGCTGCTGCTGCTGCTGCTGTTTGCTGCTGCTGTTTG       ::::::::::::     ::: aGlyAlaGlySerGlyAlaGlyAlaGly	40
653 406	2 CTGCTGCTGCTGCTGCTGCTGCTGCTGTTGCTTGTTGGAGCTGCA ::	
703 390	0 - 13	75 37
753 374	GCATCTGCTGCAGCTGCTGGGGCAGAGCCTGGGAGGGCC :::::::   :::::	802 364
363	2 AACTGGAGGCTGCTGGGGGCTGTGGTGGC :::::       7 laGlyAlaGlySerGlyAlaGlyAlaGl	3 <b>4</b>
853 47	3 GTCTGCGACTGTGGCGGGAGTT	33
894 33(	TATACAACATTTGTCCAGGGAGAGCTTGCGCCTGTGACACCCAAAGGC	943 320
319	lyAlaGlyAla	316
94	3 GGGCTGCTGCACCACCATCGGAGCTCGGACAAATTTCAGTGGTGGTT	99
31	]AlaSerIleLysValAlaValSerAlaGlyProSerAlaGlyTyrG	30

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OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                  Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Run on:
                                                                                                                                                                                                                                                                                                                                 Database
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Title:
                                              Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 atgaggaaagctggtgtggc.....cacattcgttccagccatga 1740
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-668-119-1
1740
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             February 28, 2002, 17:49:47; Search time 86.87 Seconds
                                                                                                                                                                                                                                                                                                                              Issued_Patents_NA: *
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   351203 seqs, 113238999 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                      /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
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/cgn2_6/ptodata/2/ina/6A_COMB.seq:*
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/cgn2_6/ptodata/2/ina/Backfiles1.seq:*
/cgn2_6/ptodata/2/ina/backfiles1.seq:*
SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (without alignments)
4536.338 Million cell updates/sec
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Result No.	Score	Query	Query Match Length	DB	ID	Description
1	181.2	10.4	3489	2	US-08-728-323A-1	Sequence 1,
c 2	81.	10.4	32207	Ν	US-08-770-379-20	Sequence 20
ი ა	181.2	10.4	32207	4	US-08-757-669A-20	
		9.9	543	σ	5273901-6	
ر ت	170	9.8	533	σ	5482709-5	No
6	142.6	8.2	397	ω	US-09-253-691-3	Sequence 3,
7	130.8	7.5	234	Н	US-08-469-802B-3	Sequence 3,
8	130.8	7.5	234	2	803B-	Sequence 3,
9	130	7.5	688	4	US-08-998-416-915	Sequence 915,
c 10			6530	2	US-08-146-930-1	Sequence 1,
c 11	•		6530	ω	US-08-458-240-1	Sequence 1,
	126.6		6530	υī	PCT-US93-03993-1	Sequence 1,
13	•	6.9	477	4	US-09-135-994-1	Sequence 1,
14	•		2580	w	US-09-050-863-2	Sequence 2,
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16		6.8	9600	4	US-08-910-647-1	Sequence 1,
17		6.8	10596	٢	US-07-884-811-15	Sequence 15
18		6.8	10596	_	-885-971-	Sequence 15
19	118.8	6.8	10596	1	US-08-087-783A-15	Sequence 15
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21	118.8		10596	N	US-08-194-087-15	
22	118.8		10596	თ	PCT-US93-04648-15	Sequence 15
	114.8		2793	Н	US-08-209-747-1	Sequence 1,
c 24		٠	2793	ب	US-08-458-298-1	Sequence 1,
25		6.5	203	4	US-09-043-303-7	Sequence 7,
c 26	113.4		2214	w	US-08-864-038A-1	Sequence 1,
c 27	112	,				

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45	44	<b>4</b> ω	42	41	40	39	38	37	36	ω 5	34	33	ω 2	<u>3</u> 1	30	29	t
93.6	93.6	96	96	97.4	98.8	98.8	101.8	101.8	105.8	109	110.8	110.8	110.8	110.8	111.2	111.2	H - C - H
5.4	5.4	ۍ ن	5.5	5.6	5.7	5.7	5.9	5.9	6.1	6.3	6.4	6.4	6.4	6.4	6.4	6.4	
336	336	154	154	2821	1995	1995	16442	2455	165	2190	9551	9551	786	786	195	195	000
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US-07-814-220-4	US-07-814-220-3	US-08-267-803B-6	US-08-469-802B-6	US-09-103-429A-2	US-08-317-844B-3	US-08-425-069-3	US-08-781-891-208	US-09-103-429A-1	US-09-043-303-17	US-09-625-188-19	US-08-800-644-93	US-08-056-200-93	US-08-929-414-2	US-08-403-379A-2	US-08-267-803B-2	US-08-469-802B-2	
Sequence 4	Sequence 3	Sequence 6	Sequence 6	Sequence 2	Sequence 3	Sequence 3	Sequence 2	Sequence 1	Sequence 1	Sequence 1	Sequence 93	Sequence 93,	Sequence 2	Sequence 2	Sequence 2	Sequence 2	,
, Appli	, Appli	, Appli	Appli	Appli	, Appli	, Appli	208, App	1, Appli	7, Appl	y, Appi	3, Appl	3, Appi	, Appli	, Appli	, Appli	, Appii	

## ALIGNMENTS

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RESULT 1
US-08-728-323A-1
US-08-728-323A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1, Application US/08728323A Patent No. 5948676
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Chang, Yuan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Chang, Yuan
APPLICANT: Bohenzky, Roy A.
APPLICANT: Russo, James J.
APPLICANT: Edelman, Isidore S.
APPLICANT: Moore, Patrick S.
TITLE OF INVENTION: Immediate Ea
TITLE OF INVENTION: Sarcoma-Asso
TITLE OF INVENTION: Encoding Sam
NUMBER OF SEQUENCES: 21
                                                                                                                                                                            TELEFAX: 212-391-0525
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/728,323A
                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REGISTRATION NUMBER: 08,678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 05
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-278-0400
                                                          FEATURE:
                                                                           MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: N
COUNTRY:
                  NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
CLASSIFICATION: 435
                                                                                                                                                                                                     TELEPHONE: 212-2, TELEPHONE: 212-391-0525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 10036
                                                                                                  TOPOLOGY:
                                                                                                                   STRANDEDNESS:
                                                                                                                                      LENGTH: 3489 base pairs TYPE: nucleic acid
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                                     CDS
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                                                                             DNA (genomic)
                                                                                                                   single
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                                                                                                                                                                                                                                                                                                      Patent No.
                                                                                                                                                                                                                                                                                                      Sequence 20, Application US/08770379 Patent No. 5849564
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Best Local Similarity
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                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                         APPLICANT: Edelman, Isidore S.

APPLICANT: Moore, Patrick S.

TITLE OF INVENTION: POLYPEPTIDES FROM KAPOSI'S SARCOMA-ASSOCIATED TITLE OF INVENTION: HERPESVIRUS, DNA ENCODING SAME AND USES THEREOF
                                                                                                         NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                            APPLICANT: Chang, Yuan APPLICANT: Bohenzky, R
                                                                                                                                                                                                                                                                                                                                                                                                                   2158 CAGGATGAGCAGCAGCAGC 2179
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               STATE: N
COUNTRY:
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CITY: N
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                                                                                         Cooper & Dunham LLP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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19959 CAGCAGCAGGATGAGCAGCAGGATGAGCAGCAGCAGGATGAGCAGCAGCAGGATGAG
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                   976 atggtggtgcagccagccccagtgcagccccaggtgcagcagcagcagcagcagtacag 1035
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TELECOMMUNICATION INFORMATION:
                                                                                                                                                                               856 cagaaccaaccatcacaactcccgccacagtcgcagacccagcctttggtgtcacaggcg 915
                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Palana
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/770,379
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Pred. No. 1.9e-30;
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Best Local Similarity
Matches 376; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 20, Application US/08757669A Patent No. 6183751
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (212) 391-0525 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                 19839 CAGGATGAGCAGCAGCAGCAGG 19818
                                20316 CAGCGGGAGCCACAGCAGCGGGAGCCA---CAGCAGCGGGAGCCACAGCAGCGGGAGCCA
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APPLICANT: MOOTE, PATRICK S.
TITLE OF INVENTION: UNIQUE ASSOCIATED KAPOSI'S SARCOMA VIRUS
TITLE OF INVENTION: SEQUENCES AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 45
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
                                                                                                                   496 cagcagagtgccatgcagcagtttccaagcagtagtgcagcagcagcagcagctccag 555
                                                                                                                                                                                    376 cagctgcagctccagcaggtggcgctgcagcagcagcagcagcagcagcagttccagcag 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER:
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TYPE: nucleic acid
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cagcagcagcaacagcagctgcagcgaatagcacagctgcagctccaacaacagcaacag 675
                                                                                                                                                                cagcagcagcagcagcatctaattaaattgcatcatcaaaatcagcaacagata 615
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1185 Avenue of the Americas
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Russo, James J.
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                                                                                                                                                                                                                                                                                                             Score 181.2; DB 4;
Pred. No. 1.9e-30;
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RESULT 4
5273901-6
;PATENT NO. 5273901
;PATENT NO. 5273901
;PATENT NO. 5273901
;APPLICANT: JACOBSON, JAMES W.;STRAUSBERG, ROBERT L.;WILDOWN, SUSAN D.;PODE, SHARON H.;STRAUSBERG, SUSAN L.;RUFF,MICHAEL D.;
;SUSAN D.;PODE, SHARON H.;STRAUSBERG, SUSAN L.;RUFF,MICHAEL D.;
;AUGUSTINE, PATRICIA C.;DANFORTH, HARRY D.
;TITLE OF INVENTION: GENERICALLY ENGINEERED COCCIDIOSIS
;SPORZOITE 21.5 KB ANTIGEN, AC-6B
;NUMBER OF SEQUENCES: 11
;MUMBER OF SEQUENCES: 11
;MUMBER OF SEQUENCES: US/07/581,693
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                                                                                                                                                                                                                                                                                                                       Matches 269;
                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
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556 cagcagcagcagcagcagcatctaattaaattgcatcatcaaaatcagcaacagata 615
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FILING DATE: 05-JUL-1988
APPLICATION NUMBER: 746,520
FILING DATE: 19-JUN-1985
                                                                                                                                                                                                                         98 cggcagcacctgcagcagcaacagcagcagcacctgcagcagcaacagcagcagcaacag 157
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 627,811
                                                                                                                                    cagctgcaacagcagcagctacagcaacaccagctgcagctgcagcagcagcagcag 217
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                                          caccagctgcagcagcagcagcaacaggagctgcagcagcaccagctgcagcgacag
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                                                                                                                                                                                                                                                                                                                                          9.9%;
                                                                                                                                                                                                                                                                                                                   Score 171.8; DB Pred. No. 4e-29; 0; Mismatches 1
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RESULT 5
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NUMBER OF SEQUENCES: 10
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQ ID NO:5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Patent No. 5482709
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 277;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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                                                                                                                                                                                                                                                                                                                          429 ccagcagcagcagcagcgcgcctacagcagcagcagcagcagcagcagcagcagtt 488
                                                                                                                                                                                                                                                                                                                                                                                                   518 cagcagcaaca 528
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381 gcaacaacagcagctgcagcaagagcagcagcatcagcagcaggtaagcctggggga 440
                                                                        201 gcagcagcaccagctgcagcagcagcagcagcaacaggagctgcagcagcaccagctgca
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APPLICATION NUMBER: 627,811
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FILING DATE: 12-SEP-1990
APPLICATION NUMBER: 215,162
FILING DATE: 05-JUL-1989
APPLICATION NUMBER: 746,520
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Match 9.8%;
Local Similarity 63.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 533
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                 gcaacagcagcagcagcagcagcagcagcagcaggctttggaggcccagccacc
                                                                                            gctccagcagcagcagcagcagcatctaattaaattgcatcatcaaaatcagca
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 170; DB 6; Length 533; Pred. No. 9.9e-29;
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                                                                                                                                                                                                                                                          US-08-469-802B-3
                                                                                      APPLICANT: Orr, Harry T.
APPLICANT: Ranum, Laura P.W.
APPLICANT: Chung, Ming-yi
APPLICANT: Zoghbi, Huda Y.
TITLE OF INVENTION: Gene Sequence for Spinocerebellar Ataxia
Patent No. 5741645
                                                                                                                                                                                                                   Sequence 3, Application US/08469802B Patent No. 5741645
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LENGTH: 397
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 3, Application US/09253691 Patent No. 6124100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches 184;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best
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CURRENT APPLICATION NUMBER: US/09/253,691
CURRENT FILING DATE: 1999-02-22
EARLIER APPLICATION NUMBER: KR 98-6,278
EARLIER FILING DATE: 1996-02-26
NUMBER OF SEQ ID NOS: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Dong Kyu JIN
TITLE OF INVENTION: Diagnostic Method and Kit for Neuropsychiatric Diseases
TITLE OF INVENTION: Using Trinucleotide Repeats Sequence
                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: WordPerfect 6.1/Windows
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Mueting, Raasch, Gebhardt & Schwappach,
STREET: 119 No. 5741645th Fourth Street, Suite 203
                                                    TITLE OF INVENTION: Type 1 and Method for Diagnosis NUMBER OF SEQUENCES: 47
                                                                                                                                                                                                                                                                                                                                  361 cctatcagcacag 373
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Match 8.2%; Local Similarity 72.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gcagcagcagcagcagcaacagcagcagttccaggctcagcagagtgccatgcagcagca 518
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                                                                                                                                                                                                                                                                                                                                                                        US-08-267-803B-3
                                                                                                                                                                                                  APPLICANT: Orr, Harry T.
APPLICANT: Chung, Laura P.W.
APPLICANT: Chung, Ming-yi
APPLICANT: Zoghbi, Huda Y.
TITLE OF INVENTION: Gene Sequence for Spinocerebellar Ataxia
Patent No. 5834183
                                                                                                                                                                                                                                                                                                                Sequence 3, Application US/08267803B Patent No. 5834183 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 162;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 3:
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MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION: TELEPHONE: 612-305-1217
TELEFAX: 612-305-1225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08
FILING DATE: 06-UUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Mueting, Ann M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
                 COUNTRY: USA
ZIP: 55458-1415
COMPUTER READABLE FORM:
                                                                                                                                                CORRESPONDENCE ADDRESS:
                                                                                                                                                               TITLE OF INVENTION: Type 1 and Method for Diagnosis NUMBER OF SEQUENCES: 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          370 cagacccagctgcagctccagcaggtggcgctgcagcagcagcagcagcagcagcagcagttc 429
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        490 caggctcagcagagtgccatgcagcagcagttccaagcagtagtgcagcagcagcagcag 549
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Minneapolis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
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                                                                        STREET: P.O. Box CITY: Minneapolis STATE: MN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Mueting, Raasch, Gebhardt & Schwappach, P.A. STREET: P.O. Box 581415
MEDIUM TYPE: Floppy disk
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nucleic acid
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75.7%;
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Pred. No. 2.8e-20;
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Best Local Similarity 75.7%;
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INFORMATION FOR SEQ ID NO:
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APPLICANT:
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ATTORNEY/AGENT INFORMATION:
NAME: McCormack, Myra H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM CC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                APPLICANT: Rebischung, Corinne
TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSYPII
TITLE OF INVENTION: AND USES THEREOF
NUMBER OF SEQUENCES: 1152
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: DNA
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CURRENT APPLICATION DATA:
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                                                                                                               COUNTRY:
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                                                                                                                                  Research Triangle Park
No. 6239264th Carolina
                                                                                                                                                                      3054 Cornwallis Road
                                                                                                                                                                                                                                                                                                                                             Philippsen, Peter
Pohlmann, Rainer
Steiner, Sabine
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                                                                                                                   USA
                                                                                                                                                                                                                                                                                                                               Mohr, Christine
                                                                                                                                                                                                                                                                                            Wendland, Jurgen
Knechtle, Philipp
                                                                                                                                                                                         No. 6239264artis Corporation
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Pred. No. 2.8e-20;
Pred. No. 52;
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                              Sequence 1, Application US/08146930 Patent No. 5958764 GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 915:
SEQUENCE CHARACTERISTICS:
 APPLICANT: Rothnagel,
              APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: PF
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8587
                                                                                                                                                   611 CTGCCCAACAACAATCGCAACAACAACAGCAGCAGCAGCAGCAGTCTCAGCAGCAG 666
                                                                                                                                                                         842 agcctccagttgctcagaacccaaccatcaccaactcccgccacagtcgcagacccag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION: NAME: Meigs, J. Timothy
                                                                                                                                                                                                                                                                                        491 CACAACCACAATTGAAACCACAATCACAGCAACCACAACCGGTTCCACAGCAAGTCCAGT 550
                                                                                                                                                                                                                                                                                                                                                                                                                                 311 CTCAACCGCAACTACAACAACAACAACAGCTTGGTTTACAGCCTCATCAGCCACAACTGG 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       548 agotocagcagcagcagcagcagcatctaattaaattgcatcatcaaaatcagc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                608 aacagatacagcagcagcagcagctgcagcgaatagcacagctgcagctccaacaac 667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       488 tccaggctcagcagagtgccatgcagcagcagttccaagcagtagtgcagcagcagcagc 547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           131 CTCATCCTCAGCAACAACAAGGTTCACAAGCTCAGCAGCAGCTACTTCAACAACAACAAG 190
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        428 tccagcagcagcagcgggggctacagcagcagcagcagcagcagcagcagcagt 487
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Local Similarity 54.1%;
ses 290; Conservation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: CH 0 FILING DATE: 31-DEC-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH:
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              Roop, Dennis R
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24-DEC-1997
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Joseph A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
3335 GCAGCTGGAGCCACCGCCGCCACCAGAGTACTTGCCGCCTCCGGAACCGCCGCCGCAGCC 3276
                                                                                                                                                                3455 CGTGCCGCCGCCACCGGAATAGCCGCCGCCGCCGCCGCAGCTGGATCCACCGCCACCTGA 3396
                                                                                    3395 GTAGCCGCCGCCACAGCTAGAGCCGCCGCCGCTGCTTCCACCGCCGCCGGAATAGCCGCCTCC 3336
                                                                                                                                                                                                                                                  3515 GCACTGATACTGTTGGGACGATCCGCCGCCGCCGCCGCCGAGGGAACCACCTCCGCAGCT 3456
                                                                                                                                                                                                                                                                                                                                3575 GCCCCCGGAGTAGCCGCCGCCGCAGCTGGAGCCACCGCTAGAACCGCCTCCGTAGCTCTG 3516
                                                                                                                                                                                                                                                                                                                                                                                                                  3635 GCCGCCTCCGCAGCTAGAGCCTCCGCCCCCGGAGTAGCCGCCACCGCAGCTGGAGCCTCC 3576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: October 29, ATTORNEY/AGENT INFORMATION: NAME: Warburg, Richard J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: WordPerfect (Version 5.0)
CURRENT APPLICATION DATA:
APPLICATION NATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Greenhalgh, David A.
TITLE OF INVENTION: SPECIFIC EXPRESSION
TITLE OF INVENTION: AND METHODS OF USE
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 435
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
                                    COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
COMPUTER: IBM PC compatible
OPERATING SYSTEM: IBM MS-DOS (Version 5.0)
                                                                                                                                                                                                                                                                                                                                                          420 gcagcagttccagcagcagcagcagcgcgctacagcagcagcagcagcagcagcaaca 479
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                                                                                                                                                                                                       540 gcagcagcagcagcagcagcagcagcagcagcatctaattaaattgcatcatca 599
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: 07/876,286
FILING DATE: April 30, 1992
APPLICATION NUMBER: NO. 5958764 yet assigned (204/132)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS:
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TELEX: 67-3510
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VENTION: SPECIFIC EXPRESSION VECTORS
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Pred. No. 9.4e-19;
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                                                                             APPLICATION NUMBER: 07/876,286
FILING DATE: April 30, 1992
APPLICATION NUMBER: No. 6143727 yet assigned (204/132)
FILING DATE: October 29, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA: APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM: MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
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                  NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 204/152
TELECOMMUNICATION INFORMATION:
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APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE:
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TELEPHONE:
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Greenhalgh, David A.
VENTION: SPECIFIC EXPRESSION
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(213) 489-1600
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Best Local Similarity
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TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
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STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                           --TGGAGCCACCCCGGAGTAGCTGCCGCCGCCGCAGCTGGAGCCGCCGCCGCCTCCGGA
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                                                                                                   ccagagcagcctccccatgctgtcctcgccgtcaccgggccagcaggtgcagaccccgca 1139
                                                                                                                                                                          gcagacagcagtacagacagctcaggctgcccagatggtggctcccggagtccaggtcag 1079
                                                                                                                                                                                                                    GTAGCCACCTCCGCAGCTGGAGCCGCCGCCGCCCCAGAGTAGCCACCGCCGCAGCTAGA
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                                                                      CTTGACGCCCCACCGGAGCCGCCTCCACCG---CCGCAGCTGGAACCACCTCCATAGGA 2862
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48.6%;
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Pred. No. 9.4e-19;
0; Mismatches 424;
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TELEX: 76.829
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 6530 base pairs
TYPE: NUCLEIC ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PCT-US93-03993-1/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 7.3%; Score 126.6; DB 5; Length 6530; Best Local Similarity 48.6%; Pred. No. 9.4e-19; Matches 407; Conservative 0; Mismatches 424; Indels 6;
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3335 GCAGCTGGAGCCACCGCCACCAGAGTACTTGCCGCCTCCGGAACCGCCGCCGCCAGCC 3276
                                                                                 3395 GTAGCCGCCGCCACAGCTAGAGCCGCCGCTGCTTCCACCGCCGCCGGAATAGCCGCCTCC 3336
                                                                                                                                                                  3455 CGTGCCGCCGCCACCGGAATAGCCGCCGCCGCCGCCGCCAGCTGGATCCACCGCCACCTGA 3396
                                                                                                                                                                                                                                                   3515 GCACTGATACTGTTGGGACGATCCGCCGCCGCCGCCACCGGAGGAACCACCTCCGCAGCT 3456
                                                                                                                                                                                                                                                                                                                                    3575 GCCCCCGGAGTAGCCGCCGCCGCAGCTGGAGCCACCGCTAGAACCGCCTCCGTAGCTCTG 3516
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MEDIUM TYPE: Flofpy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: 11
MOLECULE TYPE:
                                  REFERENCE/DOCKET NUMBER: D-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713/651-5325
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NAME: Paul, Thomas D.
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APPLICANT: Rothnagel, Joseph A.
APPLICANT: Greenhalgh, David A.
TITLE OF INVENTION: CONSTITUTIVE AND INDUCIBLE EPIDERMAL
TITLE OF INVENTION: VECTOR SYSTEMS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                        600 aaatcagcaacagaticagcagcagcaacagcagctgcagcgaatagcacagctgcagct 659
                                                                                                                                                                                                         540 gcagcagcagcagcagcagcagcagcagcagcatctaattaaattgcatcatca 599
                                                                                                                                                                                                                                                                                          480 gcagcagttccaggc.cagcagagtgccatgcagcagcagttccaagcagtagtgcagca 539
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             360 ggcaactccacagac cagctgcagctccagcaggtggcgctgcagcagcagcagcaaca 419
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TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  E: Fulbright & Jaworski
1301 McKinney, Suite 5100
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Thomas D.
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TYPE: DNA;
ORGANISM: Homo sapiens
US-09-135-994-1
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US-09-135-994-1
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APPLICANT: Ranum et al.
TITLE OF INVENTION: SCA7 GENE AND METHODS OF USE
FILE REFERENCE: University of Minnesota
CURRENT APPLICATION NUMBER: US/09/135,994A
CURRENT FILING DATE: 1998-08-18
EARLIER APPLICATION NUMBER: 60/256,170
EARLIER APPLICATION NUMBER: 60/256,170
EARLIER FILING DATE: 1997-08-19
NUMBER OF SEQ ID NOS: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Ver. SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                              Matches 183;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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2861 ACCACCGCCTCCGCCTCCACAGCTAGAGCCTCCTCCAGATGAGCCGCCTCCGCAGCC 2805
                                                                            588 attgcatcatcaaaatcagcaacagatacagcagcagcagcagcagctgcagcgaatagc 647
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                                                                                                                                                                                528 agtagtgcagcagcagcagcagcagcagcagcagcagcagcagcatctaattaa 587
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                                                                                                                                                                                                                                                                                 780 gccccagcagctgcagcagatgcatcacaccagcaccaccagccgccaccaccagccca 839
                                                                                                                                                                                                                                                                                                                                                                                                                  Match 6.9%;
Local Similarity 63.8%;
                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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SEQUENCE CHARACTERISTICS:
LENGTH: 2580 hascomproper
                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                            Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Silva, Robin M.
REGISTRATION NUMBER: 38,304
REFERENCE/DOCKET NUMBER: A-65638/DJB/RMS
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: Mammalian Protein Interaction Cloning TITLE OF INVENTION: System NUMBER OF SEQUENCES: 5
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APPLICATION NUMBER: US,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Hiang, Betty APPLICANT: Payan, Don
                                                                                                                                                                                                        661
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                                                                                                                                                               430 cagcagcagcagcaggcgctacagcagcagcagcagcagcagcagcagcagcagcagttc 489
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert
cagatacagcagcagcagcagctgcagcgaatagcacagctgcagctccaacaacag
                                                                                                           caggetcageagagtgecatgeageageagttceaageagtagtagtgeageageageageag
                                                                                                                                                cagacccagctgcagctccagcaggtggcgctgcagcagcagcagcagcagcagcagcagttc 429
                                       ctccagcagcagcagcagcagcagcatctaattaaattgcatcatcaaaatcagcaa 609
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Pred. No. 3.3e-17;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: VEBNA
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Local Similarity 53.2%;
les 252; Conserva+:...
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Sequence 1, Application US/09130114 Patent No. 5976807 GENERAL INFORMATION:
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APPLICANT: Damaj, Bassam B.
APPLICANT: Damaj, Bassam B.
APPLICANT: RObbins, Alan K.
TITLE OF INVENTION: Eukaryotic Cells Stably Expressing Genes
TITLE OF INVENTION: From Multiple Transfected Episomes
FILE REFERENCE: 0867/1D903US1
CURRENT APPLICATION NUMBER: US/09/130,114
CURRENT FILING DATE: 1998-08-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           430 cagcagcagcagcaggcgctacagcagcagcagcagcagcagcagcagcagcagttc 489
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Pred. No. 4.5e-17;
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Search completed: February 28, 2002, 19:18:22 Job time: 5315 sec

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Listing first 45 summaries
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Polyglutamine trac	Probe #692 used to	Probe #719 used to	Probe #708 for gen	Probe #5716 used t	Probe #13901 used	Probe #9950 for ge	Novel human polynu	Human secreted pro	Human polynucleoti	Human polynucleoti	Description		

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AAZ23778	AAX90923	AAA75454	AAF82902	AAA50254	AAX90924	AAV55831	AAI46546	AAZ44307	AAC79295	AAZ45239	AAC68948	AAZ22072	AAQ51557	AAQ84832	AAC90084	AAZ32027	AAF08420	AAA8864	AAZ45597	AAX89891	AAA59241	AAA59242	AAA59240	AAZ45602	AAA29550	AAT33007	AAQ20685	AAC84677	AAQ23092	AAV19941	AAV73805	AAF82901	AAA30290	
	Anti-sense strand	Nucleotide sequenc		Epstein Barr virus	Epstein Barr Virus	Nucleotide sequenc	Probe #15232 used	Human SCA/ genomic	Human lung cumour-	DNA encoding anglo	Mouse loricrin gen	Nucleotide sequenc	Loricrin gene. Ho		Z46970 cDNA clone.	Human METH1 relate	Fusarium venenatum	Human dentin sialo	cDNA sequence of h	Spinocerebellar at	Exons D, C, B and	Ca	tr		HIV codon altered	Mouse SRY-related	PKS 741 insert con	DNA sequence of hu	Antigen to-/a gene			Nucleotide sequenc	Kaposi s sarcolla-a	

## ALIGNMENTS

RESULT

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AAI59455 standard; cDNA; 2556

ВP

03-AUG-2000; 14-SEP-2000; 19-OCT-2000; 29-NOV-2000; 21-JAN-2000; 25-APR-2000; 09-JUL-2000; 19-JUL-2000; Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation; chemokinetic; AAI59455; WO200153312-A1. Homo sapiens. Human polynucleotide SEQ ID NO 1658. 22-OCT-2001 (first entry) 26-DEC-2000; 2000WO-US34263 26-JUL-2001. leukaemia; ss. ; 2000US-0488725. ; 2000US-0552317. ; 2000US-05598042. ; 2000US-0620312. ; 2000US-06521450. ; 2000US-0662191. ; 2000US-06631356. ; 2000US-0727344.

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Best Local :
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818 cagcagttccaggctcagcagagtgccatgcagcagcagttccaagcagtagtgcagcag 877
                             481 cagcagttccaggctcagcagagtgccatgcagcagtagttccaagcagtagtgcagcag 540
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                                                                                                                                        421 cagcagttccagcagcagcagcagcggcgctacagcagcagcagcagcagcagcagcacag 480
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                                                                                                                                                                                                                                                                                                                                    638 gggcagccgcctcct/ggacctcggggatggcccctcacagcatggctgtcgtgtctacg 697
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; SEQ ID NO 1658; 10078pp; English.
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Yang Y,
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25-APR-2000;
09-JUL-2000;
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         The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polypucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activity, chemotactic/chemokinetic activity, haemostatic activity, haemostatic activity, haemostatic activity, haemostatic
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Wang
Zhao
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03-AUG-2000;
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                                                                                                                                                                                                                                            2001-442253/47.
                                                                                                                                                                                         nucleic acids and polypeptides, useful for treating as central nervous system injuries -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        polynucleotide SEQ ID NO 5230.
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Wang Z,
Zhou P,
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                                                                                                                                                                 SEQ ID NO 5230; 10078pp; English
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2000US-0653450.
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Wehrman T,
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  cancer diagnosis and
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Xu C, Xue AJ,
R, Drmanac RT;
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Yang Y,
 therapy,
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  drug
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Note: The sequence data for this patent did
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                                             gctctgccccagcagctgcagcagatgcatcacacacagcaccaccagccgccaccacag
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Mismatches 3;
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Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral; antiallergic; hepatotropic; antidiabetic; antiinflammatory; antiulcer; vulnerary; anticonvulsant; antibacterial; antifungal; antiparasitic;
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                                                                           Human secreted prote:n coding sequence SEQ ID NO: 60.
                                                                                                                   02-FEB-2001 (first entry)
                                                                                                                                                                                                                                                                                                     1733 agccatga 1740
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1075 gtcagccagagcag:ctccccatgctgtcctcgccgtcaccgggccagcaggtgcagacc 1134
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                                                                                                                                                                                                                                                                                                                                                               cgtcctggccaacat:cgctcacctgtcttcaaccattccctgtaccgcacattcgttcc 1732
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nucleic acids, proteins, antibodies and (antiagonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer, and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune thyroiditis, diabetes mellitus, crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c) cardiovascular disorders such as myocardial ischaemias; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f) infections diseases such as viral, bacterial, fungal and parasitic infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12-MAR-1999;
11-JUN-1999;
03-DEC-1999;
                                                                                                                                                                                                                                          The invention relates to the isolation of genes AAA58990-A59039 encoding 50 human secreted proteins AAB27560-B27609. The genes can be used to generate fusion proteins by linking to the gene for the human immunoglobulin G Fc portion (SEQIDI) for increasing the stability of the fusion protein as compared to the human protein only. The genes and proteins are useful for preventing, ameliorating or treating medical conditions, e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The
                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Page 372; 428pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Isolated nucleic acid molecule encoding a human secreted protein used in preventing, treating or ameliorating a medical condition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P-PSDB; AAB27609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               09-MAR-2000; 2000WO-US06049
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder; neurological disease; infection; human; secreted protein; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2000-638175/61.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ruben SM,
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99US-0138574.
99US-0168667.
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Matches 955;
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Best Local Similarity
181 agcctgactggcggacctgctgcgggagccgctggaattggcatgcctcctcggggcccg 240
                                                     278 agcctgactggggacctgctgcgggagccgctggaattggcatgcctcctcgggggcccg 337
                                                                                                           218 cgagacattcataacaagaaatctcaagcttccgtcagtgatcctatgaatgcactccag 277
                                                                                                                         121 cgagacattcataacaagaaatctcaagcttccgtcagtgatcctatgaatgcactccag 180
                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                        54.0%;

    Mismatches

                                                                                                                                                                                                                                                                                        Score 939.2; DB 21
Pred. No. 9.9e-156;
                                                                                                                                                                                                                                                                                                       DB 21; Length 1388;
                                                                                                                                                                                                                                                                              9;
                                                                                                                                                                                                                                                                              Indels
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Sequence 1388 BP; 364 A; 378 C; 343 G; 297 T; 6 other;

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   02-JUL-1999;
02-JUL-1999;
                                             30-JUN-2000;
                                                                                                                                                            breast cancer; lung
                                                                                                                                                                                                     Novel human polynucleotide, SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           aatcagcaacagatacagcagcagcaacagcagctgcagcgaatagcacagctgcagctc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cagcagttccagcagcagcagcagcgctacagcagcagcagcagcagcagcagcaacag
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cagcctccagttgctcagaaccaaccatcacaactcccgccacagtcgcagacccagcct
                                                                                                                                                                          cytostatic; gene therapy; colon cancer; prostate
                                                                                                                                                                                                                                                                                                                                                                                             966
                                                                                                                                                                                                                                 (first entry)
                                              2000WO-US18374.
   99US-0142310.
99US-0142311.
                                                                                                                                                                                                                                                                                            cDNA; 386
                                                                                                                                                            cancer; cancer detection;
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CC The present sequence is one of 3351 sequences in a library of human CC polynucleotides. The library is used to detect differentially expressed CC genes correlated with a cancerous state of a mammalian cell and can CC detect colon, prostate, breast and lung cancer. The library can be used CC to produce probes for detection of mRNA and to produce additional copies CC of the polynucleotides. The probes can be used for chromosome mapping of CC the polynucleotide and for detection of transcription levels. Ribozymes CC or antisense oligonucleotides can be generated. The polynucleotides and CC their gene products are used as genetic or biochemical markers (e.g. in blood or tissues) that will detect the earliest changes along the CC carcinogenesis pathway and/or monitor the efficacy of therapies and CC antibodies against them can be used in pharmaceutical compositions to treat the cancers and proliferative disorders such as neoplasia, CC dysplasia and hyperplasia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Williams LT, Escobedo J, Reinhard C, Randazzo F, Crkenjakov R, Drmanac S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (CHIR )
(HYSE-)
                                                                                                                                                                                                                                                                                                                                                       Library of polynucleotides for diagnosing a cancerous state of mammalian cell and detecting cancer, particularly of the colon prostate, comprises 3351 human polynucleotide sequences -
                                                                                                                                                                                                                                                                                                                       Claim
                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-091805/10.
Sequence 386 BP; 50 A; 88 C; 138
                                                                                                                                                                                                                                                                                                                         9; Page 793; 1046pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HYSEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CHIRON CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Garcia V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Jones
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Dickson M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LW, Strache-Crain
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   G; 110
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Labat I,
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   <del>,</del> ;
     0 other
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                    Query Match
Best Local S
Matches 358
                     al Similarity
358; Conserv
                     Conservative
                                19.5%;
96.0%;
                       0;
                      Score 338.6; DB 2
Pred. No. 8.4e-51;
0; Mismatches 14
                                         DB 22;
                        14; Indels
                                          Length 386;
                        1;
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147
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                                                                                                                                                                                                                                                                                                         CATGCTCAGCAGAGTG-CATGCAGCAGCAGTTCCTAGCAGTAGTGCAGCAGCAGCACTAG
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                                                                                                                                                                                   CAACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCTTTGCAGGCCCAGCCACCA
                                                                                                                                                                                                   CAGATACAGCAGCAGCAGCAGCTGCAGCGAATAGCACAGCTGCAGCTCCAACAACAG
GTTGCTCAGAACC
                           gttgctcagaacc 862
                                                            CTGCAGCAGATGCATCACACACAGCACCACCAGCCGCCACCAGCCCCAGCAGCCTCCA
                                                                          ATTCAGCAGCCTCCGATGCAGCAGCCACAGCCTCCGCCCTCCCAGGCTCTGCCCCAGCAG
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AAI20017

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                                                                                                                                                                                                                                                                                                                                                                                                 The present invention relates to human single exon nucleic acid probes (SENP). The present sequence is one such probe. The SENPs are derived from human HeLa cells. The SENPs can be used to produce a single exon microarray, which can be used for measuring human gene expression in a sample derived from human cervical epithelial cells. By measuring gene expression, the probes are therefore useful in grading and/or staging of diseases of the cervix, notably cervical cancer.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at the probability of the probability of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 316 BP; 81 A; 104 C; 87 G; 44 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                             at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 25; SEQ ID No 9950; 487pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human genome-derivec single exon nucleic acid probes useful for analyzing gene expression in human cervical epithelial cells -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-488901/53.
241 tac 243
                             614 tac 616
                                                  181 agcagcagcagcagcagcagcatctaattaaattgcatcatcaaaatcagcaacagg 240
                                                                      554 agcagcagcagcagcagcagcatctaattaaattgcatcatcaaaatcagcaacaga 613
                                                                                                                                                                                                 434 agcagcagcaggcgg:gctacagcagcagcagcagcagcagcagcagcagcagcagtaccagg 493
                                                                                                                                                                                                                                                               374 cccagctgcagctccagcaggtggcgctgcagcagcagcagcagcagcagcagcagttccagc 433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (MOLE-) MOLECULAR DYNAMICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30-JAN-2001; 2001WO: US00670
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         09-AUG-2001.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cervical cancer;
                                                                                                                 121 ctcagcagagtgcca::gcagcagcagttccaagcagtagtgcagcagcagcagcagctcc 180
                                                                                                                                      494 ctcagcagagtgcca:gcagcagcagttccaagcagtagttgcagcagcagcagcagctcc 553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Probe; human; microurray; gene expression; cervical epithelial cell;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12-OCT-2001 (first entry)
                                                                                                                                                                             61 agcagcaggcggcgctacagcagcagcagcagcagcagcaacagcagttccagg 120
                                                                                                                                                                                                                                            1 cccagctgcagctccagcaggtggcgctgcagcagcagcagcaacagcagcagttccagc 60
                                                                                                                                                                                                                                                                                                                                      Local
                                                                                                                                                                                                                                                                                                                       242;
                                                                                                                                                                                                                                                                                                                                      Similarity
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                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                  13.9%;
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                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                            Score 241.4; DB 22; Length 316; Pred. No. 8.1e-34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rank DR;
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RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 99.6%;
Matches 242; Conservation
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03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention relates to single exon nucleic acid probes (SENP). The present sequence is one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of human genetic disorders.
614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 316 BP; 81 A; 104 C; 87 G; 44 T; 0 other;
                                                          554 agcagcagcagcagcagcagcatctaattaaattgcatcatcaaaatcagcaacaga 613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 25; SEQ ID No 13901; 654pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human placenta -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           04-FEB-2000;
26-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         09-AUG-2001
                                      181 agcagcagcagcagcagcagcatctaattaaattgcatcatcaaaatcagcaacagg
                                                                                                                                                                 494 ctcagcagagtgccatgcagcagttccaagcagtagtagtgcagcagcagcagcagctcc 553
                                                                                                                                                                                                                                                                     434 agcagcagcaggcggcgctacagcagcagcagcagcagcagcaacagcagcagttccagg 493
                                                                                                                                                                                                                                                                                                                                                                      374 cccagctgcagctccagcaggtggcgctgcagcagcagcagcagcagcagcagttccagc 433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (MOLE-) MOLECULAR DYNAMICS INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30-JAN-2001; 2001WO-US00663.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               genetic disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200157272-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Probe; microarray; human; placenta; antenatal diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Probe #13901 used to measure gene expression in human placenta sample.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17-OCT-2001 (first entry)
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                                                                                                                                                                                                                                    61 agcagcagcaggcggctacagcagcagcagcagcagcagcaacagcagcagttccagg 120
                                                                                                                                                                                                                                                                                                                                        1 cccagctgcagctccagcaggtggcgctgcagcagcagcagcaacagcagcagttccagc 60
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tac 616
                                                                                                                                       ctcagcagagtgccatgcagcagcagttccaagcagtagtgcagcagcagcagcagctcc 180
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2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-0236359.
2000GB-0024263.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 241.4; DB 22; Length 316; Pred. No. 8.1e-34;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
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21-SEP-2000;
27-SEP-2000;
                                                                                                                                                                                                                                                                          The present invention relates to novel single exon nucleic acid probes. The present sequence is one such probe. The probes are useful for measuring human gene expression in a human breast sample, where the prohybridises at high stringency to a nucleic acid expressed in the human breast. The probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human breast, staging, those diseases with polygenic actiology. The diseases include: breast cancer, disorders of development, inflammatory diseases of the breast, fibrocystic changes, proliferative breast disease and non-carcinoma tumours.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              09-OCT-2001
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30-JUN-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel single exon nucleic acid in a human breast .
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                                                                                                                                                                                                          Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           inflammatory disease;
                                                                                                                                                                                                                                                 Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      241 tac
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ctcagcagagtgccatgcagcagcagttccaagcagtagtgcagcagcagcagctcc
                                                                                             cccagctgcagctccagcaggtggcgctgcagcagcagcagcagcagcagcagttccagc 433
                                        agcagcagcaggcggctacagcagcagcagcagcagcagcagcagcagcagttccagg
                           agcagcagcaggcggctacagcagcagcagcagcagcagcaacagcagcagttccagg
                                                                              cccagctgcagctccagcaggtggcgctgcagcagcagcagcagcagcagttccagc
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                                                                                                                                                                                                           316 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID No 5716; 322pp; English.
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2000US-0632366.
2000US-0234687.
2000US-0236359.
                                                                                                                                        Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  to measure gene expression in human breast
                                                                                                                                                                                                           81 A; 104 C; 87 G;
                                                                                                                                                   13.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           proliferative breast disease; non-carcinoma tumour.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    316
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                                                                                                                                        0;
                                                                                                                                                   Score 241.4; DB 2
Pred. No. 8.1e-34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           probe used to measuring gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rank DR;
                                                                                                                                         Mismatches
                                                                                                                                                                                                             44 T; 0 other;
                                                                                                                                                                   DB 22; Length
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                                                                                                                                                                                                                                                                                                          inflammatory diseases
                                                                                                                                                                                                                                                                                                                                                                               where the probe
                                                                                                                                                                     316;
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Query Match
Best Local
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                                                                                    microarray, which can be used for measuring human gene expression in a sample derived from human cervical epithelial cells. By measuring gene expression, the probes are therefore useful in grading and/or staging of diseases of the cervix, notably cervical cancer.

Note: The sequence data for this patent did not form part of the printe specification, but was obtained in electronic format directly from WIPC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Probe; human; microarray; gene expression; cervical epithelial cell;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Probe #708 for gene expression analysis in human cervical cell sample.
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                                                                                                                                                                                                                    Claim 25;
                                                                                                                                                                                                                                                                                  WPI; 2001-488901/53
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cervical cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12-OCT-2001
                                                   Sequence 436 BP; 105 A; 127 C;
                                                                                                                                                                                The present invention relates to human single exon nucleic acid probes (SENP). The present sequence is one such probe. The SENPs are derived
                                                                                                                                                                                                                                            analyzing
                                                                                                                                                                                                                                                                                                           Penn
                                                                                                                                                                                                                                                                                                                                   (MOLE-)
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27-SEP-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121
                                                                                                                                                                 (SENP). The present sequence is one such probe. The SENPs are derived from human HeLa cells. The SENPs can be used to produce a single exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              241
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 Local Similarity
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                                                                                                                                                                                                                                                 genome-derived single exon nucleic acid probes useful for
                                                                                                                                                                                                                                                                                                                                   MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               243
                                                                                                                                                                                                                    SEQ
                                                                                                                                                                                                                                            gene expression
                                                                                                                                                                                                                                                                                                           Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                          2000US-0180312.
2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-0236359.
2000US-0236359.
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                                                                                                                                                                                                                    ID No 708; 487pp; English
 13.9%;
                                                                                                                                                                                                                                                                                                             Chen W,
                                                                                                                                                                                                                                            in human cervical epithelial cells
 Score 241.4; DB 2
Pred. No. 8.4e-34;
                                                   117 G;
                                                                                                                                                                                                                                                                                                             Rank DR;
                                                    87 T; 0 other
               22;
               Length
                                                                                           part of the printed directly from WIPO
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RESULY
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                                                                                                   Matches 242; Conservative
                                                                                                                                      Query Match
Best Local :
374 cccagctgcagctccagcaggtggcgctgcagcagcagcagcaacagcagcagttccagc 433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
                                                                                                                                                                                                                                                                                             The present invention relates to single exon nucleic acid probes (SENP). The present sequence is one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in sample; derived from human placenta. The probes are useful for antenatal diagnosis of human genetic disorders.
                                                                                                                                                                                                                                             Sequence 436 BP; 105 A; 127 C; 117 G; 87 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 25; SEQ ID No "19; 654pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-488897/53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               analyzing gene expression in human placenta
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 04-OCT-2000; 2000GB-0024263.
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26-MAY-2000; 2000US-)207456.
30-JUN-2000; 2000US-)608408.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         307
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                                                                                                                               Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     agcagcagcagcagcagcatctaattaaattgcatcatcaaaatcagcaacaga 613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               genome-derived single exon nucleic acid probes useful for
zing gene expression in human placenta -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2000US-J207456.
2000US-J608408.
2000US-J632366.
2000US-J234687.
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                                                                                                                            13.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chen W,
                                                                                                   0,
                                                                                                                        Score 241.4;
Pred. No. 8.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rank DR;
                                                                                                Mismatches
                                                                                                                     8.4e-34;
                                                                                                                                                    DB 22; Length 436;
                                                                                         1; Indels
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AAI00701
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      The present invention relates to novel single exon nucleic acid probes. The present sequence is one such probe. The probes are useful for measuring human gene expression in a human breast sample, where the probe hybridises at high stringency to a nucleic acid expressed in the human breast. The probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human breast, particularly those diseases with polygenic aetiology. The diseases include: breast cancer, disorders of development, inflammatory diseases of the breast cancer, disorders of development, inflammatory diseases of the breast, fibrocystic changes, prolliferative breast disease and non-carcinoma tumours.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at fip. wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              04-FEB-2000;
26-MAY-2000;
30-JUN-2000;
31-JUN-2000;
31-AUG-2000;
21-SEP-2000;
27-SEP-2000;
                                                                                                                                                                                                                                                               Claim 25; SEQ ID No 692; 322pp; English.
                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-476286/51.
                                                                                                                                                                                                                                                                                                    Novel single exon nucleic acid probe used to measuring gene expression in a human breast -
                                                                                                                                                                                                                                                                                                                                                                                                                          (MOLE-) MOLECULAR DYNAMICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               04-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Probe #692 used to measure gene expression in human breast sample.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAI00701;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29-JAN-2001; 2001WO-US00661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            09-AUG-2001.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              human; breast disease; breast cancer; development disorder;
                                                                                                                                                                                                                                                                                                                                                                                           Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; 2000US-0180312.
2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-0236559.
2000US-0236559.
                                                                                                                                                                                                                                                                                                                                                                                         Chen W, Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               non-carcinoma tumour.
                                                                                                                                                                                         where the probe
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SO

Sequence 436 BP; 105

A; 127 C; 117

G;

87 T; 0 other;

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B δÃ

Matches 242; Query Match Best Local Similarity

Conservative

0; Mismatches Score 241.4; Pred. No. 8.

Indels Length

0;

Gaps

8.4e-34; DВ 22;

13.9%; 99.6%;

374 cccagctgcagctccagcaggtggcgctgcagcagcagcagcagcagcagcagttccagc 433

cccagctgcagctccagcaggtggcgctgcagcagcagcagcagcagcagcagttccagc 246

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RESULT 11
AAB775507
ID AAB77555
XX AAF7555
XX O9-MAY
DE POly91
XX Animal
KW Heat S
KW Hoarkin
KW Parkin
KW Cancer
OS Drosop
XX 12-AUG
PR 12-AUG
PR 12-AUG
PR 12-AUG
PR 18-JAN
PR 19-MAY
XX 12-AUG
PR 18-JAN
PR 19-MAY
XX 12-AUG
PR 19-MAY
XX 12-AUG
PR 18-JAN
PR 19-MAY
XX 12-AUG
PR 18-JAN
PR 19-MAY
XX 12-AUG
PR 11-AUG
PR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Animal model; polyglutamine tract; neurodegenerative disorder; HDJ1; heat shock protein 40; tetratricopeptide repeat protein 2; TPR2; stroke myeloid leukaemia factor 1; MLF; human; fruit fly; Alzheimer's disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             09-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAF75507 standard; DNA; 486
      The present invention describes a method of screening for genes which modulate polyglutamine toxicity using animal models with polyglutamine sequences that cause toxicity in the animal. The model is preferably brosophila, and toxic polyglutamine sequences include the human and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200112238-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Polyglutamine tract coding sequence #2.
                                                                                                                                                                                                                                                              Identifying genes or other compounds that modulate polyglutamine toxicity, useful for treating Alzheimer's disease, Parkinson's disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22-FEB-2001
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   Drosophila, and toxic polyglutamine sequences include
                                                                                                                                                                                                                                                                                                                                                                                                                                     Benzer S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (CALY ) CALIFORNIA INST OF TECHNOLOGY.
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18-JAN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12-AUG-1999;
                                                                                                                                                                                                                                     Creutzfeldt-Jakob disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      agcagcagcaggcggcgctacagcagcagcagcagcagcagcaacagcagcagttccagg 493
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99US-0148934.
2000US-0177047.
2000US-0205720.
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                                                                                                                                                                275pp;
                                                                                                                                                                       English
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 486 BP; 193 A; 164 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 head trauma
                                                                                                                                                          latency-associated nuclear antigen; LANA; gamma-2 herpes virus; Human herpes virus 8; HHV8; rhadino virus cis-acting element; RVCAE; Kaposi's sarcoma; primary effusion lymphoma; PEL; human immunodeficiency virus; HIV; multicentric Castleman's disease;
                                                                                                                                                                                                                                                                                      AAA30290;
                                                                                                                                                                                                                                                                                                             AAA30290 standard;
                       misc_signal
                                                           misc_signal
                                                                                                                                   Kaposi's sarcoma-associated herpesvirus
                                                                                                                                                                                                            Kaposi's sarcoma-associated herpesvirus; KSHV; rhadino virus
                                                                                                                                                                                                                                     Kaposi's sarcoma-associated herpesvirus LANA gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        373 acccagctgcagctccagcaggtggcgctgcagcagcagcagcagcagcagttccag 432
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        atacagcagcagcagcagctgcagcgaatagcacagctgcagctccaacaacagcaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gctcagcagagtgccatgcagcagcagttccaagcagtagtgcagcagcagcagctc
                                                                                                                                                                                                                                                                                                                                                                         cagcagcaacaacagcagcagcaacagact 447
                                                                                                                                                                                                                                                                                                                                                                                     cagcagccaccgatgcagcagccacagcct 762
                                                                                                                                                                                                                                                                                                                                                                                                                         cagcagcagcagcagcagcagcagcagcagcagcagctttggaggcccagccaccaatt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cagcagcagcagcagcagcatctaattaaattgcatcatcaaaatcagcaacag
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                                                                                                                                                                                                                                                             (first
                                                             /product= "LANA"
40..50
                        190..210
                                                                                   /*tag=
                                   /note= "nuclear localisation signal,
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/note= "nuclear localisation signal,
                                                                                                            Location/Qualifiers
                                                  /*tag=
                                                                                                                                                                                                                                                                                                               DNA;
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68.2%;
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Pred. No. 4.4e-
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Best Local :
1798 cagcagcaggatgagcagcaggatgagcagcagcaggatgagcagcagcagcaggatgag 1857
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (KSSV) latency—associated nuclear antigen (LANA) gene KSHV is also known as Human Herpes Virus 8 (HHY8) and belongs to the rhadino virus, or gamma-2 herpes virus class. The LANA protein is necessary for the efficient persistence of rhadino virus DNA in mammalian cells. Persistent rhadino virus infection is implicated in a variety of diseases e.g. kaposi's Sarcoma (KS), Primary Effusion Lymphoma (PEL) and multicentric Castleman's disease. In addition, KS is a common malignancy in HTV patients. KSHV persists in host cells in a latent form. One of the few genes expressed from the latent viral DNA is LANA, LANA associates with both human chromosomes and with the rhadino virus cis-acting element (RVCAE), thereby providing a tethering function: the KSHV DNA episome is "tied" to the host chromosomes. This allows the viral DNA to persist in the host cohromosomes. This allows the viral DNA to persist in molecules that inhibit LANA interaction with RVCAE, thereby interfering with the latency cycle of this virus. Potential antiviral treatments for the host call after a series of the viral bank directions for the host call. The present sequence with RVCAE.
                                                                                1738 cagcagcgggagcca@agcagcgggagccacagcagcgggagccacagcagcaggatgag 1797
                                                                                                                                                                  1681 cagcgggagccacag:agcgggagcca---cagcagcgggagccacagcagcgggagcca
                                                                                                                                                                                                                                                  1561 cagcaggagccacagragcaggagccacagcagcaggagccacagcagcaggagccacag 1620
                                                                                                                                                                                                                                                                                                                                                                                                                          1501 cagcaggagccacaa: agcaggagccacagcagcaggagccacagcagcaggagccacag 1560
                        676 cagcagcagcagcagcagcagcagcaggcatttggaggcccagccaccaattcag 735
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 3489 BP; 1053 A; 862 C; 1137 G; 437 T; 0 other;
                                                                                                             616 cagcagcagcaacagcagctgcagcgaatagcacagctgcagctccaacaacagcaacag 675
                                                                                                                                                                                                                                                                                                            496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence is the Kaposi's sarcoma-associated herpesvirus, (KSHV) latency-associated nuclear antigen (LANA) gene. KSHV is also known
                                                                                                                                                                                             556 cagcagcagcagcagcagcatctaattaaattgcatcatcaaaatcagcaacagata 615
                                                                                                                                                                                                                                                                                                                                                               436 cagcagcagcggcg;tacagcagcagcagcagcagcagcagcagcagttccaggct 495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the above mentioned liseases may therefore be based on LANA deregulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Fig 6; 70pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Treating or preventing a disease associated with rhodino virus infection in a mammal which includes Kaposi's Sarcoma and Primary
                                                                                                                                                                                                                                                                                                                                                                                                                                                  376 cagctgcagctccag.aggtggcgctgcagcagcagcagcagcagcagcagttccagcag 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P-PSDB; AAY96255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19-NOV-1998;
21-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19-NOV-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (KIEF/) KIEFF E D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25-MAY-2000
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                                                                                                                                                                                                                                                                                              cagcagagtgccatgcagcagcagttccaagcagtagtgcagcagcagcagcagctccag
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99US-0298568.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 181.2; DB Pred. No. 3.8e-23
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RESULT 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAF8290
                                                                                                                                       A composition for use in gene therapy comprises an expression vector that includes a nucleic acid sequence encoding a nucleic acid bindi
                                                                                                                                                                                        P-PSDB; AAB62331
                                                                                                                                                                                                                                 Robertson ES,
                                                                                                                                                                                                                                                                                          01-OCT-1999;
                                                                                                                                                                                                                                                                                                                     29-SEP-2000; 2000WO-US26908
                                                                                                                                                                                                                                                                                                                                                    12-APR-2001.
                                                                                                                                                                                                                                                                                                                                                                                 WO200125484-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Histone H1; tethering protein; LANA; gene therapy; multiple sclerosis; Parkinson's disease; Huntington disease; diabetes; human herpesvirus 8 KSHV; latency-associated nuclear antigen; LANA; ds.
                                                                                                                                                                                                                                                              (UNMI ) UNIV MICHIGAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kaposi's sarcoma associated herpesvirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2158 caggatgagcagcagcagg 2179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nucleotide sequence of KSHV tethering protein, LANA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29-JUN-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAF82901 standard; DNA; 3489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1036 acagctcaggctgcccagatgg 1057
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2098 caggagcagcaggatgagcaggagcagcaggatgagcaggagcagcaggatgagcagcag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2038 cagcagcaggatgagcagcagcaggatgagcagcaggatgagcagcagcaggatgag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1978 cagcagcaggatgagcagcagcaggatgagcagcagcaggatgagcagcagcaggatgag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1918 cagcagcaggatgagcagcaggatgagcagcagcaggatgagcagcagcaggatgag 1977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1858 cagcagcaggatgagcagcaggatgagcagcagcaggatgagcagcagcaggatgag 1917
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAF82901;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        976 atggtggtgcagccgccagtgcagccccaggtgcagcagcagcagcagcagcagtacag 1035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          916 caageteteeetggacaaatgttgtataeeceaaceaectgaaatttgteegageteeg 975
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                                                                                                                                                                                                    2001-281736/29.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cagaaccaaccatcacaactcccgccacagtcgcagacccagcctttggtgtcacaggcg 915
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                                                                                                                                                                                                                                                                                          99US-0410399
                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
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The invention provides a composition comprising nucleic acid, histone HI protein and expression vector operationally encoding a protein suitable for tethering the nucleic acid to the histone HI protein, where the tethering protein is LANA. The composition is useful in aiding the retention of the viral DNA in the host cell. The viral vector encodes a protein suitable for tethering DNA to Histone HI. Methods for screening

Disclosure; Fig 9A; 60pp; English.

protein

acid binding

KSHV LUR DNA (nucleotides 105,301-137,507).

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RESULT 1
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1621
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                                                                                                                                                                                                                                                                                                                                                                                                                    1918
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                                                                              AAV73805 standard;
                                                                                                                                                            2158 caggatgagcagcagcagg
                  25-FEB-1999
                                                AAV73805;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cagctgcagctccagcaggtggcgctgcagcagcagcagcagcagcagcagttccagcag 435
                                                                                                                                                                                                                                                                                                                                                                          cagaaccaaccatcacaactcccgccacagtcgcagacccagcctttggtgtcacaggcg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cagcagcaggatgagcagcaggatgagcagcaggatgagcagcaggatgag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cagcagcagcagcagcagcatctaattaaattgcatcatcaaaatcagcaacagata
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cagcagagtgccatgcagcagttccaagcagtagtgcagcagcagcagcagctccag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cagcagcaggcggcgctacagcagcagcagcagcagcagcagcagcagttccaggct 495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cagcagcagcagcagctgcagcgaatagcacagctgcagctccaacaacagcaacag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cagegggagecacageggggggeca---eageagegggagecacageagegggageca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          acagctcaggctgcccagatgg 1057
                                                                                                                                                                                                                        caggagcagcaggatgagcaggagcaggatgagcaggagcagcaggatgagcagcag
                                                                                                                                                                                                                                                     atggtggtgcagcagccccagtgcagccccaggtgcagcagcagcagcagcagtacag
                                                                                                                                                                                                                                                                                                                                                     cagcagcaggatgagcagcaggatgagcagcaggatgagcagcagcaggatgag
                                                                                                                                                                                                                                                                                                                                                                                                                   cagcagcaggatgagcagcaggatgagcagcaggatgagcagcaggatgag
                                                                                                                                                                                                                                                                                                                                                                                                                                     cagatgcatcacacagcaccaccagccgccaccagccccagcagcctccagttgct 855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cagecacegatgeagecaceagecteegeceteecaggetetgecceageagetgeag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cagcagcaggatgagcagcaggatgagcagcaggatgagcagcagcagcaggatgag
                                                                                                                                                                                                                                                                                        cagcagcaggatgagcagcaggatgagcagcagcaggatgagcagcagcaggatgag
                                                                                                                                                                                                                                                                                                                     caagctctccctggacaaatgttgtatacccaaccaccactgaaatttgtccgagctccg
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                (first entry)
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                                                                                                                                                             2179
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Pred. No. 3.8
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Best Local Similarity
                                                                                                                                                                                                                                                                                                  This sequence is a fragment of the Kaposi's sarcoma-associated herpesvirus (KSHV) LUR (long unique region). This fragment contains coding regions for ORF65 which encodes capsid protein IV, ORF66, ORF67 which encodes tegument protein IV, ORF68 which encodes a glycoprotein, ORF69, K12 which encodes kaposin, K13, ORF72 which encodes cyclin D, ORF69, K12 which encodes kaposin, K13, ORF72 which encodes cyclin D, ORF73 which encodes immediate early protein (IEP), K14 which encodes OX-2 (V-adh), ORF74 which encodes G-protein coupled receptor, ORF75 which encodes tegument protein/FGARAT, K15, KSHV is a new human Herpesvirus (HHV8) believed to cause Kaposi's sarcoma (KS) which is the most common form of neoplasm occurring in persons with acquired immune deficiency syndrome (AIDS). The DHFR protein is useful for vaccination, prophylaxis, diagnosis and treatment of a subject with Kaposi's sarcoma and for detecting expression of a DNA virus associated with Kaposi's
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        dihydrofolate reductase; LUR; long unique region; vaccine; prophylax diagnosis; treatment; HHV8; capsid protein IV; tegument protein IV; glycoprotein; kaposin; cyclin D; immediate early protein; IEP; OX-2; v-adh; G-protein coupled receptor; FGARAT; ds.
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cagcagcagcagcagcagcagcagcagcaggctttggaggcccagccaattcag
                                  cagcagcagcaacagctgcagcgaatagcacagctgcagctccaacaacagcaacag
                                                                                                   CAGCGGGAGCCACAGCAGCGGGAGCCA - - - CAGCAGCGGGAGCCACAGCAGCGGGAGCCA
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Pred. No. 5.1e-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAV19941 standard; DNA; 137507 BP
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           complement (88410..88910)
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comp.ement (27137...27424)
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/projuct= complement-binding protein
8699..11236
                                   /product= glycoprotein L
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complement (17261..17875)
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1142..2794
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                                                                                                            glycoprotein M
                                                                                                                                                                                                                                                                interferon regulatory factor 1
     This sequence represents the long unique region and terminal repeat of the Kaposi's sarcoma-associated herpes virus (KSHY). KSHY is also known as human herpes virus 8 (HHV8). This sequence contains the DNAs of the invention which encode KSHY polypeptides selected from: (a) viral can be invention which encode KSHY polypeptides selected from: (a) viral frequency protein (MIP) II; (b) viral interleukin-6 (II-6); (c) viral IRF 1; (d) complement-binding protein; glycoproteins B, M or L; (d) capsid protein IV encoded by ORF65; and (e) immediate early protein encoded by ORF63 that belied probes for the nucleic acid, proteins encoded by it, and antibodies (Ab) specific for the proteins are useful for concluded by ORF63; had (e) immediate early protein encoded by it, and antibodies (Ab) specific for the proteins are useful for concluded by ORF63; and (e) it have a second in the protein gamples. HHV8 infections can be treated with antisense error triplex forming molecules or agents that bind specifically to the protein. Ab may be used for prophylaxis or treatment of HHV8 infection, while the protein can be used in protective vaccines. Ab may also be used to differentiate between lymphomas, and HHV8 may be implicated in many cother lymphoproliferative diseases such as lymphomas, leukaemia, splenomegaly and mycosis fungoides. Cells and animals containing the used as targets for antivital drugs, e.g. dihydrofolate reductase gene can be inhibited with methotrexate. These can also be used to determine the inhibited with methotrexate. These can also be used to determine can be used to determine the inhibited with methotrexate. These can see the second as containing frames.
Sequence 137507 BP; 32579 A; 37795 C; 35758 G; 31375 T; 0 other;
                                                     81 open reading frames.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New nucleic acid encoding Kaposi's sarcoma associated herpes virus proteins - useful for, e.g. detecting levels of HHV8 in, and preparation of vaccines for treatment of, HIV patients
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25-JUL-1996;
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96US-0708678.
96US-0728323.
96US-0747887.
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/product= interferon regulatory factor 2
89600..90541
/*tag= i
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Qy Q Db γΩ ρy QΨ δÃ В γQ 망 ρ В В Ş Ъ B Query Match 10.4
Best Local Similarity 55.1
Matches 376; Conservative 125199 CAGGAGCAGCAGGATGAGCAGGAGCAGCAGGAGCAGGAGCAGGATGAGCAGCAG 125140 125319 CAGCAGCAGGATGAGCAGCAGCAGGATGAGCAGCAGCAGCAGCAGCAGCAGGATGAG 125260 125379 CAGCAGCAGGATGAGCAGCAGCAGGATGAGCAGCAGGATGAGCAGCAGGATGAG 125320 125439 CAGCAGCAGGATGAGCAGCAGGATGAGCAGCAGGATGAGCAGCAGGATGAG 125380 125499 CAGCAGCAGGATGAGCAGCAGGATGAGCAGCAGCAGGATGAGCAGCAGCAGGATGAG 125440 125139 CAGGATGAGCAGCAGCAGCAGG 125118 1036 acagctcaggctgcccagatgg 1057 496 916 676 cagcagcagcagcagcagcagcagcagcaggctttggaggcccagccaccaattcag 735 616 cagcagcagcaacagcagctgcagcgaatagcacagctgcagctccaacaacagcaacag 675 556 976 atggtggtgcagcagccccagtgcagccccaggtgcagcagcagcagcagcagcagtacag 1035 736 cagecacegatgeageagecacageetteegeetteegegetetgeeecageagetgeag 795 cagcagcagcagcagcatctaattaaattgcatcatcaaaatcagcaacagata 615 caagctctccctggacaaatgttgtatacccaaccaccactgaaatttgtccgagctccg 975 cagcagagtgccatgcagcagcagttccaagcagtagtgcagcagcagcagcagctccag 555 cagaaccaaccatcacaactcccgccacagtcgcagacccagcctttggtgtcacaggcg 915 10.4%; Score 181.2; DB 19; Length 137507; 55.1%; Pred. No. 6.2e-23; tive 0; Mismatches 303; Indels 3; G 3; Gaps 1;

Search completed: February 28, 2002, 19:22:15 Job time: 4978 sec

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pir2:T23107
pir2:T47141
pir2:T48814
pir2:T48814
pir2:T48877
pir2:T3828
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Query length: 1740
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Date: Feb 28, 2002 7:24 PM
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-Q=/cgn2_1/USPf0_spool/USO9668119/runat_28022002_084716_19297/app_query.fasta_1.1824
-DB=FIR_68 -QFMY=fastan -SUFFIX=rpr -GAPOP=12.000 -GAPDXT=4.000
-MINMATCH=0.100 -LOOPCL=0.000 -LOOPEXT=0.000 -FGAPOP=4.500
-QGAPDXT=0.050 -XGAPOP=10.000 -XGAPDXT=0.500 -FGAPOP=6.000
-FGAPDXT=7.000 -YGAPOP=10.000 -YGAPDXT=0.500 -DELDP=6.000
-DELEXY=7.000 -START=1 -MATRIX=Dlosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0
-ALIGN=15 -MODE-LOCAL -OUTFMT=pfs -MATRIX=DRM=ext -MINLEN=0
-ALIGN=15 -MODE-LOCAL -OUTFMT=pfs -GON1_1_89 -NCPU=6 -ICPU=3
-MAXLEN=20000000000 -USER=USO9668119_@CGN1_1_89 -NCPU=6 -ICPU=3
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5.2e-09
4.5e-09
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6.7e-10
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3.2e-10
4.6e-10
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1.5e-11
1.6e-11
2.3e-11
2.1e-11
2.6e-11
3.4e-11
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2.1e-14
1.5e-13
2.3e-13
4.0e-12
3.4e-12
4.1e-12
                                                                                                                                                                                        6.1e-09
7.9e-09
7.2e-09
7.2e-09
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1.5e-09
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4.8e-09
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3.1e-09
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Documentation
                                                                                                            antifreeze glycoprotein precurs
hypothetical protein KO6A9.la
transcription factor shn - fru
glutenin high molecular weight
                                                                                                                                                                                                                                                                    | hypothetical protein 1 - Africa
| fibroin - Chinese oak silkmth
| stripe a/b protein - fruit fly
| omega secalin precursor (clone
! regulatory protein SNF5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | ALR protein - human
| ALR protein - human
                                        ! female sterile homeotic prote
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          neurogenic locus mam protein
high molecular mass nuclear an
transcription activator GAL11
fibroin - Chinese oak silkmoth
hypothetical protein ZK84.1 - C
trfA protein - silme mold (Did
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       d-box-binding factor - slime md in hypothetical protein C24A8.3 in hypothetical protein C37A2.2 in hypothetical protein 87B1.5 in hypothetical protein 87B1
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eye development protein canoe
hypothetical protein T05A10.1
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CYC8 protein - yeast (Saccharon
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                                                                                transcription activator GAL11
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pir2:S18235
pir2:T25795
pir2:B30843
pir2:T06982
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Map position: 12
C; Superfamily: human ALR protein
C; Keywords: alternative splicing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R; Prasad, R.; Zhadanov, A.
Oncogene 15, 549-560, 1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: mRNA
A; Residues: 1-4957 < PRA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    seq_name: pir2:T03455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Align seg 1/1 to: T03455 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3240 roGlnGlyProHisArgGlnValLeuMetThrGlnSerArgValLeuSer 3256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3224 .proAlaGlnValAlaValLeuGlnGlnGlnHisProGlyAlaLeuGlyP 3240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3214 ProProGlnGlyProGlnGlyMetLeuGly.....
                                                                                                                                                                                                                                                                                                                                                 3273 lThrAlaGlnGlnGlnGlnGlnGlnGlnHisGlnGlnGlnGlySerM 3290
                                                                                                                                                                  3307 ProLysLeuSerAlaGlnProMetGlySerLeuGlnGlnLeuGlnGlnGl 3323
                                    512 AGCAGCAGTTCCAAGCAGTAGTGCAG...CAGCAGCAGCAGCTCCAGCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             326 GGATGGCCCCTCACAGCATGGCTGTCGTGTCTACGGCAACTCCACAGACC 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       276 CATGGGACAGCCAATGTCTCTCTCAGGGCAGCCGCCTCCTGGGACCTCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             226 CCTCCTCGGGGCCCGGGACAGTCTCTGGGGGGGGGGGTAGCTTTGGTGC 275
                                                                                                                          GCAGCAGCAGCACCAGCAGCAGTTCCAGGCTCAGCAGAGTGCCATGC 511
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                                                                                     nGlnGlnLeuGlnGlnGlnGlnGlnGlnGlnGlnGln.....G
                                                                                                                                                                                                                                                           etAlaGlyLeuSerHisLeuGlnGlnSerLeuMetSerHisSerGlyGln 3306
                                                                                                                                                                                                                                                                                                                                                                                            GGCGCTGCAGCAGCAGCAGCAACAGCAGCAGTTCCAGCAGCAGCAGCAGC 445
                                                                                                                                                                                                                                                                                                                                                                                                                                    SerProGlnLeuAlaGlnGlnGlyGlnGlyLeuMetGlyHisArgLeuVa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Quality:
Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Zhadanov, A.B.; Sedkov, Y.; Bullrich, F.; Druck, T.; Rallapalli, R.; Ya
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     43.586
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1.587
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324.00
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281.10
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                                                                                                                                                                                                                .....CTACAGCAGCA 461
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1.4e-08
1.4e-08
1.7e-08
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359
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hypothetical protein F53F10.
glutenin high molecular weigh
glutenin low molecular weigh
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                                               558
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3645	roGlnLeuArgHisLeuSerProGlnGlnGlnGlnGlnLeuGlnAlaLeu 3	629
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950 3612	GTGTCACAGGCGC.AAGCTCTCCCTGGACAAATGTTGTATACCCAACC ::::::::::::::::::::::::::::	901 3598
900 3597	TTGCTCAGAACCAACCATCACAACTCCCGCCACAGTCGCAGACCCAGCCT S	ο υ
850 3583	CACACACAGCACTACCAGCGGCGCACCAGCAGCCCCAGCAGCAGCCTCCAG	י ס כ
U	OHisLeuLeuAlaGlnProSerValSerLeuGlyAspGlnProGl	்
804		
3549	lyGlySerHisGlyGlnLeuGlySerGlySerSerSerGluAlaSerSer	3533
804		804
804 3533	TCTGCCCCAGCAGCTGCAGCAG	777 3516
	::: nProGlnProGlnProSerSerLeuGlnLeuGlnProProLeu	0
776	. CAGCCACAGCCTCCGCCCTCCCAG	UI
_ vi	AspSerClnLenLenLenWalcln	3483
3483	yGlyProLeuAlaIleGlyThrThrProGluSerMetAlaThrGluProG	່່ດ
750		75
3466	AspProAlaValSer:erGluAlaThrGluGlyProSerThrHisGlnGl	3450
750		750
3449	lyAlaLeuGlyProThrLeuLeuThrGlyLysGluGlnAsnThrVal	3433
750		750
3433	<b>-</b> -	3416
750	AGCAGCCACCGATGCA	717
3416	lnGlnGlnGlnGlnGln	0
716	TO THE TO DECIDE ON THE	69
	<b>X</b>	659 383
658 3383	ACAGATACAGCAGCA(:CAACAGCAGCTGCAGCGAATAGCACAGCTGCAGC	3366
608 3366	CAGCAGCAGCAGCAGCATCTAATTAAATTGCATCATCAAAATCAGCA	O O

9 4 4 7 7 8 8 8 8 8 7 7 7 7 7 7 7 7 7 7 7	93CCCATGCTGTCCCCGCGCGCCAGCGGGCCAGCAGGTGCAGCAGGTGCAGCAGGTGCAGCAGGTGCAGCAGGTGCAGCAGGTGCAGCAGGTGCAGCAGGTGCAGCAGGTGCAGCAGGTGCAGCAGCAGGTGCAGCAGCAGGTGCAGCAGCAGGTGCAGCAGCAGCAGTGCAGCCCCCCCC
	<u></u>
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1363	CTCACCTGGACCTTTAAACACACCTGTGAACCCCAGCTCTGTCATGAGCC	1314
on H		4047
04		4031
1263	rioriosiyAlabedselinksiyriovalbe	1219
1218	TCACAGCCCAACTCCAACGTCAGCTCTGGC	1188
1187 4016	CAGTCGATGCCCCCTCCCCCCAGCCGTCCCCGCAGCCCGGCCAGCCAGCCCAGCCCAGCCCAGCCCAGCCCAGCCCAGCCCAGCCCAGCCCAGCCCAGCCCAGCCCAGCCAGCCCAGCCCAGCCCAGCCCAGCCCAGCCCAGCCCAGCCCAGCCCAGCCCAGCCAGCCCAGCCCAGCCCAGCCAGCCCAGCCAGCCCAGCCCAGCCAGCCCAGCCAGCCCAGCCAGCCCAGCCAGCCCAGCCCAGCCAGCCCAGCCAGCCCAGCCCAGCCCAGCCCAGCCCAGCCCAGCCCAGCCCAGCCCAGCCCAGCCAGCCCAGCCAGCCAGCCCAGCCAGCCAGCCCAGCCAGCAACACAACA	1138 4000
1137 3999	CCCATGCTGTCCTCGCCGTCACCGGGCCAGCAGGTGCAGACCCCG    :::   ::::	1093 3984
1092 3984	GCTCCCGGAGTCCAGGTCAGCCAGAGCAGCCTC	1060 3967
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950 3917	TTGGTGTCACAGGCGCAAGCTCTCCCTGGACAAATGTTGTATACCCAACC::::::::::	901 3903
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804		804
804 3838	TCTGCCCCAGCAGCTGCAGCAGATGCAT	777 3821
3821	roGlnProGlnPr	3805
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3804	ysProSerLeuSerGlyAspSerGln	3788
750		750
3788	$y {\tt GlyProLeuAlaIleGlyThrThrProGluSerMetAlaThrGluProG}$	3771

367 rGlyTyrProGlnAsn\alala
GATGGCCCCTCACAGCITGGCTGTCGTGTCTACGGCAACTCCACAGACCC 37
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248 CTCTGGGCGGGATGGGTAGCTTTGGTGGCCATG 279 ::        334 snalaGlyGlyTyrGlrThrSerGlnGlnGlnValAlaAsnGlnVal 350
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148 GCTTCCGTCAGTGATCCTATGAATGCACTCCAGAGGCCTGACTGGCGGACC 197
Align seg 1/1 to: T2039: from: 1 to: 796
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1364 CAGCTGGCTCCAGCCAK(GCTGAGGAGCAGCAGCAGCTGGACAAGCTGAAG 1413
4063 ProThrHisProGlyThrProLysProGlnGlyPr 4074

640		626
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767	AGCCACCAATTCAGCAGCCACCGATGCAGCCAGCCACAGCCTCCGC	718
475	lnGlnGlnAsnGlnTyrGlyGlyMetGlnProAsnProTyrValGln	459
717	CAGCAGCAGCAGCAGCAGCAGCAGCAGCAGGCTTTGGA	677
5 \	ACADEMOCIAN ADEACACADE LOCADE CONTROL OF THE ACADEMOCIAN ADEACADE ADEACADA ADEACADE ADEACADA ADEACADA ADEACADA ADEACADA ADEACADA ADEACADA	4
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626	ATCTAATTAAATTGCATCAACAAATCAGCAACAGATACAGCAGCAGC	577
425		412
576	AGCAGCAGCAGCAGCTCCAGCAGCAGCAGCAGCAGCAGCA	527
411		403
526	AGCAGCAGTTCCAGGCTCAGCAGAGTGCCATGCAGCAGCAGTT	477
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42 42	
1121 TGGCCCGGTGACGGCGAGGACAGCATGGGGAGGCTGCTCTGGCTGACCTG 1072	•
1165 ACGGCTGGGGGGGAGGGGGCATCGACTGCGGGGTCTGCACCTGC 1122 ::	
1215 AGAGCTGACGTTGGAGCTGTGAGCTGGGCTGGGCTGGCGGGG 1166	
1265 GGCTGCGGTGAGGGCCAGGAAGCTACTGGGAGATGGGCAGGGCC 1216         ::::::     9 GlyCysGlySerSerCysGly	
Align seg 1/1 to: A38346 from: 1 to: 230	₽
uS-09-668-119-1/rev x A38346	al U
Alignment_scores:  Quality: 431.00 Ratio: 3.241 Gaps: 26 Percent Similarity: 39.583 Percent Identity: 30.655	a 1
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R; Wood, L.; Mills, M.; Hatzenbuhler, N.; Vogeli, G. 7. Biol. Chem. 265, 21375-21380, 1990 7.Title: Serine-rich ultra high sulfur protein gene expression in murine hair and skin d 7.Reference number: A38346; MUID:91065960 7.Accession: A38346	A A A J R
<pre>eq_documentation_block: iltra-high-sulfur keratin 1 - mouse ;;Species: Mus musculus (house mouse) ;Date: 28-Jun-1991 #sequence_revision 28-Jun-1991 #text_change 24-Sep-1999 ;;Accession: A38346</pre>	000 E
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1404 CAAGCTGAAGCTGTCGAAGTACATCGAGCCCCTGCGCCGC 1446  ::: :::::: !:                699 pSerLysAsnGluSerThrLysLysThrGluThrLeuLeuArgAspThrT 716	
1375 AGCCAGGCTGAGGAGCAGCAGTACCTGGA 1403 ::::::	
1325 CTTTAAACACCTGTGAACCCCAGCTCTGTCATGAGCCCAGCTGGCTG	
1278 AGTGACGGCGCGGACCCCACAGAACTTCAGTGTCCCCTCACCTGGAC 1324 :::	
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1071	_ G	1022
43	alc	47
1021 47	GCTGCTGCTGCACCTGGGGCTGCACTGGGGGCTGCTGCACC 9           SCYSCYSLYSProValCys	981
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930	ACACCAAAGGCTGGGTCTGCGACTGTG	881
59	CysGlyGlyCy	æ
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68	ySerSerCysGlyGlyCysGlySerCys	77
830	GGCGGCTGGTGGTGTGTGTGATGCATCTGCTGCAGCTGCTGGGG	781
78	lyserserCys	81
780	GAGGCTGTGGCTGCTGCATCGGTGGCT	737
82	ysGlySerSerCysCys	89
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90	ValProVal	98
695	TGCTGTTGC	669
, ,		
115		131
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493	TGCTGTTGCTGCTGCTGCTGCTGC	459
173		186
458	GCGCCGCCTGCTGCTGCTGCTGGAACTGCTGCTG	418
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373	TCTGTGGA 366	
220	LyCysGly 222	

seq\_documentation\_block:
ultra-high-sulfur keratin 2 - mouse
C; Species: Mus musculus (house mouse)

seq\_name: pir2:B38346

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C;Date: 31-Mar-1992 #seq.ence_revision 31-Mar-1992 #text_change 24-Sep-1999 C;Accession: A38666; B38:46 R;Wood, L.; Mills, M.; Hatzenbuhler, N.; Vogeli, G. J. Biol. Chem. 266, 4024, 1991 A;Title: Serine-rich ultra high sulfur protein gene expression in murine hair and skin A;Reference number: A386(0; MUID:91154184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Note: this is a correction
R;Wood, L.; Mills, M.; Hatzenbuhler, N.; Vogeli, G.
J. Biol. Chem. 265, 21375-21380, 1990
J. Biol. Chem. 265, 21375-21380, 1990
A;Title: Serine-rich ultra high sulfur protein gene expression in murine hair and skin A;Reference number: A38346; MUID:91065960
A;Accession: B38346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     alignment_scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: GB:M37759; NID:g200961; PIDN:AAA40106.1; PID:g200962
A;Note: the sequence reported in this paper has been corrected. See A38660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: DNA
A; Residues: 1-223 <WO2>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Quality: 427.00 Length: 256
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Percent Similarity: 49.219 Percent Identity: 37.891
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    766 GCGGAGGCTGTGGCTGCATCGGTGGCTGCTGAATTGGTGGCTGGGCC 717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          866 GGTTGGTTCTGAGCAACTGGAGGCTGCTGGGGGCTGTGGTGGCGGCTGGTG 817
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         916 GCGCCTGTGACACCAAAGGCTGGGTCTGCGACTGTGGCGGGAGTTGTGAT 867
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            966 GACAAATTTCAGTGGTGGTTGGGTATACAACATTTGTCCAGGGAGAGCTT 917
                                                                                                                                                                                                                                                                                              92 oCysCysSerSerGly?ysGlySerSerCysCysGlnSerSerCysCysL 109
                                                                                                                                                                                                                                                                                                                                                                                                                                         76 GlnSerSerCysCysLysProCysCysCysGlnSerSerCysCysLysPr 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        62 ...GlyGlyCysGlySerCys...GlyGlyCys...LysGlyGlyCysCys 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   39 GlyCysLysGlyGlyCysGlySerCysGlyGlyCysLysGlyGly..... 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26 ysCysCysValPro.....ValCysSerCys...SerSerCysGly 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17 .....CysGlySerSerCysCysLysProValC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 CysCys.....GlyCysSerGlyGlyCysGlySerSerCysGlyGly.. 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                alignment_block:
US-09-668-119-1 x T44768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Introns: 1/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R;Chen, L.; DeVries, A.L.; Cheng, C.H.C.
Proc. Natl. Acad. Sci. U.S.A. 94, 3817-3822, 1997
A;Title: Convergent evolution of antifreeze glycopeptides in Antarctic notothenioid f A;Reference number: 222834; MUID:97268653
A;Recession: T44768
A;Rocession: T44768
A;Rocession: T44768
A;Rocession: T44768
A;Rocession: T44768
A;Rocession: T44768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 antifreeze glycopeptide AFGP polyprotein precursor [imported] - Boreogadus saida C;Species: Boreogadus saida C;Species: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jul-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: DNA
A; Residues: 1-507 < CHE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: EMBL:U43200; NID:g2078482; PIDN:AAC60129.1; PID:g2078483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           seq_name: pir2:T44768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Align seg 1/1 to: T44768 from: 1 to: 507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Accession:
                             334 CCTCACAGCATGGCTGTCGTGTCTACGGCAACTCCACAGACCCAGCTGCA 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     184 CTGACTGGCGGACCTGCTGCGGGAGCCGCTGGAATTGGCATGCCTCCTCG 233
                                                                                                                                                                                                                                                                                                                                284 AGCCAATGTCTCTCAGGGCAGCCGCCTCCTGGGACCTCGGGGATGGCC 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               234 GGGCCCGGGACAGTCTCTGGGCGGGATGGGTAGCTTTGGTGCCATGGGAC 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              214 ...CysAlaProValCys 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         198 ysCysGlnSerSerCysCysLysProCysCysGlnSerSerCys... 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     436 GCTGCTGGAACTGCTGCTGTTGCTGCTGCTGCAGCGCCACCTGCTGG 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           473 ....recrecrecrecrecreraececececec.....recr 437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   169 CysGlnSerSerCys......CysLysProCysCysCysGlnSe 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  152 lnSerSerCysCysLysProCysCysSerSerGlyCysGlySerSerCys 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          386 AGCTGCAGCTGGGTCTGT 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        181 rSerCysCysLysProCysCysCysGlnSerSerCysCysLysProCysC 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           512 TGCATGGCACTCTGCTGAGCCTGGAACTGC.....TGCTGTTGC..... 474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          553 GGAGCTGCTGC.....TGCTGCACTACT...GCTTGGAACTGCTGC 513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      137 ....LysProCysCysGysGlnSerSerCysCysLysProCysCysCysG 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            588 TTTAATTAGATGCTGCC......TGCTGC.....TGCTGCTGCT 554
                                                                                                             41 ......AlaThrProAlaThr..AlaAla 47
                                                                                                                                                                                                                                                                                                                                                                                                       18 rGluGlnHisGlnLeuLeu.....ValAlaA 27
                                                                                                                                                                                                                                                        27 rgProAlaAlaAlaAlaArgAlaAlaThrProAlaThrAla..... 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 LeuThrGlySerCysLeuLeuGlyProSerCysThrSerSerProArgTy 18
Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    399.50
1.297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  54.225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length: 568
Gaps: 20
Percent Identity: 29.225
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, 48	rAlaAlaThrAla	4. [
64		<u>`</u>
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81	laAlaThrAlaAlaThrAlaAlaTh	7
16 98	GCAGTTCCAAGCAGTAGTGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG	14
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14	hrP	.31
03	TCAGCAACAGATACAGCAGCAGCAACAGC	35
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36	ATAGCACAGCTGCAGCT	
48	hralaalaThralaalaThralaalaThrSeralaThrAlaalaThral	
64	aklaArgAlaAlaThrProAlaThrAlaAlaThrProAlaThrProAlaT 1	.81
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14	::::::::       roAlaArgAlaAlaArgAlaAlaThrProAlaThrAlaP	
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3	hrProAlaThrAlaAlaThrProAlaThrAlaAlaThrAlaAlaT	247
21	TCCCTGGACAAATGTTGTATACCCAACCACCACTGAAATTTGTCCGA	970
48	laProThrAlaAlaThrPr	55
71	GTGGTGCAGCAGCCCCCA	866
55	ArgAlaAlaArgAlaAlaThrProAl	272
99	:	1028
272	aAlaThrProAlaThrProAlaThrProAlaThrAlaAlaThrAspAla	882
200	**CAGACAGCTCAGGCTGCCCA	0054
	THE TABLET IN PROPERTY OF THE	
305	OAlaThrAlaAlaThrProAlaThrProAlaThrAlaAlaThrAlaAlaT	322
105	CCGTCACCGGGCCAGCAGGTGCAGACCCCGCAGTCGAT	1148
322	hrAlaAlaThrAlaAlaThrPro	338
149	CCCTCCCCCCAGCCGTCCCCGCAGCCCAGCCAGCCAGCTCAC	1192
339	AlaThrProAlaThrAlaAlaThrProAlaThrAlaAlaThrAlaAlaTh	355

Cross-references: GB:D49534; NID:g705386; PIDN:BAA08478.1; PID:g705387 Genetics: F1yBase:FBgn0000340 Superfamily: GLGF domain homology	A; Cross-references: C; Genetics: A; Gene: cno A; Cross-references: C; Superfamily: GLGF F; 848-924/Domain: GL alignment_scores: Quality: Percent Similarity
fruit fly (Drosophila melanogaster) er vision 03-Oct-1995 #text_change 21-Jul Kondo, S.; Ueda, R.; Togashi, S.; Hira rotein containing a GLGF/DHR motif and :95212910 red with conceptual translation	seq.documentation_block: eye development protein canoe - C;Species: Drosophila melanogast C;Date: 03-Oct-1995 #sequence_re C;Accession: A56158 R;Miyamoto, H.; Nihonmatsu, I.; Genes Dev. 9, 612-625, 1995 A;Title: canoe encodes a novel p A;Reference number: A56158; MUID A;Accession: A56158 A;Status: preliminary; not compa A;Molecule type: mRNA A;Residues: 1-1893 <miy></miy>
:A56158	seq_name: pir2:A56
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ACCGACCAAACA	1631 ACCGACCA     481 ThrAlaAl
GAAACTCAAGAATGACATGCGGTGCCCACTCCCCCACCGCCCCCGGTGCC 1630    :::   :::    :::	1581 GAAACTCA 469
TCGAAGCGGTGTCCCCTGAAGACCTTGCAAAAGTGTGAGATCGCCCTGGA 1580   :::      :::      oAlaThrGlyAlaThrProAlaThrAlaPro 468	1531 TCGAAGCGGTGT   :::    458 oAlaThrGly
AAAAGGACCTGAGTAAGATGAAGAGCCTTCTGGACATTCTGACAGACCCC 1530 :::         ArgAlaAlaThrPr 458	1481 AAAAAGGACCTGAG ::: ::: 454 ArgAlaAla
CGAGCCCCTGCGCCGCATGATCAACAAGATCGACAAGAACGAAGAACAAGAA 1480 ::::: :::   ::: :::	1431 CGAGCCCC ::::: 437 laAlaThr
GCTGAGGAGCAGCAGTACCTGGACAAGCTGAAGCAGCTGTCGAAGTACAT 1430 ::::::::::    ::::::: ::::::::::::::::	1381 GCTGAGGA: 421 rAlaAlaT
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CCCACAGAACTTCAGTGTCCCCTCACCTGGACCTTTAA 1330 	1293 CCCACAGA     388 rAlaAlaT
CTGCCCAGCCCTCACCGCAGCCCCAGAGCCCCAGTGACGGCGCGGAC 1292 ::: ::    ::: ::	1243 CTGCCCAG :: 372 AlaArgAl
ralaala.ThralaalaThralaalaThralaalaThrProalaargAla 371	355 rAlaAla.

642 1271	618 GCAGCACCAACAGCAGCYTGCAGCGA	
617 125 <b>4</b>	ATACA :::   nLeuProLeuGl	
591 1237	ATTAAATT3	
57 <b>4</b> 1221	2 CCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC	
551 1204	CAAGCAGTAGTGCAGCAGCAGCAGCAGCT :::::: 	
522 1187	AGGCTCAGCAGAGTGCCATGCAGCAGCAGTTC	
472 1174	436CAG:AGCAGGGGGGGGGTACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG	
435 1157	CCAGCAG	
420 1140	AGCAGGTGGCGCTGCAGCAGCAGCAGCAGCA        ::: 	
370 1124	ATGGCTG1 TyrAsnGl	
320 1107	GCAGCC ::::: snGluAr	
270 1090	nGluGlnGlyPheT	
256 1074	CCTCCTCGGGGCCCGG    :::    eu3lyGlnProAsnGlySerc	
212 1057	CACTCCAGAGCCIGACTGGCGGACCTGCTGCGGGAGCC ::   :::::    :::   erLeuHisAsnAsnThrSerGlyMetGlyGlyIleGlyGlyAla	
168 1040	CATTCATAA JAAGAAATCTCAAGCTTCCGTCAGTGATCCT    :::      :::::::::: AsnSerLysSerArgSerThr	
118 1033	CAAGACCCGGGACGAATACCTTTCTCTCGTGGCCAGGCTC       ::	
68 1023	19 GCACACAGTAAATCCASCAAGGATATGGAGAGCCATGTTTTCCTGAAGGC	
	Align seg 1/1 to: A56158 from: 1 to: 1893	
	US-09-668-119-1 x A56158	ω

CTGGGCCTGCCCAGTA
1094 CCATGCTGTCCTCGCCGTCACCGGGCCAGCAGGTGCAGACCCGGG
1044 GGCTGCCCAGATGGTGGCTCCCGGAGTCCAGGTCAGCCAGAGCAG :::                1500 nGluLeuPheArgLeuAlaGlyGlyGlyGlnValSerAlaIleGl
994 CCAGTGCAGCCCCAGGTGCAGCAGCAGCAGCAGACAGGAGACAG :::          :::       1486GluGluGlnAspGlnGluGlnGlnTyrAspLysGluAsnV
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915 GCAAGCTCTCCCTGGACAATGTTGTATACCCAACCACCACTGAAA ::: :::
901TrGGTGTCAC :::   : 1436 MetArgArgGluHisIleArgGlnTrpArgGluGlnGlnIleSerG
884 AGTCGCAGACCCAGCCT
846 TCCAGTTGCTCAGAACCAACCATCACAACTCCCG            :::      1402 oProLysGlySerTyrValalaSerAsnGlnGlyAsnAsnArgPro
838CAGCAG
815 ACCACCAGCCGCCACCACAGCCC
778 .CTGCCCCAGCAGCTGCAGCAGATGCATCACACACACAG
730 ATTCAGCAGCCACCGATGCAGCCAGCCACAGCCTCCGCCCTCCCAGGC :::   :::    :::
701 AGCAGCAGGCTTTGGAGGCCCAGCCACCA
651 GCTGCAGCTCCAACAACAGCAACAGCAGCAGCAGCAGCAGCAGCAGCAG
ο .
71 etGlnAsnValAsnAspPheAlaGlyGlyTyrGlnAsnGlySerL
642

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alignment_scores:
Quality:
Ratio:
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A; Introns: 188/3; 240/3; 420/1; 570/3; 596/1; 732/3; 778/3; 851/3; 1359/2; 1394/2; 1434,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
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A;Cross-references: EMBL:Z68108; PIDN:CAA92133.1; GSPDB:GN00028; CESP:T05A10.1
A;Experimental source: clone T05A10
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R;Sulston, J.
submitted to the EMBL Data Library, November 1995
submitted to the EMBL Data Library, November 1995
A;Reference number: Z19898
A;Accession: T24490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         seq_documentation_block:
hypothetical protein T05A10.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
C;Accession: T24490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             alignment_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               seq_name: pir2:T24490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Gene: CESP:T05Al0.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Quality: 397.00
Ratio: 1.481
Percent Similarity: 44.741
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1612 AsnGlnLeu...ThrMetLeuAspLysAspAsnAsnAsnGlu 1624
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1595 luArgHisLeuHisThrGluHisProIleSerAsnLeuAlaLysGluLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1382 CTGAGGAGCAGCAGTACCTGGACAAGCTGAAGCAGCTGTCGAAGTACATC 1431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1432 GAGCCCCTGCGCCGCATGATCAACAAGATCGACAAGAACGAA 1473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1282 ACGGCGCGGACCCCACAGAACTTCAGTGTCCCCTCACCTGGACCTTTAAA 1331
575 AGCATCTAATTAAATTGCATCAT.....CAAAATCAGCAACAGATACAG 618
                                                                                                                                            525
                                                                                                                                                                                               201
                                                                                                                                                                                                                                                   475 CAACAGCAGCAGTTCCAGGCTCAGCAGAGTGCCATGCAGCAGCAGTTCCA 524
                                                                                                                                                                                                                                                                                                      461
                                                                                                                                                                                                                                                                                                                                                                                                                167 aGlnAlaArgGlnGlnGlnGlnAlaGlnLeuAlaAlaIleGlnGlnG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       411 GCAGCAACAGCAGCAGTTCCAGCAGCAGCAGCAGCGGCGCGCTACAGCAGC 460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             151 AlaArgHisGlnAlaGluGlnGlnAlaGlnGlnGlnAlaGlnGlnGlnAl 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 361 GCAACTCCACAGACCCAGCTGCAGCTCCAGCAGGTGGCGCTGCAGCAGCA 410
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                                                                                                                                                                                            GlnGlnGlnPheGln...GlnGlnGlnLeuGlnGlnGlnGlnLeuGl 216
                                                                                                                                                                                                                                                                                                                                                             AG......CAGCAGCAGCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            yAlaProSerSerProSerLysSerGlnLysSerAlaSerPheAlaAsnG 1595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SerIleLeuLysHisAsnArgTyrSerGluGlyGlyValGlyProSerGl 1578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AGCAGTAGTGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length: 599
Gaps: 24
Percent Identity: 29.549
                                                                                   233
                                                                                                                                                                                                                                                                                                                                                             474
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N 5	TGTCCCCTCACCTGGACCTTTAAACACACCTGTGAACCCCAGCTCT	0
1307 505	Se AG	125; 48;
1257 488	TCCTGCCCAGCCCCTCA ::: alalaValThrThrAla	1201 47:
1207 472	AACTCCAACG ;;; ;;;;;; ;;	116: 45:
55	CCGCAGTCGATGCCCCCCCCCCCCAG	<b>4</b> 3
1134 438	CGGGCCAGCAGGTGCAGACC        ::: snGluGlnGlnArgMet	108
1084 422	CAGATGGTGGCTCCCGGAGTCCAGGTCAGCCAGA     :::	104:
1040 405	ACAGCAGTACAGACAGC    :::   nArgThrValSerGlnAlaLeuGlnTyrIl	102: 38:
1020 388	GTGGTGCAGCAGCCCCAGTGCAGCCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCA	97: 37:
970 373	AAATGTTGTATACCCAACCACTGAAATTTGTCCGAG    :::       heuleuLeuGlnGlnGlnAlaG	92: 35:
920 356		90. 34:
906 340	TCACAACTCCCGCCACAGTCGCAGACCCAGCCTTTGGTG	85 <sup>7</sup>
856 324	CACACAGCACCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG	807 313
806 312	CAGCCTCCGCCCTCCCAGGCTGCCCCAGCAGCTGCAGCAGATGCATCA	757 300
756 299	AATTCAGCAGCCACCGATGCAGCCA	70° 28:
706 283	AACAGCAACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCA	26
656 266	CAGCAACAGCAGCTGCAGCGAATAGCACAGCTGCA    ::::::   :::     HisvalGlnSerArgGlnMetGlnProSerGlnGlnSerGl	61: 25:
249	${\tt nGinValLeuGlnIleSerGlnAlaGlnGlnGlnAlaGln}$	23:

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A;Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R;Newfeld, S.J.; Tachida, H.; Yedvobnick, B.
J. Mol. Evol. 38, 637-641 1994
A;Title: Drive-selection equilibrium: homopolymer evolution in the Drosophila gene maste
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   seq_documentation_block:
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C:Species: Drosophila virilis
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 17-Nov-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1621 ....CCCCGGTGCCACCGACCAAACAGCAGTACCTATGCCAGCCGCTCCT 1666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1573 GCCCTGGAGAAACTCAAGAATGACATGCGGTGCCCACTCCCCCACCGC.. 1620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1549 ......AAGACCTTGCAAAAGTGTGAGATC 1572
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1525 ......GACCCCTCGAAGCGG. 1539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1486 .....GACCTGAGTAA;ATGAAGAGCCTTCTGGACATTCTGACA..... 1524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1474 ..... GACAGAAA, AAAG ..... 1485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1443 CCGCATGATCAACAAG ...ATCGACAAGAACGAA...... 1473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1393 CAGTACCTGGACAAGCTGAAGCAGCTGTCGAAGTACATCGAGCCCCTGCG 1442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    652 oGluCysIleTyrCys:\( \text{ysLeuThrPheProAsnGluAlaGlyLeuGlnA } \) 669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          619 euPheGluLeuSerGlySerLysHisPheMetGlySerLeuThrSerGly 635
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           711 .....ProLeuAlaAlaHisThrProSerAsnMetPro 721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                694 aLeuLysArgArgHisThrHisGlnAspAlaThrLeuAlaMetHisSer. 710
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              636 GlnProLeuLeuArgP::oIleGlnAlaHisAsnAspProAsnTyrThrPr 652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            602 oGlyProLysAspSerArgMetLeuGlnAlaAlaSerArgSerGlnSerL 619
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 586 SerSerValAspHisA;pSerAsnSerGlyGlySerThrArgThrSerPr 602
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     686 AlaGlnGlu......GlyAsnProHisSerAl 694
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          669 laHisGluValValCy;3GlyLysLysLysGluLeuGluLysAlaGlnIle 685
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  569 spProValIleArgLy;sLysArgProTyrHisArgGlnIleGlyAlaGln 585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                552 raspHisIleSerArg[leIleSerGluAsnGluValIleLeuGlnGlyA 569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     539 .....SerSerSerSysAlaAlaSerSerGlyAsnGluSerMetSe 552
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    723 nGlnGlnHisLeuProProGlnPheHisGlnLysAlaProGlyGlyG 740
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      610 GlyGlyProThrAlaGlyGlyGlyGlyGlyGly......AsnGlyPr 623
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            804 AsnMetGlyValProMetGlyGlyAlaGlyAsnPheAlaLySGlnGlnGl 820
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             476 AACAGCAGCTTCCAGGCTCAGCAGAGT......504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              773 nAlaMetGlnGlnGlnGln.....GlnGlnGlnGlnGlnGlnGlnG 787
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    426 GTTCCAGCAGCAGCAGCAGCGGCGCTACAGCAGCAGCAGCAGCAGCAGC 475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              757 PheTyrSerSerProAsnAspPheAspLeuLysHisLeuGlnGlnGlnGl 773
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               415 .....CAACAGCAGCA 425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    740 lyProGlyMetAsnValGlnGlnAsnPheLeuAspIleLysGlnGluLeu 756
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              379 .....CTGCAGCTCCAGCAGGTGGCGCTGCAGCAGCAGCAG..... 414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 372 GACCCAG...... 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   707 GlyGlyFheProAsnAspPheAlaMetGlyProAsnProThrGlnGl 723
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     322 TCGGGGATGGCCCCTCACAGCATGGCTGTCGTGTCTACGGCAACTCCACA 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      690 lyGlnGlyGlnGlnGlnGlnGlnGlnGlnProArgTyrAsnAspTyr 706
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 673 nAlaProGlnGlnGlnGlnGlnHisGlyGlnMetMetGlyGlyProG 690
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        657 HisValProProHisGlyMetGlnGlnGlnGlnFroGlnGlnGlnGlnGl 673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        640 etAlaGluGlnHisGlnHisLysSerAlaMetGlyGlyMetGlyGlyPhe 656
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           623 oGlyGlyLeuMetSerGluHisSerLeuAlaAlaGlnThrLeuLysGlnM 640
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     190 GGCGGACCTGCTGCGGGAGCCGCTGGAATTGGCATGCCTCCTCGGGGCCC 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        244 ...... CAGTCTCTGGGCGGGATGGGTAGCTTT 270
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90	3 ATAGCACAGCTGCAGCTCCAACAACAGCAACAGCAGCAGCAGCAGCAGCAGCAGCAG	692 920
9	3 GCAGCAGCAGCAGCCTTTGGAGGCC	720
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72	0	720
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95	4 IleGlnValSerAlaGlyGlnHisLeuHisLeuSerSerAspMetLysSe	970
72	1CAGCCAC	727
97	0 rAsnValSerValAlaAlaGlnGlnGlyValPhePheSerGlnGlnA	987
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10;	.yGlyProAsnGlyProGlnGlnGlnGlnProA	1037
84	7CCAGTTGCTCAGAACCA	867
103	AspGlyPheSerLeuSerGln	1053
10:	68 TCACAACTCCCGCCACAGTCGCAGACCCAGCCTTTGGTGTCACAGGCGCA ::::::         :::         ::::::         54 MetasnPheThrGlnGlnGlnGlnGlnAlaAlaAlaAlaAlaAlaAl	917 107(
9	TCTCCCTGGACAAATGTTGTATA	967
10'	70 aAlaAlaAlaGlnGlnGlnAla	1079
و	GAGCTCCGATGGTGGTGCAGCAGCCCCCAGTGCA	0
0	0AlaAlaAlaGlnGlnGlnGlnGLnValProProAsnMetArgGL	106.
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11	11AlaAlaGlnAlaGlnAlaAlaAlaAsnAlaAsnGlyGlyPro	112
11	18 GCCAGCAGGTGCAGACCCCGCAGTCGA	114
11	.25 lyGlyAsnValProLeuMetGlnGlnGlnGlnGlnThrPro	
<u>س</u> ا د	.47 CCCCCTCCCCCCCAGCCGTCCCCGCAGCC	119
ب <u>د</u> ب د		o i
_	46 vserd vasnalaservald v	

A;Cross-references: EMBL:235981; NID:g536449; PIDN:CAA85069.1; PID:g536450; MIPS:YBR1	
Accession Molecule 1	
prences nucleo H.; Ma The I	
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A;Fitle: Analysis of a 70 kb region on the right arm of yeast chromosome II. A;Fitle: Analysis of a 70 kb region on the right arm of yeast chromosome II. A;Reference number: S48255; MUID:95208357 A;Reference number: S48255; MUID:95208357	
A;Residues: 1-965 <man> A;Residues: 1-965 <man> A;Cross-references: EMBL:X66247; NID:g3548; PIDN:CAA46973.1; PID:g3550 R;Mannhaupt, G; Stucka, R.; Ehnle, S.; Vetter, I.; Feldmann, H. Vosct 10 1363-1381 1994</man></man>	
A;Title: Molecular analysis of yeast chromosome II between CMD1 and LYS2: the excisio A;Reference number: \$25364; MUID:92327848 A;Accession: \$25365 A;Molecule type: DNA	
ce_revision 17-Apr-1993 #text_change 11-Jan-2000; S45980; S25404; S25405; A30906; S44692; Ehnle, S.; Vetter, I.; Feldmann, H.	
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•	
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1424 AGTACATCGAGCCCCTGCGCCGCATGATCAACAAGATCGACAAGAACGAA 1473 ::::            :::         1228 nIleMetArgAlaGlnAlaMetGlnHisGlnGln	
1386 GGAGCAGCAGTACCTGGACAAGCTGAAGCAGCTGTCGA 1423     ::      :: :::::    1212 GlyGlyProValProAlaAlaSerGlnAlaLysPheLeuGlnGlnGlnGl 1228	
1358 TGAGCCCAGCTGGCTCCAGCCAGGCTGA	
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1297 CAGAACTTCAGT	
1247 CCAGCCCCTCACCGCAGCCCTCCCAGAGCCCAGTACCCCCGCCACCCCCCCC	

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SerThrAlaGlu	ACCTGGAC	GTCATG    ::: ValGlnProThrV	TCAGTGTCCCCTC       erValserProse	CTCACCGCAGCCC :::    nGluProProGln	AACGTCAGCTCTG	CCCCCCAGCCGTC	CTCGCCGTCACCG  :::        :rAsnGlnSerPro	ATGGTGGCTCCCG :::    :LeuValAsnThrA	CCCAGGTGCAGCA         ::::: roGlnValLysLy	ATGGTGGT ::: rHisAlaIlePr	GGACAAATGTTG :::::: SerSerSerThr	CACAGTCGCAGA ::: lnLysArgTyrM	GCAGCCTCC	CTGCAGCAGATG       :::::: LeuGlnSerVal	CAGC:::: InAlaMetGluH	aggcccagccacc :::      leThrGlnProTh	ACAGCAACAGCAG  ::: nLysGlyValSer	CAGCAGCAGCAAC               GlnGlnGlnGlnG
ThrIleGlu TGATCAACAAGA	AAGCTGAAGCA	AGCCCAG      alserserGlus	ACCTGGACCTTT                 rThrLysProLe	ETCCCAGAGCCCA :::        GluAlaSerPro	GCCC :: snSe	CCCGCAGCCCGG	3GGCCAGCAGGTG  ::: DAlaValValGlu	GAGTCCAGGTCA :::::::::::: AlaThrSerIleG	.GCAGCAGACAG :   ::: :sGlnLysLeuA	GCAGCAGCCCCC     	TATACCCAACCA::::   :::: HisThrGluAsn.	CCAGCCTTTGG ;;; tGluGlyAlaI	AGTTGCTCAGAA  :::     :: oLeuIleGlnHi	CATCACACACAG :::         GlnHisProGln	CTCCGCCCTCCC	AATTCAGCAGCC :::     rValileGlnAl	CAGCAGCAGCAG    ::: ValGlnMetLeu	AGCAGCTGCAGC             lnGlnLeuGlnP
euSerThrAla CGACAAGAACG	GTCGAAGTAC	CTGGCTCCAGCC :::::::::: erSerThrThrL	AAACACACCTGT         uAsnThrGluPr	.GTGACGGCGCGG ::: AlaGluGluAla	CTCCCAGTAGC		3CAGACCCCGCAG :::::: 1SerAsnThrAsn	AGCCAGAGCAGCC ::::::::::::::::::::::::::	CAGTACAGACAGC ::::: snSerProAsnSe	A       OAlaThrGlyIle	CCACTGAAATTT(      AsnThrLysSerl	TGTCACAGGG :: :: : leHisThrLeuV	CCAACCATCACA::::: :::    ::::: :::    :::::::::::::	CACCACCAGCCGC:::	AGGCTCTGCCC.::             erGlnLeuProP	ACCGATGCAGCA :::    aHisGlnLeuGl	CAGCAGCAGCAG :::        RsnProGlnGln	GAATAGCACAGC ::: roLeuProArgG
ThrVal AAGACA	ATCGAGC	AGGCTGA 1 ::   :: ysAlaAs 8	GAACCCC 1::: coGluSer 8	ACCCCAC 1	TTCCTGCC 1::: ValileG1 7	CACAGCCC 1       erGlnGlu 7	GTCGATGC 1:::: nAsn 7	CTCCCCAT 1 LysserGl 7	CTCAGGCT 1 ::::: erAsnIle 7	eThrAsnA 7	GTCCGAGC 9	CGCAAGCT 9	AC     nAsnValL	CCACCACA        GlnProGl	roGlnGln	GCCA      nProPheS	CAGCAGGC	TGCAGCTC

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seq_documentation_block:
RAE-28 - mouse
C:Species: Mus sp. (mouse)
C:Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 01-Dec-2000
C:Accession: I53172: I66850; I66851
R:Nomura, M.; Takihara, Y.; Shimada, K.
Differentiation 57, 39-50, 1994
A:Title: Isolation and characterization of retinoic acid-inducible cDNA clones in F9 cel
Drosophila polyhomeotic protein.
A;Reference number: I53172; MUID:94350162
A;Accession: I53172
A;Accession: I68850
A;Accession: I68850
A;Accession: I68850
A;Accession: I66850
A;Accession: I66851
A;Accession
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             seq_name: pir2:I53172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             lignment_block:
US-09-668-119-1 x I53172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Align seg 1/1 to: I53172 from: 1 to: 1012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1479 AAAAAAGGACCTGAGTAAGATGAAGAGCCTTCTGGACATTCTGACAGACC 1528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1579 GAGAAACT 1586
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1529 CCTCGAAGCGGTGTCCCCTGAAGACCTTGCAAAAGTGTGAGATCGCCCTG 1578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        909 laAlaThr 911
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          892 uAlaGluProAlaAlaSerArgAspAlaGluLysGlnGlnAspGluThrA 909
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             879 GluAsnGly.....ThrThrGluAlaSerAlaProSerThrGluGl 892
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        228 T.....CCTCGGGGCCCGGGACAGTCTCTGGGCGGGATGGGTA 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     178 CAGAGCCTGACTGGCGGACCTGCGGGAGCCGCTGGAATTGGCATGCC 227
310 CCTCCTGGGGACCTCGGGGATGGCCCCTCACAGCATGGCTGTCGTGTCTAC 359
                                                                                                                                                                                                               266 GCTTTGGTGCCATGGGACAGCCAATGTCTCTCTCAGGGCAG.....CCG 309
                                                                                                                                                                                                                                                                                                          276 oGlySerMetGlyProGlyGlyGlyGlyGlnAlaProGlyGlyLeuGlyG 293
                                                                                                                                  293 InLeuProSerSerGly.....LeuThrGlyGlySerCysPro 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                385.50
1.417
50.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length: 544
Gaps: 24
Percent Identity: 27.390
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1208	AGCCGTCCCCGCAGCCGGCCAGCCCAGCTCACAGCCCAACTCCAACG	UT.
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560	::: AlaLeuGlyLeuAlaGlnLeuAlaAlaAlaValPro	4
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548	::::::::::::::::::::::::::::::::::::::	532
1058	TGCAGCAGCAGCAGCAGCAGTACAGACAGCTCAGGCTGCCCA	1009
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517	IleGlnSerLysProProValAlaProIleLysProProGl	503
979	TGTATACCCAACCACTGAAATTTGTCCGAGCTCCGATG	930
502	ProGluProThrSerLysProProIlePro	493
929	CACAGTCGCAGACCCAGCCTTTGGT	880
492	ValGlnProMetLeuGlnSerSerProLeuThrLeuPr	476
879	CTCCAGTTGCTCAGAACCAACCATCACAACTCCCG	844
476	ValProProSerGlnSerGlnGlnAl	465
843	ACCAGCCGCCACCACCAGCCCCAGCAG	801
464	ProGlnValProProThrGln	454
800	AGCCACAGCCTCCGCCCTCCCAGGCTCTGCCCCAGCAGCTGCAGCAGAT	751
453	:::     ::: 	437
750	GCAGCAGGCTTTGGAGGCCCAGCCACCAATTCAGCAGCCACCGATGCAG	701
437	sLeuGlnLeuAlaGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnG	420
700	CTGCAGCTCCAACAACAGCAACAGCAGCAGCAGCAGCAGCAGCAGCAG	651
420	:::::    :::        nHisArgGlnSerGlnLeuLeuHisThrAlaThrHi	404
650	AGCAACAGATACAGCAGCAGCAACAGCAGCTGCAGCGAATAGCACA	604
403	ValIleGlnGlnG	389
603	GCAGCAGCAGCAGCAGCATCTAATTAAATTGCATCAAAAAT	560
389	rGlnIleGlnProHisSerLeuIleGlnGlnGlnGlnGlnIleHisLeuG	372
559	AGCAGCAGTTCCAAGCAGTAGTGCAGCAGCAGCAGCAGCTCCAGCAGC	510
372	ThralaThrProAlaProSerGlnThrLeuIleSerSerAlaThrTyrTh	356
509	GCAGCAGCAACAGCAGCAGTTCCAGGCTCAGCAGAGTGCCAT	460
355		339
459	CAGCAGCAGTTCCAGCAGCAGCAGCAGCGGCGCGCTACAGCA	410
339	GGCAACTCCACAGACCCAGCTGCAGCTCCAGCAGCTGGCGCTGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG	360 322
	ghysgrymngryvarvargineroLeuercoAldAldGuriirvari	

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seq_documentation_block:
    G-box-binding factor - s.
    C; Species: Dictyostelium
    C; Date: 06-Jan-1995 #sem
alignment_block:
US-09-668-119-1 x A53185
                                                                                                                                                                                                                                                                                                                A;Cross-references: GB:L29075; NID:g456561; PIDN:AAA21021.1; PID:g456562 C;Superfamily: G-box binding factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R;Schnitzler, G.R.; Fischer, W.H.; Firtel, R.A. Genes Dev. 8, 502-514, 1994
A;Title: Cloning and characterization of the G-box binding factor, an essential componen A;Reference number: A53185; MUID:94170994
A;Accession: A53185
                                                                                                                                                                                      alignment_scores:
                                                                                                                                                                                                                                                                        C; Keywords: DNA binding; transcription factor; zinc finger
                                                                                                                                                                                                                                                                                                                                                                         A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-708 <SCH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                seq_name: pir2:A53185
                                                                                         Percent Similarity: 43.185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -box-binding factor - slime mold (Dictyostelium discoideum)
Species: Dictyostelium discoideum
Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 24-Sep-1999
Accession: A53185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1608 ACTCC...CCCACCGCC.................CCCGGTGCCACCGACCAA 1639
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1558 CAAAAGTGTGAGATCGCCCTGGAGAAACTCAAGAATGACATGCGGTGCCC 1607
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1508 TTCTGGACATTCTGACAGACCCCTCGAAGCGGTGTCCCCTGAAGACCTTG 1557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1640 ACAGCAGTA. . CCTATGCCAGCCGCTCCT 1666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1458 GATCGACAAGAACGA&GACAGAAAAAAGGACCTGAGTAAGATGAAGAGCC 1507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1408 CTGAAGCAGCTGTCG&AGTACATCGAGCCCCTGCGCCGCATGATCAACAA 1457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1358 TGAGCCCAGCTGGCTCCAGCCAGGCTGAGGAGCAGCAGTACCTGGACAAG 1407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1308 TGTCCCCTCACCTGG&CCTTTAAACACACCTGTGAACCCCAGCTCTGTCA 1357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1273 ..... AGCCCAGTGFCGGCGCGCACCCACAGAACTTC.....AG 1307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1209 CAGCTCTGCCCCTGCCCCATCT...CCCAGTAGCTTCCTGCCCAGCCCCT 1255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     707 ValAlaLeuAlaProThrProSerAlaPro 716
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            690 ysAlaGluProValAlaSerLeuAsnAlaAsnProProAsnSerAspLeu 706
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  682 GluGlu.....GlyGluL 690
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        666 alLeuProThrLysAlaSerProAlaAlaGluSerPro...LysValIle 681
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     649 gLysAlaGluSerGluGluArgAspAspLeuSerAlaLeuAlaSerV 666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               635 rValHisLeuProGlyLysAlaGlnThr.....644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           602 hrLeuAlaProValGlnGlyThrAlaHisValValLysGlyGlyProThr 618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            585 aAlaProGlyAlaLetGlnGluCysProProAlaLetAlaAlaGlyMetT 602
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .....LeuAlaValLysAr 649
                                                                                                                                                         Quality:
                                                                                                                         Ratio:
                                                                                                                             383.00
1.272
                                                                       Gaps: 23
Percent Identity: 24.390
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Align seg 1/1 to: A53185 from: 1 to: 708
279 snAsnSerAsnAsnAsnAsnAsnAsnAsnAsnAsnAsnAsnSerHisGln 295
                                                                     846 ...... 846
                                                                                                                                                        262 oGlnSerLeuSerAsnSerGlyAsnAsnAsnAsnAsnAsnAsnAsnAsnAsnA 279
                                                                                                                                                                                                                                       846 T...... 846
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   153 MetGlnGlnGlnHisHisGlnGlnMetGlnGlnGlnGlnHisHi 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            246 GlnGlnHisGlnGlnGlnAsnGlnIleGlnMetValProGlnGlnPr 262
                                                                                                                                                                                                                                                                                                                                                                                                         796 CAGATGCATCACACACCACCACCACCACCACCACCACCCCAGCAGCC 845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   746 TGCAGCAGCCACAGCCTCCGCCCTCCCAGGCTCTGCCCCCAGCAGCTGCAG 795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     219 nGlnGlnHisHisGlnHisSerGlnProGlnGlnGlnHisGlnHisA 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               696 GCAGCAGCAGCAGGCTTTGGAGGCCCAGCCACCAATTCAGCAGCCACCGA 745
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              203 GlnGlnGlnHisHisGlnGlnGlnGlnGlnGlnGlnGlnHisHisGl 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            646 GCACAGCTGCAGCTCCAACAACAGCAACAGCAGCAGCAGCAGCAGCAGCA 695
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      186 euGlnGlnHisGlnHisGlnHisGlnGlnGlnGlnGlnGlnHis 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            605 AGCAACAGATACAG......CAGCAGCAACAGCAGCTGCAGCGAATA 645
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    169 sGlnGlnMetGlnGlnGlnGlnHisHisGlnGlnMetGlnHisHisGlnL 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              555 GCAGCAGCAGCAGCAGCAGCATCTAATTAAATTGCATCATCAAAATC 604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      505 GCCATGCAGCAGCAGTTCCAAGCAGTAGTGCAGCAGCAGCAGCAGCTCCA 554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               455 AGCAGCAGCAGCAGCAGCAACAGCAGCAGTTCCAGGCTCAGCAGAGT 504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         122 nGlnGlnAlaGlnGlnAsnGlnProProGlnGlnAsnGln........... 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            405 GCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCGGCGCGCTAC 454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           106 ProAsnGlnAsnProHisTyrAsnTyrGlnTyrGlnLeuMetPheMetGl 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     358 ... ACGGCAACTCCACAGACCCAGCTGCAGCTCCAGCAGGTGGCGCTGCA 404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              279 GGGACAGCCAATGTCT.....CTCTCAGGGCAGCCGCCTCCTGGGACCT 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        238 .....CCGGGACAGTCT...CTGGGCGGGATGGGTAGCTTTGGTGCCAT 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      230 CTCGGGGC..... 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   180 GAGCCTGACTGCGGACCTGCTGCGGGAGCCGCTGGAATTGGCATGCCTC 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 130 CATAACAAGAAATCTCAAGCTTCCGTCAGTGATCCTATGAATGCACTCCA 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    89 spGlyGlnTyrProAspMetProAsnMetValAspGlnTyrGlnTleHis 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 72 eLeuLeuProProSerSerIleMetSerSerAsnValPheProSerHisA 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          56 PheProProThrSerSerLeuLeuGlyGlySerSerAsnThrProSerPh 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                39 euProSerIlePheThrThrAlaGlnAsnGlnMetAsnProProIleLeu 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22 nThrIleGlyGlySerAspLeuSerAsnIleSerAlaLeuProLeuProL 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6 HisHisGlnGlyAsnSerSerSerSerSerSerSerSerProSerGl 22
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9	  roSerValLeuGlnSe	6
1257	CCAGTAGCTTCCTGCCCAGCCCCTC	1231
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1230	H :	1230
546	ThrSerSerSe	530
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513	sLysArgTyrPheCysLysGluCysLysLysProPheThrProValGlyA	496
1158		1158
496	CysPr	480
1158	cccc	1144
479	Φ-	472
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472	GlnAsnThrLe	455
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1074	CAGGCTGCCCAGATGGTGGCTCCCGGAGTCCA	1036
438		422
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933 394	AGTCGCAGACCCAGCCTTTGGTGTCACAGGCGCAAGCTCTCCCTGGACAA	884 379
379	lnValProGlnG	362
883	CCGCCAC	871
362	GluAlaAlaSerTrpLysHisAspLysArgArgTrpTrpCysLysGluCy	346
870		870
345	luLysLysAspSerSerGlyGlnThrIleProLysCysThrArgCysAsn	329
870		870
329	oSerProSerThrLysGlyLysArgLysHisHisGluThrSerAsnSerG	312
870		870
312	::::     :::     :uSerGlnAsnAsnThrSerGlySerAsnThrPr	296
870	TGCTCAGAACCAACCATCA	847

202GCGGGAGCCGCTGGAATTGGCATGCCTCCT 231 :::    :::   :::	110 TTATCCATTTTCGAGACATTCATAACAAGAAATCTCAAGCTTCCGTCAGT 159 ::::::::::::::::::::::::::::::::::::	60 CCTGAAGGCCAAGACCCGGGACGAATACCTTTCTCTCGTGGCCAGGCTCA 109    :::    :::            ::::::::    :: 562 ProAsnProGlnGlnMetargTleProGlnAlaGlnAsnGlnMetG1 578	Align seg 1/1 to: T25563 from: 1 to: 1307	alignment_block: US-09-668-119-1 x T25563	alignment_scores: Quality: 383.00 Length: 758 Ratio: 1.182 Gaps: 33 Percent Similarity: 42.744 Percent Identity: 23.483	A;Gene: CESP:C24A8.3 A;Gene: CESP:C24A8.3 A;Map position: X A;Introns: 42/3; 116/2; 165/1; 200/3; 233/3; 275/1; 318/1; 358/3; 397/3; 590/3; 606/3	A; Residues: 11307 <nel> A; Residues: 11307 <nel> A; Cross-references: EMBL:U80845; PIDN:AAB37980.1; GSPDB:GN00028; CESP:C24A8.3 A; Experimental source: strain Bristol N2; clone C24A8</nel></nel>	A;ACCESSION: T25563 A;Status: preliminary; translated from GB/EMBL/DDBJ A:Molecule type: DNA	R;Nelson, J.; Gattung, S. submitted to the EMBL Data Library, December 1996 A;Description: The sequence of C. elegans cosmid C24A8. A;Reference number: Z20051	<pre>seq_documentation_block: hypothetical protein C24A8.3</pre>	seq_name: pir2:T25563	1448 TGATCAACAAGATCGACAAGAACGAAGAACAAGAAAAAGGAC 1488 :::::::::::::::::::::::::::::::::::	1426TACATCGAGCCCTGCGCCGCA 1447 ::: 646 rGlyAlaLeuLeuSerSerAsnGlyIleAsnLeuAlaAsnLeuGlyAsnP 663	1378 CAGGCTGAGGAGCAGTACCTGGACAAGCTGAAGCAGCTGTCGAAG 1425 630 ProProLysSerSerSerLeuAsnAsnLeuAsnSerPheSerAsnTh 646	1337 CTGTGAACCCCAGCTCTGTCATGAGCCCAGCTGGCTCCAGC 1377 :::       :::::: ::: :::            613 lnAlaAsnSerIleLysProAspGlyGlyIleLeuIleSerGlyLeuSer 629	1290 GACCCCACAGAACTTCAGTGTCCCCTCACCTGGACCTTTAAACACAC 1336        :::                ::: 596 rCysSerProAsnProSerLeuProSerTleGlyGlyAsnLeuAsnSerG 613	580 SerSerIleSerGlnSerProLeuGlnLeuAsnTyrGlnThrProTh 596
		TTATCCATTTTCGAGACATTCATAACAAGAAATCTCAAGCTTCCGTCAGT::::::::::	CCTGAAGGCCAAGACCCGGGACGAATACCTTTCTCTCGTGGCCAGGCTCA     :::    :::            ::::::::    ProAsnProGlnGlnGlnMetArgIleProGlnAlaGlnAsnGlnMetGl TTATCCATTTTCGAGACATTCATAACAAGAAATCTCAAGCTTCCGTCAGT : :::          :::::     nGlnArgIleProGlnValSerProGlnGlnMet.Gln	seg 1/1 to: T25563 from: 1 to: 1307  60 CCTGAAGGCCAAGACCCGGGACGAATACCTTTCTCTCGGTGGCCAGGCTCA    :::    :::	lignment_block: US-09-668-119-1 x T25563  Align seg 1/1 to: T25563 from: 1 to: 1307  Align seg 1/1 to: T25563 from: 1 to: 1307  60 CCTGAAGGCCAAGACCCGGGACGAATACCTTTCTCTCGTGGCCAGGCTCA	lignment_scores: Quality: 383.00 Ratio: 1.182 Percent Similarity: 42.744 Percent Identity: 23.483  lignment_block: US-09-668-119-1 x T25563 Align seg 1/1 to: T25563 from: 1 to: 1307  Align seg 1/1 to: T25563 from: 1 to: 1307  60 CCTGAAGGCCAAGACCCGGGACGAATACCTTTCTCTCGTGGCCAGGCTCA    :::    :::       :::::::    562 ProAsnProGlnGlnGlnMetArgIleProGlnAlaGlnAsnGlnMetGl 110 TTATCCATTTTCGAGGACATTCATAACAAGAAATCTCAAGCTTCCGTCAGT :::::::    578 nGlnArgIleProGlnValSerProGlnGlnMet.Gln	200/3; 233/3; 275/1; 318/1; 358/3; 397/3; 590/3; 606,  Length: 758 Gaps: 33 Percent Identity: 23.483  Percent Identity: 23.483  Percent Identity: 23.483  Percent Identity: 23.483  Percent Identity: 23.483	; PIDN:AAB37980.1; GSPDB:GN00028; CESP:C24A8.3 ristol N2; clone C24A8 200/3; 233/3; 275/1; 318/1; 358/3; 397/3; 590/3; 606, 200/3; 233/3; 275/1; 230/3; 200/	ed from GB/EMBL/DDBJ ; PIDN:AAB37980.1; GSPDB:GN00028; CESP:C24A8.3 ristol N2; clone C24A8 200/3; 233/3; 275/1; 318/1; 358/3; 397/3; 590/3; 606, 200/3; 23	ary, December 1996 C. elegans cosmid C24A8. C. elegans cosmid C24A8. ed from GB/EMBL/DDBJ ; PIDN:AAB37980.1; GSPDB:GN00028; CESP:C24A8.3 ristol N2; clone C24A8  Length: 758	eq_documentation_block: pypothetical protein C24A8.3 - Caenorhabditis elegans species: Caenorhabditis elegans spate: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000 spacession: T25563 species: 1-007	Caenorhabditis elegans ns evision 15-Oct-1999 #text_change 18-Feb-2000  ary, December 1996 C. elegans cosmid C24A8.  ed from GB/EMBL/DDBJ  ; PIDN:AAB37980.1; GSPDB:GN00028; CESP:C24A8.3  ristol N2; clone C24A8  Length: 758 Gaps: 33  Percent Identity: 23.483  Percent Identity: 23.483	CGAAGACAGAAAAAGGAC 1488 :::::::::::::::::::::::::::::::::::	TACATCGAGCCCCTGCGCCGCA 1447 ::: :::::::::::::::::::::::::::::::	rGGACAAGCTGTAAGCAGCTGTTCGAAG 1425   :::::   ::::   :::  suannasnLeuAansGerPheSerAanTh 646   :::::  :::      ::::   :::      :::::       :::::       :::::       :::::       :::::       ::::       :::::      :::::      :::::      ::::::	TCTGTCATGAGCCCAGCTGGCTCCAGC 1377	CCCTCACCTGGACCTTTAAACACAC 1336

. 32	95	45 79	13 62	73 45	28	16	99	83 4	66	149	139	116	999				241 639	232 622
	GCTGCAGCAGATGCAT(:ACACACAGCAGCACCAGCCGCCACCA83;	ATGCAGCAGCCACAGCUTCCGCCCTCCCAGGCTCTGCCCCAGCA 78	roGlnAsnI	CAGCAG:AGCAGCAGCAGCAGCA :::::       ::   roAsnIleLysArg;lnProGlnHisG!	GCAGCGAAYRAGCACAGCTGCAGCTCCAACA ::::::::    :::    pArgGlnMətProGlnMetGlnGlnProGl	TGCA FCATCAAAATCAGCAACAGATACAGCAGCAGC                  Hi.3HisGlnAsnGlnProProMetGlnGlyAsnP	etAsnLeu	CAGCAGCAG    :::      InserGlnSerIleHisGlySerMet	CCAT3CAGCAGCAGTTCCAAGCAGT    :::         aGlnGlnProGlnAsnMetGlnIl		GCGCTACAGCAGCAGCAG 	AGTTCCAGCAG	nGlnAsnMetAsnAsnGlySerProHis	CTACGGCAACTCCACAGACCCAGCTGCAGCTCCAGCAGGTGGCG. 3 :::::	GCCCCTCACAGCATGGCTGTC 3 :::	TCCTGGGACCTCGGGGATG3	GTGCCATGGGACAGCCAAT 2    :::::     nLeuMetAsnArgProSe 6	roHisGlnMetGlnGlnGlyGlyGlyFroMetSerMetAsnArgProPro
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1407	TGAGCCCAGCTGGCTCCAGCCAGGCTGAGGAGCAGCAGCAGCTGGACAAG ::    :::	1358
20	.::     :::    nArgProProAlaAsnLysAlaAspMetThrValIleArgAspAlaIleV	18
א ני	AAACACACCTGTGAACCCCAGCTCTGTCA	N
1328	GTGACGGCGGACCCCACAGAACTTCAGTGTCCCCTCACCTGGACCTTT	1279 1169
1278 1168	CACCGCAGCCCTCCCAGAGCCCA ::	1256 1152
1255	CGTCAGCTCTGGCCCTGCCCCATCTCCCAGTAGCTTCCTGCCCAGCCCCT  :::::::    :::::::          ::::::	1206
1205	CCCCAGCCGTCCCCGAGCCGGCCAGCCCAACTCCAA    :::	NU
1155	CGCCGTCACCGGGCCAGCAGGTGCAGACCCCGCAGTCGATGCCCCCTCCC	10
1105	CCCCATGCTGTCCT                 	09
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0	roLysProArgTyrArgGlyLysLysAsnProAlaGlnGluProPro	05
1050	0	105
105	2 GCCCCAGGTGCAGCAGCAGCAGCAGTACAGCTGCAGGTGCGCCCC	104:
0	AsnMetAlaAsnIleGlnAsnGlnGlnAsnLeuGlnAsnProProIle	02
100	TGCAGCAGCCCCCAGT	98:
981 102	7 AACCACCACTGAAATTTGTCCGAGCTCCGATGGTG	9 <b>4</b> 7 1010
946 101	7 GCCTTTGGTGTCACAGGCGCAAGCTCTCCCTGGACAAATGTTGTATACCC	897 995
995	/CCGCCACAGTCGCAGACCCA	97
7	lnGlnGlyGlnProMetGlnGlnValHisGlnGlyGlyHisGlnGluGl	ı o
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962	5 rLysLeuValProGlnGlnArgGlnGlnAsnGlnGlnLysMetP	94
л		838
4	9 GlnThrIleArgIleAsnGlyGluHisAlaIleIleAsnGlyMetGlnT	92
837	7	83
928	2 erGlnMetMetGlnProValValThrAspAsnPheGluProAspAsnAsp	91

709 oGlyMetProProProGlnGlyAlaPheProProGlyTyrLeuProGlyG 726	387 CCAGCAGGTGGCGCTGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 436
993 993	
GlnGlnGlyGlnMetValGlnGlnProGlyTyrProGlyGlnGlyTyrPr	CACAGCATGGCTGTCGTGTCTACGGCAACTCCACAGACCCAGCTGCAGCT
:::    lyGlnGlnGlnGlnGlnGlnGlnArgMetGlnMetMetGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnG	287 CAATGTCTCTCAGGGCAGCCGCCTCCTGGGACCTCGGGGATGGCCCCT 336    ::
	249 TCTGGGCGGGATGGGTAGCTTTGGTGCCATGGGACAGC 286 :::    :::::    ::::      419 nIleThrProGlnProGlySerLeuGlyProMetGlySerLeuGlyProP 436
643 LysLysLysArgProThrLysLysGlnLysGluAlaAlaAlaAlaAlaAlaAl 659 883CAGTCGCAGACCCAGCCTTTGGTGTCACAGGCGCAAGCTCTCCCTG 928	211 GCTGGAATTGGCATCCTCGGGGCCCGGGACAGTC 248 :::       :::
882	
836 CCCAGCAGCCTCCAGTTGCTCAGAACCAACCATCACAACTCCCGCCA 882	x T30160
786 GCAGCTGCAGCAGATGCATCACACACAGCACCACCAGCGCCACCACAGC 835	Percent Similarity: 39.640 Percent Identity: 27.027
748CAGCAGCCACAGCCTCCCGCCCTCCCAGGCTCTGCCCCA 785        :::        ::   :: 597 AlaGinGinPheArgProProProGinGinSerGinGinProIleProPr 613	A; map position: 1 A; Introns: 46/1; 124/1; 159/1; 231/1; 508/3; 740/3; 891/1; 931/1; 975/1; 1014/3; 1083/3
580 laGlyProGlnGlyGlnMetIleGlnArgMetAsnSerTyrProGlyAsn 596	A;Gene: CESP:C37A2.2
747 747	A;Experimental source: strain Bristol N2; clone C37A2
730	A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: DNA A;Residues: 1-1234 <let> A;Residues: 1-1234 <let> A;Residues: 1-1234 <let></let></let></let>
	submitted to the EMBL Data Library, April 1997 A; Description: The sequence of C. elegans cosmid C37A2. A; Reference number: Z20746 A; Reference number: T30160
692 AGCAGCAGCAGCAGCAGCT711	C.Species: (Genoribabilitis elegans C.Species: (Genoribabilitis elegans C.Species: (Genoribabilitis elegans C.Species: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999 (C.Accession: T30160
642 AATAGCACAGCTGCAGCTCCAACAACAGCAACAGCAGCAGCAGCAGCAGC 691     :::::	seq_name: pir2:T30160
592 CATCATCAAAATCAGCAACAGATACAGCAGCAGCAGCAGCAGCTGCAGCG 641    :::          :::	1599 GCGGTGCCCACTCCCCCACCGC 1620        :::        1263 .ArgIleProMetDroAlaArg 1269
542 AGCAGCAGCTCCAGCAGCAGCAGCAGCAGCAGCATCTAATTAAATTG 591          503 lnGlnGln	1549 AAGACCTTGCAAAAGTGTGAGATCGCCCTGGAGAAACTCAAGAATGACAT 1598 :::    :::   1254GluLysLeuThrIleIleIleProPro
	1499 TGAAGAGCCTTCTGGACATTCTGACAGACCCCTCGAAGCGGTGTCCCCTG 1548 ::::::::       :::::: ::::::::::::::::
451 CTACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGTTCCA 491    :::::	1455 CAAGATCGACAAGAAGAGAGAGAGAAAAAGGACCTGAGTAAGA 1498 ::::::::::::
437 AGCAGCAGGCGGCG	1408 CTGAAGCAGCTGTCGAAGTACATCGAGCCCCTGCGCCGCATGATCAA 1454    :::       :::   ::::::: 1218TyrValCysGluGluLeuAsnArgLeuMetAr 1228
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	<pre>seq_documentation_block: hypothetical protein 87B1.5 - fruit fly (Drosophila melanogaster)</pre>
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	1526 A1550 
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US US All	1319 CTGGACCTTTAAACA(ACCTGTGAACCCCAGCTCTGTCATGAGCCCAGCT 1368
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ali	1219 CCTGCCCCATCTCCC1.GTAGCTTCCTGCCCAGCCCCTCACCGCAGCCCTC 1268
C; SC C; SC C; SC	1169 CGCAGCCCGGCCAGCCCAGCCCAACCTCCAACGTCAGCTCTGGC 1218      ::
A) 60 A) 60 A) 7. 7. 7. 7. 7. 7. 7. 7. 7. 7. 7. 7. 7.	1147CCCCCTCCCCCCCAGCCGTCCC 1168
A; M A; R	809
A; A	
R; D; Gen A; Fn	1103 CCTCGCCGTCACCGGC(CCAGCAGGTGCAGACCCCGCAGTCGATG 1146
A; R A; R	1077 CAGCCAGAGCCTCCCCATG
A; R	1036 ACAGCTCAGGCTGCCCAGATGGTGGCTCCCGGAGTCCAGGT 1076 :::        :::             743 GlnGlnArgMetAlaMetPheGlnGlnGlnAlaGlnGlyGlnGlnPr 759
C; D C; D C; D	994CCAGTGC:GCCCCAGGTGCAGCAGCAGCAGCAGCAGTACAG 1035    :::       :::
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03	nGlnSerSerThrProLeuValThrSerSerThrValAlaSer	2
00	CGAGCTCCGATGGTGGTGCAGCAGCCCCAGTGCAGCCCCAG	σ
966 1016	TC	927 999
926 999		983
982	SerValSerSerThrThrProAlaGlyIleAlaThrSerSe	6
891	GCTCAGAACCAACCATCACAACTCCCGCCACAGT	853
966	GlnHisHisGlnS	
'nυ	PROPROPROPROPROPROPROPROPROPROPROPROPROP	807
0	AGCCTCCGCCCTCCCAGGCTCTGCCCCAGCAGCTGCAGCAGATGCATC	757
756 939	GGCTTTGG	้ จั
706 926	TCCAACAACAGCAACAG ::        alGlnAlaGlnValGln	
909	lisAsnGlnLeuI	9 1
9		7
624	· · · · · · · · · · · · · · · · · · ·	601
600 876	CAGCAGCATCTAATTAAATTGCATCATCAA         HisGlnGlnAlaLeuAlaAsnAlaThrGlnGlnIleL	571 859
570 859	AlaGlnAl	843
	lAsnAlaGlnGlnGlnGlnAlaValAlaGlnGlnGlnGlnAlaVal	i N
534	CAGGCTCAGCAGAGTGCCATGCAGCAGCAGTTCCAAGCAGTAGT	488
487 826	P - >	450 809
449 809	 ; ; aAlaIleGlnM	412 793
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1315 1194	TTCAGTGTCCCCT	1303 1177
1302 1177	AAC	1300 1161
1299 1160	ACGGCGCGGACCCCACAG     :::    ::: lySerProLysThrProValSerGlyLysAspThrCysThrThrProLys	1282 1144
1281 1144	CAGTAGCTTCCTGCCCAGCCCTCACCGCAGCCCTCCCAGAGCCCAGTG.  ::::::               :::             ::: OThrLysGluThrProSerLysGlyProThrAlaThrLeuValProTleG	1233 1127
1232 1127	AACTCCAACGICAGCTCTGGCCCTGCCCCATCTCC	1198 1112
1197 1112	CGCAGCCCGGCCAGCCCAGCTCACAGCCC :::           :::             :::   1SerValThrSerThrAlaValThrSerSerProG1yG1nLeuValLeuL	1169 1095
1168 1095	CCAGCAGGTGCAGACCCCGCAGTCGCAGCCCTCCCCCCAGCCGTCCCCCCCAGCCGTCCCCCCCC	1119 1079
1078	   1         1	1062

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! P54258 rattus norvegicus

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SCOTE_List:

Sequence
Sequence
Sequence
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Swissprot_39:CFD_DROME + 305.50
Swissprot_39:CFD_DROME + 305.50
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Query: US-09-668-119-1
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-FGAPOP=6.000 -FGAPEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500
-DELOP=6.000 -FGAPEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500
-DELOP=6.000 -FGAPEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500
-TRANS-human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE-PCt
-THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE-LOCAL -OUTENT-Pfs
-NORM-ext -MINLEN=0 -MAXLEN=200000000
USER-USO9668119_@CGN1_1_42 -NCPU=6 -ICPU=3 -LONGLOG -NO_XLPXY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Results were produced by the GenCore software, Copyright (c) 1993-2000 Compugen Ltd.
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                                                                                                                                                                                                                                                                                      4 i Q93074 homo sapiens (human)
i P10385 trikicum aestivum (which i P26371 homo sapiens (human).
5 i P15941 homo sapiens (human).
5 i P15941 homo sapiens (human).
6 i P29617 drosophila melanogast i Q01617 drosophila melanogast i P3241 drosophila melanogast i P3241 drosophila melanogast i P3572 saccharomyces cerevis i P35732 saccharomyces cerevis i P35732 saccharomyces (human) i P18164 drosophila melanogast i P36404 drosophila melanogast i Q9273 homo sapiens (human) i P18171 drosophila melanogast i P38365 saccharomyces cerevis i P38465 saccharomyces cer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | P24856 notothenia coriiceps | | | P32857 kluyveromyces lactis | P13709 drosophila melanogast | P13709 drosophila melanogast | P18480 saccharomyces cerevis | P08489 triticum aestivum (while | P10388 triticum aestivum aes
                                                                                                                                                                                                                             P17437 xenopus laevis (africa
P48997 mus musculus (mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P36417 dictyostelium discoid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P21519 drosophila melanogast
P39769 drosophila melanogast
O75690 homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P54259 homo sapiens (human
P15714 eimeria tenella ant
P28968 equine herpesvirus ty
                                                                        P08488 triticum aestivum P04727 triticum aestivum
                                                                                                                                                     P34314 caenorhabditis elega
O14497 homo sapiens (human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P08640 saccharomyces cerev
                                             triticum aestivum
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SwissProt_39:DRPL_RAT + 282.00 200.67 0.0001
SwissProt_39:BRM_DROWE + 282.00 198.79 0.0001
SwissProt_39:TBGU_EBY + 281.00 194.35 0.0001
SwissProt_39:ZEST_DROVI + 280.50 203.41 0.0002
SwissProt_39:HDC_DROWE + 280.00 199.85 0.0002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               seq_name: SwissProt_39:SSN6_YEAST
EMBL; M23440; AAA34545.1;
EMBL; M17826; AAA35103.1;
EMBL; X66247; CAA46973.1;
EMBL; X78993; CAA55615.1;
EMBL; Z35981; CAA85069.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-90124639; PubMed-2404612; MEDLINE-90124639; PubMed-2404612; Sikorski R.S., Boguski M.S., Goebl M., Hieter P.A.; Sikorski R.S., Boguski M.S., Goebl M., Hieter P.A.; and a required for mitosis and RNA RNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mannhaupt G., Stucka R., Ehnle S., Vetter I., Feldmann H.;
"Molecular analysis of yeast chromosome II between CMD1 and IXS2: the
excision repair gene RAD16 located in this region belongs to a novel
group of double-finger proteins.";
Yeast 8:397-408(1992).
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[2]
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01-APR-1990 (Rel. 14, Last sequence update)
01-FEB-1995 (Rel. 31, Last annotation update)
GLUCOSE REPRESSION MEDIATOR PROTEIN.
SSN6 OR CYCB OR YBR112C OR YBR0908.
                                                                                                                                                                                                                   use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Saccharomyces cerevisiae (Baker's yeast).

Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                  or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          synthesis.";
Cell 60:307-317(1990)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Schultz J., Carlson M.; Schultz J., Carlson M.; "Molecular analysis of SSN6, a gene functionally related to the protein kinase of Saccharomyces cerevisiae."; Mol. Cell. Biol. 7:3637-3645(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. MEDLINE-89211964;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TPR REPEATS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=92327848; PubMed=1626431;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-S288C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. MEDLINE=88065502; PubMed=3316983;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Trumbly R.J
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Cloning and characterization of the CYC8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=4932;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FUNCTION: IT IS INVOLVED IN REPRESSION BY A1-ALPHA2 AND ALPHA2 AND IN OTHER SYSTEMS AS A GENERAL REPRESSOR OF TRANSCRIPTION. THIS PROTEIN HAS NO OBVIOUS DNA-BINDING DOMAINS. IT MIGHT NOT INTERACT DIRECTLY WITH DNA BUT WITH DNA-BOUND PROTEINS.
SUBCELLULAR LOCATION: NUCLEAR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIMILARITY: CONTAINS 10 TPR REPEATS. SIMILARITY: TO YEAST GALL AND CCR4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       73:97-111(1988).
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3149
618
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! P03186 epstein-barr virus
! Q24762 drosophila virilis
! Q9n2m8 drosophila melanog
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alignment_block:
US-09-668-119-1 x SSN6_YEAST
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Ratio: 1.477 Gaps: 17
Percent Similarity: 53.484 Percent Identity: 29.713
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Align seg 1/1 to: SSN6_YEAST from: 1 to: 966
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SEQUENCE
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REPEAT
                                                                                                                                                                          547 LysalaGlnAlaGlnAlaGlnAlaGlnGlnGlnGlnGlnGlnGlnGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                513 nAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        280 GGACAGCCAATGTCT.....CTCTCAGGGCAGCCGCCTCCTGGGACCTC 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro, IPR001440; TPR.

Pfam; PF00515; TPR; 10.

SMART; SM00028; TPR; 9.

Transcription regulation; Repressor; Repeat; TPR repeat;
595 GlnLeuGlnGlnLys(lyValSerValGlnMetLeuAsnProGlnGlnGl 611
                                                                                  605 AGCAACAGATACAGCAGCAGCAACAGCAGCTGCAGCGAATAGCACAGCTG 654
                                                                                                                                                                                                                                                                                                                                                                                                                                                  555 GCAGCAGCAGCAGCAGCAGCATCTAATTAAATTGCATCATCAAAATC 604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             505 GCCATGCAGCAGTTCCAAGCAGTAGTGCAGCAGCAGCAGCAGCTCCA 554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     530 laGlnAlaGlnAlaGlnAlaHisAlaGlnAlaGlnAlaGlnAlaGlnAla 546
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   488 TCCAGGCTCAG......CAGAGT 504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             438 GCAGCAGGCGGCGCTPCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGT 487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                497 GlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGlnAlaGl 513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        388 CAGCAGGTGGCGCTGCAGCAGCAGCAGCAGCAGCAGCAGTTCCAGCAGCA 437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          480 erAlaThrMetTyrSerAsnGlyAlaSerProGlnLeuGlnAlaGlnAla 496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        361 ......GCAACTCCACAGACCCAGCTGCAGCTC 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          463 aSerMetValGlnGlnGlnHisProAlaGlnGlnThrProIleAsnSerS 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                447 GlyAsnProLeuAsnThrArgIleSerAlaGlnSerAlaAsnAlaThrAl 463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SGD; S0000316; CYC8.
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966 AA;
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TPR 2.

TPR 3.

TPR 4.

TPR 5.

TPR 6.

TPR 9.

TPR 9.

TPR 10.

TP
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1572	CAGACCCCTCGAAGCGGTGTCCCCTGAAGACCTTGCAAAAGTGTGAGATC	1523
9	:::::::::	87
1522	GACAGAAAAAAGGACCTGAGTAAGATGAAGAGCCTTCTGGACATTC	1473
1472 876	TCGAGCCCCTGCGCCGCATGATCAACAAGATCGACAAGAAAGA	1430 860
860	GGCTGAGGAGCAGCAGTACCTGGACAAGCTGAAGCAGCTGTCGAAGTACA :   :::::::   ::: sAlaAsnAspGlnSerThrAlaGluThrIleGluLeuSerThrAlaT	1380 844
4 4	:	82,4
827	salaalaSerValSerProSerThrLysProLeuAsnThrC	u no
1341	CCCACAGAACTTCAGTGTCCCCTCACCTGGACCTTTAAACACA	1292
1291 811	CCTGCCCAGCCCCTCACGCAGCCCTCCCAGAGCCCAGTGACGCGCGCG	1242 794
1241 794	CAGCCCAACTCCAACGTCAGCTCTGGCCCTGCCCCCATCTCCCAGTAGCTT         ::::::	1192 781
1191 780	CGATGCCCCCCCCCCCAGCCGTCCCCGCAGCCCGGCCAGCCCAGCTCA :: : :       sn	1142 778
1141 778	CCCCATGCTGTCCTCGCCGTCACCGGGCCAGCAGCTGCAGACCCCGCAGT:::   :::       :::        :::	1092 761
1091 761	CAGGCTGCCCAGATGGTGGCTCCCGGAGTCCAGGTCAGCCAGAGCAGCCT::::::::::	1042 745
1041 744	GTGCAGCCCCAGGTGCAGCAGCAGCAGACAGCAGCAGACAGA	997 728
996 728	CCGAGCTCCGATGGTGGTGCAGCAGCCCCCA	966 711
965 711	H 0	916
915 694	CTCCCGCCACAGTCGCAGACCCAGCCTTTGGTGTCACAGGCG	874 678
873 678	ACCACAGCCCCAGCAGCCTCCAGTTGCTCAGAACCAACCATCACAA.	828 661
827 661	CAGCAGCTGCAGCAGATGATCACACACAGCAGCAGCAGCCGCC	784 645
783 644	CACAGCCTCCGCCCTCCCAGGCTCTGCCC	755 628
75 <b>4</b> 628	GCAGGCTTTGGAGGCCCAGCCACCAATTCAGCAGCCACCGATGCAGCAGC	705 611

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alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          seq_name: SwissProt_39:GBF_DICDI
                                                                                                                                             alignment_block:
                                                                                                                            US-09-668-119-1 x GBF_DICDI
                                                                                                                                                                            Percent Similarity:
                                                                                            Align seg 1/1 to: GBF_DICDI from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1573 GCCCTGGAGAAACT 1586
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Late development in Dictyostelium."; Genes Dev. 8:502-514(194).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
01-JUN-1997 (Rel. 35, Last annotation update)
G-BOX BINDING FACTOR (GBF).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Schnitzler G.R., Fischer W.H., Firtel R.A.; "Cloning and characterization of the G-box binding factor, an essential component of the developmental switch between early and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Dictyostelium discoideum (Slime mold).

Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           907 luThrAlaAlaThr 911
                                                              130 CATAACAAGAAATCTCAAGCTTCCGTCAGTGATCCTATGAATGCACTCCA 179
                                                                                                                                                                                                                                                                                                                                                                                                                      TRANSFAC; T00315; -. DictyDb; DD02046; gbfA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; L29075; AAA21021.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A., AND PARTIAL SEQUENCE
180 GAGCCTGACTGGCGGACCTGCTGCGGGAGCCGCTGGAATTGGCATGCCTC 229
                                                                                                                                                                                                                                                                                                                                                                                                        Transcription regulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=94170994; PubMed=8125261;
                              6 HisHisGlnGlyAsnSerSerSerSerSerSerSerSerProSerGl 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FUNCTION: CAMP-RESPONSIVE TRANSCRIPTIONAL ACTIVATOR REGULATING LATE GENE EXPRESSION. ESSENTIAL COMPONENT OF THE DEVELOPMENTAL SWITCH BETWEEN EARLY AND LATE DEVELOPMENT. BINDS TO A NUMBER OF CA/GT-RICH GENE REGULATORY ELEMENTS.
SUBCELLULAR LOCATION: NUCLEAR (POTENTIAL).
                                                                                                                                                                                                            Quality:
                                                                                                                                                                                            Ratio:
                                                                                                                                                                                                                                                368
81 510
1 21
263
292
557
79268 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                           383.00
1.272
43.185
                                                                                                                                                                           Length:
Gaps:
Percent Identity:
                                                                                                                                                                                                                                                                                                                                                                                                       Activator; DNA-binding; Nuclear protein;
                                                                                                                                                                                                                                                                                          POLY-ASN.
                                                                                                                                                                                                                                                                                                                         GLN-RICH.
                                                                                                                                                                                                                                                                                                                                         POLY-SER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                          B4B6D8F04FACACCA CRC64;
                                                                                            to: 708
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           708 AA.
                                                                                                                                                                            : 697
: 23
: 24.390
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Š	310 OSerDroSerThriveClwIveArgIvgHieHieCluThrSerAenSerG	
87	870	
31:	296 LeuAsnAsnLeuThrLeuSerGlnAsnAsnThrSerGlySerAsnThrPr	
870	TGCTCAGAACCAACCA	
295	279 snAsnSerAsnAsnAsnAsnAsnAsnAsnAsnAsnAsnAsnSerHisGln	
84	846	
279	l 262 oglnSerLeuSerAsnSerGlyAsnAsnAsnAsnAsnAsnAsnAsnAsnA	
84	846 T	
26	:::   :::    :::  46 GlnGlnHisGlnGlnGlnGl	
84	AGATGCATCACACACAGCACCACCAGCCGCCACCACAGCCCCAGCAGC	
79	746 TGCAGCAGCAGCACAGCCTCCGCCCTCCCAGGCTTGCCCCAGCAGCTGCAG	
23		
74	96 GCAGCAGCAGCATTTGGAGGCCCAGCCAATTCAGCAGCCACCG	
21	646 GACAGCTICCAGCACAGCACAGCAGCAGCAGCAGCAGCAGCAGCAGCA	
202	605 AGCAACAGATACAGCAGCAGCAACAGCAGCTGCAGCGAATA	
186	555 GCAGCAGCAGCAGCAGCAGCATCTAATTAAATTGCATCATCAAAATC :      :::	
169	:::         ::: :::              ::: :::	
554	TGCAGCAGCAGTTCCAAGCAGTAGTGCAGCAGCAGCAGCAGCTCC	
504	455 AGCAGCAGCAGCAGCAGCAGCAGCAGCAGTTCCAGGGTCAGCAGAGAGT	
136	405 GCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCGCGCGCCTAC	
	106 ProAsnGlnAsnProHisTyrAsnTyrGlnTyrGlnLeuMetPheMetGl	
105	9 spGlyGlnTyrProAspMetProAsnMetValAspGlnTyrGlnIleH1	
357	3 CGGGGATGGCCCCTCACAGCATGGCTGTCGTCGTCTT	
32 <u>2</u>	279 GGGACAGCCAATGTCTCTCTCAGGGCAGCCGCCTCCTGGGACCT :	
	6 PheProProThrSerSerLeuLeuGlyGlySerSerAsnThrProSer	
278	8CCGGGACAGTCTCTGGGCGG	
55	230 CTCGGGGC	
ט ע	o characte	
4	o nubrileClvClvCerMenIeSerMenIleSerMlaIeuProLeuPr	

-		
870		870
329	${\tt luLysLysAspSerS} \\ \& r{\tt GlyGlnThrIleProLysCysThrArgCysAsn}$	345
870		870
346	${\tt GluAlaAlaSerTrpLysHisAspLysArgArgTrpTrpCysLysGluCy}$	362
871	AACTCCCGCCAC	883
362	: :	379
884	CAGACCCAGCCTTTGGTGTCACAAGGCGCAAGCTCTCCCTGGACAA	933
379	nAlaGlnLeuGlnProLeuGlnAsnHisAsnGlnIleIleProGln	394
934	TGTTGTATACCCAACCACCACTGAAATTTGTCCGAGCTCCGATGGTGGT	983
395	uTrpAspSerGlnGlnAsnAsnSerSerGl	405
984	AGCAGCCCCAGTECAGCCCCAG	1008
405	roProThrGlnProGlnAsnAsnMetAsnGlnIleAsnHisG	422
600	TGCAGCAGCAGCAGACAGCAGTACAG	1035
422	uLeuGlnGlnHisGlnGlnAlaGlnLeuGlnAlaHisLeuAsn	438
036	CTCAGGCTGCCCAGATGGTGGCTCCCGGAGTCCAG	1074
439	AlaSerAsnClnGlnValProProGlnLeuGlnGlnGlnIleAs	455
1075	GTCAGCCAGAGCAGCCTCC	0
φ.	GTCCTCGCCGTCACCGGGCCAGCAGGTGCAGACCCCGCAGTCG	1143
472	SerThrSerValSer	479
.144	CCC	1158
480	roProCysProLeuCysArgGlyIleSerSerTrpLysHisAspLy	496
.158		1158
496	Thr	513
.159	GCCGTCCCCGCAGCCCGGCCAGCCCAGCCTCACAGCCCAAC	1200
513	erProSerSerSerProSerSerProLysLys	529
.201	CCAACGTCAGCTCTGGCCCTGCCCCAT	229
530	SerThrSerSerSerSerS	546
.230	日	1230
546	IleIleAsnAsnAsnAsnAsnAsnAlaAsnSerSerL	63
231	CCCAGTAGCTTCCTGCCCAGCCCCTC	257
563	nLeuSerProProPro	579
258	AGCCCTCCCAGAGCCCAGTGA	.289
580	SerIleSerGlnSerProLeuGlnLeuAsnTyrGlnTh	96
290	AACTTCAGTGTCCCCTCACCTGGACCTTTAAACAC	336
596	nProSerLeuProSerIleGlyGlyAsnLeuF	13

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seq_name: SwissProt_39:MAM_DROME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            seq_documentation_block:

        Neurogenesis; Nuclear protein; Repeat.

        DOMAIN
        20
        84
        GLN-RICH.

        DOMAIN
        127
        190
        ARG/LYS-RICH.

        DOMAIN
        196
        219
        GLN-RICH.

        DOMAIN
        259
        304
        ASN-RICH.

        DOMAIN
        355
        388
        GLY/ASN-RICH.

        DOMAIN
        392
        406
        GLN-RICH.

        DOMAIN
        407
        440
        GLY-RICH.

  DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "The Drosophila neurogenic locus mastermind encodes a nuclear protein unusually rich in amino acid homopolymers.";

Genes Dev. 4:1688-1700(1990).

-1- FUNCTION: MAY HAVE A REGULATORY FUNCTION POSSIBLY IN ASSOCIATION WITH THE N GENE PRODUCT.

-1- SUBCELLULAR LOCATION: NUCLEAR.
-1- DEVELOPMENTAL STAGE: DURING EARLY NEUROGENESIS MAM PRODUCTS ARE UBLOUTCOUSLY LOCATED. DURING LATER STAGES THEY ACCUMULATE IN THE CENTRAL NERVOUS SYSTEM.
-1- MISCELLANEOUS: THE PROTEIN HAS MANY AA HOMOPOLYMERIC DOMAINS: 21
POLY-GLN RUNS (FROM 5 TO 16 AA IN LENGTH), 4 POLY-GLY (6 TO 10 AA), 3 POLY-ASN (3 X 5 AA), 1 POLY-ALA (10 AA) AND 1 POLY-THR (5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1448 TGATCAACAAGATCGACAAGAACGAAGACAGAAAAAAAGGAC 1488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1426 .....TACATCGAGCCCCTGCGCCGCA 1447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1378 CAGGCTGAGGAGCAGCAGCTGCGACAAGCTGAAGCAGCTGTCGAAG. 1425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1337 CTGTGAAC......CCCAGCTCTGTCATGAGCCCAGCTGGCTCCAGC 1377
                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P21519;
01-MAY-1991 (Rel. 18, Created)
01-MAY-1991 (Rel. 18, Last sequence update)
01-MAR-1992 (Rel. 21, Last annotation update)
                                                                                                                                                                                                             PIR; A33106; A33106.
PIR; A36391; A36391.
                                                                                                                                                                                                                                                             EMBL; X54251; CAA38152.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-91065516; PubMed=1701150;
Smoller D., Friedel C., Schmid A., Bettler D., Lam L.,
Yedvobnick B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Drosophila melanogaster (Fruit fly).

Dukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Eukaryota; Neoptera; Endopteryota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      663 roLeuSerGlnLeuAsnLysLysGlnLysLysArgSerAsp 676
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              646 rGlyAlaLeuLeuSerSerAsnGlyIleAsnLeuAlaAsnLeuGlyAsnP 663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         630 ProProLysSerSerSerSerLeuAsnAsnLeuAsnSerPheSerAsnTh 646
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 613 lnAlaAsnSerIleLysProAspGlyGlyIleLeuIleSerGlyLeuSer 629
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NEUROGENIC PROTEIN MASTERMIND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MAM_DROME
                                                                                                                                                                                       FlyBase; FBgn0002643; mam
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIMILARITY: TO OTHER NUCLEAR PROTEINS OF DROSOPHILA, TO CERTAIN YEAST AND MAMMALIAN REGULATORY PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
ARG/LYS-RICH (BASIC).
GIN-RICH.
ASN-RICH.
GLY/ASN-RICH.
GLY-RICH.
GLY-RICH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1596 AA.
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713 511 730	500	460 696	680	459	443 663	406 646	630	405	359 613	327 596	283 580	233 570	183 553	136 537	Align se	alignment US-09-66	alignment Percent	FT DOMA. FT SEQU
3 inGlnHisLe	0 AGAGTGCCCATG 5						0 GlnHisLysAsnAlaMetG			7 GATGGCCCCTCACAGCATGGCTGTCGTGTCTA 358	3 CAGCCAATGTCTCTCTCAGGGCAGCCGCCTCCTGGGACCTCGGG 326 :::    ::: ::                   ::	3 GGGGCCCGGGACAGTCTCTGGGCGGGATGGGTAGCTTTGGTGCCATGGGA 282 :::      ::::::::	3 CCTGACTGGCGGACCTGCTGCGGGAGCCGCTGGAATTGGCATGCCTCCTC 232 :         :::     :::   :::   :::    3 sSerGluGlyGlyLeuGlyHisGlyPheGlyGlyPheGlyLeuGlyLeuA 570	6 AAGAAATCTCAAGCTTCCGTCAGTGATCCTATGAATGCACTCCAGAG 182     ::: :::::::    :::   :::   ::: 7 LysValGluProProAsnAlaGlnAspLeuIleAsnSerLeuAsnValLy 553	seg 1/1 to: MAM_DROME from: 1 to: 1596	nt_block: 668-119-1 x MAM_DROME	nt_scores: Quality: 378.00 Ratio: 1.615 Ratio: 1.605 Gaps: 24 t Similarity: 45.000 Percent Identity: 30.192	MAIN 700 714 GLN-RICH.  MAIN 700 714 GLN-RICH.  MAIN 759 816 GLN-RICH.  MAIN 987 996 5 X 2 AA TANDEM REPEATS OF G-V.  MAIN 1060 1079 ALA-RICH.  MAIN 1092 1107 8 X 2 AA TANDEM REPEATS OF V-G.  MAIN 1237 1252 7 X 2 AA TANDEM REPEATS OF G-V.  MAIN 1237 1252 7 X 2 AA TANDEM REPEATS OF G-V.  MAIN 1492 1496 POLY-THR.  MAIN 159 1592 ASP/GLU-RICH (ACIDIC).  MAIN 159 1596 AA; 167717 MW; B944D86EF359D605 CRC64;

1220 1018	CAGCCCGGCCAGCCCAGCTCACAGCCCAACTCCAACGTCAGCTCTGGCCC	1171 1002
1001	;;; lyGlyGlyValGlyValGlyValGlyValGlyValGlyAsnGlyGl	œ
1170	AGCCGTCCCC	1153
1152 985	CTCGCCGTCACCGGGCCAGCAGGTGCAG ::::   :::	1104 968
Ō	GlnGlnGlnProGlyGly	961
1103	ATGGTGGCTCCCGGAGTCCAGGTCAGCCAGAGCAGCCTCCCCATGCTG	1054
960	CCCAGGTGCAGCAGCAGCAGCAGCAGTACAGCTCAGGCTGCCCAG    :::              lnGlnAlaGlnGlnGlnGlnGln	1004 953
ੇ ਹਾ	sSerAsnValSerValAlaAlaGlnGlnGlyValPhePheSerGl	w
1003	ATTTGTCCGAGCTCCGATGGTGGTGCAGCAGCCCCCAGTGC	960
937	GCCAAGCTCTCCCTGGACAAATGTTGTTATACCCAACCACCACCACCACCACCACCACCACCACCA	913 921
1 N	etLysGlnThrGlnGlnLeuHisIleSerGlnGlnGlyGlyGlyAlaG	0
912	GTCGCAGACCCAGCCTTTGGTGTCACAG	884
904		834 888
888	lyGlnGlnAsnAsnProAsnThrGlyProGlyGlyAsnThrPr	872
833	cagcaccaccaccagccgccaccac	811
871	GlyAlaGlyProGlnGlnGlnGlnGlnArgGlyAsnAlaGlyAs	Ü
810	CCAGGCTCTGCCCCAGCAGCTGCAGCAGATGCATCACACA.	767
856	  GlyAsnGlnGlnProGlyAsnLeuAlaGlnGlnGlnG	841
766	AGCAGCCACCGATGCAGCAGCCACAGCC	730
841	roAsnAlaAlaAlaAsnPheLeuAsnCysProProArgGlyGlyPro	825
729	ccacca	724
824	AsnGlnAs	808
723	GCAGCAGCAGCAGCAGCAGCAGGCTTTGGAGGCCCAG	683
808	nGlnGlnValProGlnGlnGlnLeuGlnGlnGlnGlnGlnGlnGlnGlnGlnG	791
682	CTGCAGCGAATAGCACAGCTGCAGCTCCAACAACAGCAACAGCAGCAG	633
9	AATICAGCAACAGSHACAGG AATICAGCAACAGSHACAGG AATICAGCAACAGSHACAGG AATICAGCAACAGGHACAGG AATICAGCAACAGGHACAGGA AATICAGCAACAGGHACAGGA AATICAGCAACAGGHACAGGA AATICAGCAACAGGHACAGGA AATICAGCAACAGGHACAGGAGAGAGAGAGAGAGAGAGAGAGAG	775
		,
600 774	CTAAT	551 763
763	yrSerSerGlnAsnAspPheAspLeuLysArgLeuGlnGlnGlnGlnGl	746
5		538

1221 TGCCCCATCT 1230

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seq_name: SwissProt_39:PHP_DROME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 199-1584 FROM N.A.

SEQUENCE OF 199-1584 FROM N.A.

BEDLINE-92039031; PLOMEd=1937015;

Deatrick J. Daly M., Randsholt N.B., Brock H.W.;

The complex genetic locus polyhomeotic in Drosophila melanogaster potentially encodes two homologous zinc-finger proteins.";

Gene 105:185-195 (1951).

-I- FUNCTION: BINDS TO POLYTENE CHROMOSOMES. SEEMS TO INTERACT WITH PC. MAY INTERACT WITH PROTEINS ALREADY BOUND TO PROMOTER COMPLEXES AND MAY BE A NEGATIVE REGULATION OF PROMOTER SEGMENTATION GENES. PLAYS A ROLE IN REGULATING THE EXPRESSION OF
               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way endified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE-Imaginal disks;

MEDLINE-92146557; PLbMed-1346609;

Decamillis M., Chenr N.S., Pierre D., Brock H.W.;

"The polyhomeotic gene of Drosophila encodes a chromatin protein that shares polytene chromosome-binding sites with Polycomb.";

Genes Dev. 6:223-23;(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         documentation_block
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1018 nValProser 1021
                                                                                                                                                                                                                                          FlyBase; FBgn0004861; ph-p. InterPro; IPR001660; SAM. Pfam; PF00536; SAM; 1.
                                                                                                                                                                                                                                                                                                  EMBL; X63672; CAA45211.1;
EMBL; M64750; -; NOT_ANNO
PIR; S23632; S23632.
                                                   CONFLICT
                                                                                           DOMAIN
                                                                                                                                 DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER PAIR RULE GENES SUCH AS EVE, FTZ, AND H.

ISUBCELIULAR LOCATION: NUCLEAR.

ITISSUE SPECIFICITY: SALIVARY GLANDS.

ISUBLARITY: CONTAINS 1 SAM DOMAIN.

ISIMILARITY: CONTAINS 1 SAM DOMAIN REGULATOR PROTEIN RAE-28.

ISIMILARITY: TO POUSE EARLY DEVELOPMENT REGULATOR PROTEIN RAE-28.

ICCAUTION: IT IS UNCERTAIN WHETHER MET-1 OR MET-9 IS THE INITIATOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Drosophila melanoga:ter (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
                                                          Zinc-finger; Developmental protein; DNA-binding; Nuclear protein.

74 30 POLY-GLN.

DOMAIN 411 4 50 GLN-RICH.

DOMAIN 494 520 GLN-RICH.

DOMAIN 619 650 GLN-RICH.

DOMAIN 775 950 GLN-RICH.

DOMAIN 1233 1230 SER/THR-RICH.

ZN.FING 1365 1337 C4-TYPE.
                                                                                                                                                                                                                             SMART; SM00454;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-FEB-1995 (Rel. 3., Created)
01-FEB-1995 (Rel. 3., Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
POLYHOMEOTIC-PROXIMAL CHROMATIN PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PHP_DROME
           ĀΑ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                             SAM;
                                                                                                                                                                                                                                                                                                                      NOT_ANNOTATED_CDS.
                               14.L5
           167297 MW;
MISSING (IN REF. 2).
D -> A (IN REF. 2).
MW; A6DF0CF9106E1891 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT; 1589 AA.
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alignment_block:
US-09-668-119-1 x PHP_DROME
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Align seg 1/1 to: PHP_DROME from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Percent Similarity: 46.438
893 LeuHisAsnGlnLeuIleGlnGlnGlnLeuGlnGlnGlnAlaGlnAlaGl 909
                                                                                                                                                                                                                                                                                                                                                                                                                                                 826 alAsnAlaGlnGlnGlnGlnAlaValAlaGlnGlnGlnGlnAlaValAla 842
                                                                                                                  876 alAlaProAsnGlnPheIleThrSerHisGlnGlnGlnGlnGlnGlnGln 892
                                                                                                                                                                                                                                                                                  843 GlnAlaGlnGlnGlnArgGluGlnGlnGlnGlnValAlaGlnAlaGl 859
                                                                                                                                                                                                                                                                                                                                                                                        535 CAGCAGCAGCAGCAGCTCCAGCAGCAGCAGCAGCAG......570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        488 TCCAGGCT...CAGCAGAGTGCCATGCAGCAGCAGTTCCAAGCAGTAGTG 534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           412 CAGCAACAGCAGCAGTTC.....CAGCAGCAGCAGCAGCAGCGGC 449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                776 lnGlnGlnLeuGlnLeuPheGlnLysGlnGlnIleLeuGlnGlnGlnGln 792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       371 AGACCCAGCTGCAGCTC.....CAGCAGGTGGCGCTGCAGCAGCAG 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                759 nAsnGlyGlnThrLeuHisAlaAlaThrAlaAlaGlyValAspLysGlnG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      321 CTCGGGGATGGCCCCTCACAGCATGGCTGTCGTGTCTACGGCAACTCCAC 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         747 ...........ValValMetSerThrThrGlyThrProIleThrLeuGl 759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            271 GGTGCCATGGGACAGCCAATGTCTCTCTCAGGGCAGCCGCCTCCTGGGAC 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   221 GCATGCCTCCTCGGGGCCCGGGACAGTCTCTGGGCGGGATGGGTAGCTTT 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            740 n.....AlaAlaGlyAsnL 745
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     171 TGCACTCCAGAGCCTGACTGGCGGACCTGCTGCGGGAGCCGCTGGAATTG 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        724 ThrThrValGlnGlnGlnGlnAlaThrAsnLeuGlnGlnValValAs 740
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 CGAGACATTCATAACAAGAAATCTCAAGCTTCCGTCAGTGATCCTATGAA 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     707 ysThrGluIleGlyGlnValAlaGlyGlnAsnLysValValGlyHisLeu 723
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              690 aLysMetArgAsnLysGlnGlnProValArgProAlaLeuAlaThrLeuL 707
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        88 .....CTTTCTCTCGTGGCC.....AGGCTCATTATCCATTTT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    69 CAAGACCCGGGACGAATAC......87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19 GCACACAGTAAATCCAGCAAGGATATGGAGAGCCATGTTTTCCTGAAGGC 68
                                                         ......CAACAGCAGCTGCAGCGAATAGCACAGCTGCA 656
                                                                                                                                                                                                                               nAlaGlnHisGlnGlnAlaLeuAlaAsnAlaThrGlnGlnIleLeuGlnV 876
                                                                                                                                                                     .....AATCAGCAACAGATACAGCAGCAG 624
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Quality:
Ratio:
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1.114
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657 909	GCTCCAACAACAGCAACAGCAGCAGCAGCAGCAGCAGCAGCAG	26
707 926	AGGCTTTGGAGGCCAGCCAGCCAACTTCAGCAGCCACCGATGCAGCAGCCACCCATCCGATGCAGCAGCCACCGATGCAGCAGCCACCGATGCAGCAGCCACCGATGCAGCAGCCACCGATGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG	39
757 940	CAGCCTCCGCCCCCAGGCTCTGCCAGCAGCTGCAGCAGATGCATCA E	51
807 952	CACACAGCAGCACCAGCC	43
844 967	ACCATO	90
891 980	SerSerAlaLeuGlnAlaAlaLeuSerAlaSerGlvAlaIlePheGlnTh	)17
918	AGCTCTCCCTGGAC	142
943	roGiğiniCýsserserserserrotniserservaiva	.013
		1029
	CAGTGCAG.	024
025	TACAGACAGCTCAGGCTGCCCAG	1053
.046	AlaThrIleAlaGlyGlyThrGlnGlnProGlnGl	1062
053		1053
.063	${\tt ProProSerLeuThrProThrThrAsnProIleLeuAlaMetThrSerMe}$	1079
.054	ATGGTGGCTCCCGGAGTC	1078
7	tAsnAlaThrValGlyHisLeuSerThrAlaProProValThrVal	1096
.079 1096	GCCAGAGCAGCCTCCCCATGCTGTCCTCGCCGTCACCGGGCCAGCAGGTG:	1128
128	0	1128
111	LeuLeuSerThrAlaSerSerGlyGlyGlyGlySerIleProAlaThrPr	1127
1129	AGACCCCGCAGTCGATGCCC	1149
1127	hrProSerLys	1144
L150	CCTCCCCCCAGCCGTCCCCCGCAG	1173 1160
1174	CCCGGCCAGCCCAGCTCACAGCC	1196
1197	GCTTCCT	1246
1177	 SerThrL	1194

1	JNC JCH JCH ATR ATR OLF OLF -20 -20 ERA			COUNTER COUNTE	eq_name:	1637 CAAAC!  :::   1325 rArgG	1587 CAAGAATGAC :::    1319 AsnGlu	1549 AAGACC ::   1304 snVall	1499 TGAAGAG: : 1290s	1449 GATCAA     111 1276 hrSerC	1399 CTGGAC   ::   1259 rAlaVa	1351TCTG :::: 1244 hrThrI	1309 .GTCCCCTC ::: :: 1227 sLeuAlaTh	1276 CCAGTG     1211 Proprc	1194 erLysG
HAIR FOLLICLES.  DOMAIN: MAINLY COMPOSED OF CYS-RICH (CR), GLY-RICH RICH (SR) REPEATS.  SIMILARITY: BELONGS TO THE UHS KERATIN FAMILY.	ZZ7:137-148(1999).  ZZ7:137-148(1999).  SUCH AND HAIR CONSIST OF MICROFIBRILS EMBEDDED I SUCH AS WOOL AND HAIR CONSIST OF MICROFIBRILS EMBEDDED I MATRIX OF OTHER PROTEINS. THE MATRIX PROTEIN INCLUDE THE SULFUR AND HIGH-TYROSINE KERATINS, HAVING MOLECULAR WEIGHT OF THE MICROFIBRILS CONTAIN THE LARGER, INCLEDED AND MICROFIBRILS CONTAIN THE LARGER, INCREATINS (40-56 KDA).	Pu J., tio	rdata; Craniata; Vertebrata; E Imates; Catarrhini; Hominidae;	(Rel. 40, Created) (Rel. 40, Created) (Rel. 40, Last sequence update) (Rel. 40, Last annotation update) (Rel. 40, Last annotation update)	Prot.	CAAACAGCAGTACCTATGCCAGCCGCTCCTGGAT 1670 	TGACATGCGGTGCCACTCCCCCACCGCCCCCGGTGCCACGAC	AAGACCTTGCAAAAGTGTGAGATCGCCCTGGAGAAACT::	AAGAGCCTTCTGGACATTCTGACAGACCCCTCGAAGCGGTGTCCCCTG :::::	ATCAACAAGATCGACAAGAACGAAGACAGAAAAAAGGACCTGAGTAAGA                    :: rSerCysThrSerThrThrThrThrThrThrSerSerIle	CTGGACAAGCTGAAGCAGCTGTCGAAGTACATCGAGCCCCTGCGCCGCAT   :::    :::    :::                 ralavalSerThrAlaSerThrThrThrThrSerSerGlyThrPheIleT	TCTGTCATGAGCCCAGCTGGCTCCAGCCAGGCTGAGGAGCAGCAGTAC ::::::	CTCACCTGGACCTTTAAACACACCTGTGAACCCCAGC :::	CAGTGACGGCGCGGACCCCACAGAACTTCAGT	erLysGlyAlaThrThrProThrSerLysGlnSerAsnAlaAlaValGln
(GR) AND SER-	MAL DERIVATIVES DDED IN A RIGID UDE THE HIGH- R WEIGHTS OF GER, LOW-SULFUR ING	.; two human UHS	uteleostomi; Homo.	IN B) (UHS			1636 1325	1586 1318 .	1548 1304	1498 1289	1448 1276	1398 1259	1350 1244	1308 1227	1210

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alignment_scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1015 GCTGCACCTGGGGCTCCACTGGGGGCTGCTGCACCATCGGAGCTCGG 966
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1265 GGCTGCGGTGAGGGGCCTGGGAAGCTACTGGGAGATGGGGCAGGGCC 1216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1065 GGGAGCCACCATCTGCGCAGCCTGAGCTGTCTGTACTGCTGTCTGCTGCT 1016
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1115 GGTGACGGCGAGGAC&GCATGGGGAGGCTGCTCTGGCTGACCTGGACTCC 1066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1165 ACGGCTGGGGGGAGCGGGCATCGACTGCGGGGTCTGCACCTGCTGGCCC 1116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   715 CCAAAGCCTGCTGCTGCTGCTGCTGC.....TGCTGCTGCTGCTGT 672
671 TGCTGTTGTTGGAGCT3CAGCTGTGCTATTCGCTGCAGCTGCTGTTGCTG 622
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        865 GTTGGTTCTGAGCAACTGGAGGCTGCTGGGGGCTGGTGGTGGCGGCTGGTGG 816
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               915 CGCCTGTGACACCAAAGGCTGGGTCTGCGACTGTGGCGGGAGTTGTGATG 866
                                                            108 lySerSerCysCysGlnSerSerCysCysLysProCysCysSerGlnSer 124
                                                                                                                                                                                                                                                                                                                                                                                    815 TGCTGTGTGATGCATCTGCTGCAGCTGCTGGGGCAGAGCCTGGGAGGG 766
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               965 ACAAATTTCAGTGGTCGTTGGGTATACAACATTTGTCCAGGGAGAGCTTG 916
                                                                                                                                                                                                                                                        765 CGGAGGCTGTGGCTGCATCGGTGGCTGCTGAATTGGTGGCTGGGCCT 716
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               69 rCysGlyGlySerLysGly......AspCys...GlySerCysGlyG 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            63 ......GlyArgGlySe 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               47 ysCysValProAlaCysSerCysSerSerCysGlySerCysGlyGly... 62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16 .....GlyCysGlySerGlyCysGlyGlyCysGlyS 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HSSP; P04355; 2MRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   ly.........SerLysGlyGlyCysGlySerCysGly.......................91
                                                                                                                                                                                                                                                                                                                       .....CysSerGlnCysSerCysTyrLysProCys...... 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Quality:
Ratio:
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194 AA;
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3.149)
39.161
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seq_documentation_block:
ID AMYH_YEAST STAN
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O1-AUG-1988 (Rel. 08, Created)
O1-FBE-1995 (Rel. 31, Last sequence update)
O1-FBE-1995 (Rel. 40, Last annotation update)
G10-AUG-2001 (Rel. 40, Last annotation update)
G10COAMYLASE S1/S2 PRECURSOR (EG 3.2.1.3) (GLUCAN 1,4-ALPHA-GLUCOSIDASE) (1,4-ALPHA-P-GLUCAN GLUCONTDROLASE).
STAL OR STA2 OR MAL5 OR YIRO19C.
Saccharomyces cerevisiae (Baker's yeast).
Saccharomyces cerevisiae (Baker's yeast).
Saccharomycetales; Saccharomycetaceae; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomycetes;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Barrell B.G., Badcock K., Bankier A.T., Bowman S., Brown D., Churcher C.M., Connor R., Copsey T., Dear S., Devlin K., Fraser A., Gentles S., Hamlyn N., Horsnell T.S., Hunt S., Jagels K., Jones M., Louis E., Lye G., Moule S., Moule T., Odell C., Pearson D., Rajandream M.A., Riles L., Rowley N., Skelton J., Smith V., Walsh S.V., Whitehead S., Submitted (DEC-1994) to the EMBL/GenBank/DDBJ databases.
the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is
                                                                                                              -I- CATALYTIC ACTIVITY: HYDROLYSIS OF TERMINAL 1,4-LINKED ALPHA-D-GLUCOSE RESIDUES SUCCESSIVELY FROM NON-REDUCING ENDS OF THE CHAINS WITH RELEASE OF BETA-D-GLUCOSE.
-I- SIMILARITY: TO S.POMBE SPEC215.13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       STAI
                                                                                                                                                                                                                                     from Saccharomyces cerevisiae."; FEBS Lett. 239:179-184(1988).
                                                                                                                                                                                                                                                                                  Pardo J.M., Ianez E., Zalacain M., Claros M.G., Jimenez A. "Similar short elements in the 5' regions of the STA2 and
                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 1-31 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-87194600; PubMed=3106330;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 1-242 AND 762-1331 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-S288C / AB972;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          190 ysGlnCys 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     421 GCTGTTGC 414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                173 rCysCysLysProCysCysSerGlnSerSerCysCysValProIleCysC 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              471 CTGCTGCTGCTGCTGTAGCGCCGCCTGCTGCTGCTGCTGGAACTGCT 422
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    146 ysLysProCysCysSerGlnSerSerCysCys......Lys 157
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                                                                                                                                                                                                                                                                                                                                   MEDLINE=89031230; PubMed=3141213;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Yamashita I., Nakamura M., Fukui S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=4932;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  571 GCTGCTGCTGCTGCTGCAGCTGCTGCTGCTGCACTACTGCTTGG 522
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Gene fusion is a possible mechanism underlying the evolution of
                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteriol. 169:2142-2149(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT; 1367 AA
                                                                                                                                                                                                                                                                                SGA genes
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alignment_block:
US-09-668-119-1 x AMYH_YEAST
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Quality:
Ratio:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Align seg 1/1 to: AMYH_YEAST from: 1 to: 1367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Percent Similarity:
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EMBL; M16164; AAA35015.1; -.
EMBL; M16165; AAA35015.1; -.
EMBL; X13857; CAA32069.1; -.
PIR; B26877; B26877.
PIR; A26877; A26877.
PIR; S48478; S48478.
SGD; S0001458; MUC1.
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CARBOHYD
                                      477
                                                                                                                                                                            444
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                346 rSerThrThrGluSerSerSerAlaProVal.ProThrProSerSerSer 362
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Signal; Multigene family. SIGNAL 1 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hydrolase; Glycosidase; Polysaccharide degradation; Glycoprotein;
ACCAATTCAGCAGCC.....ACCGATGCAGCCACAGCCTCCGCCCT 769
                                                                 CAGCAGCAGCAGCAGCAGCAGCAGCAGCAGGCTTTGGAGGCCCAGCC 725
                                                                                                     rProSerSerSerThrThrGluSerSerSerAlaProValThrSerSerT 477
                                                                                                                                                                                                      GCAGCAGCAACAGCAGCTGCAGCGAATAGCACAGCTGCA......656
                                                                                                                                                                                                                                            rGluSerSer.SerAlaProValThrSerSerThrThrGluSerSerSer 443
                                                                                                                                                                                                                                                                             CAGCAGCAGCATCTAATTAAATTGCATCATCAAAATCAGCAACAGATACA 617
                                                                                                                                                                                                                                                                                                                                                                                                      ......AACAGCAGCAGTTCCAGGCTCAGCAGAGTGCCATGCAGCAGC
:::||||||::::||| :::|||
                                                                                                                                                                                                                                                                                                                                                                                                                                                      ThrThrGluSerSerAlaProValThrSerSerThrThrGluSerSe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TACGGCAACT......CCACAGACCCAGCTGCAGCTCCAGC 391
                                hrThrGluSerSerAlaProValProThrProSerSerSerThrThr 493
                                                                                                                                                                         AlaProValThrSerSerThrThrGluSerSerSerAlaProValProTh 460
                                                                                                                                                                                                                                                                                                                                                  roThrProSerSerSerThrThrGluSerSerSerAlaProValThrSer 412
                                                                                                                                                                                                                                                                                                               SerThrThrGlu.....SerSerSerAlaProValThrSerSerThrTh 427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .....GCTCCAACAACAACAACAG 675
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 21 POTENTIAL.
22 1367 GLUCOAMYLASE S1/S2.
210 1367 SER/THR-RICH.
817 817 N-LINKED (GLCNAC. . .) (POTENTIAL).
874 874 N-LINKED (GLCNAC. . .) (POTENTIAL).
1367 AA; 136110 MW; 91COOEZDBD61AA9D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            339.50
1.102
56.204
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Gaps: 22
Percent Identity: 26.825
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           379
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1582	GAAGCGGTGTCCCCTGAAGACCTTGCAAAAGTGTGAGATCGCCCTGGAGA	1533
768		765
1532	0000	1483
1482 764	AGCCCCTGCGCCGCATGATCAACAAGATCGACAAGAACGAAGACAGAAAA :::    :::::: :::   :::   ::: AlaProValThrSerSerThrThrGluSerSerSerAlaProVal	1433 750
1432 749	GTACCTGGACAAGCTGAAGCAGCTGTCGAAGTACATCG	1395 733
1394 733	CCCAGCTCTGTCATGAGCCCAGCCAGGCTGAGGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG	1345 717
1344 716	CACAGAACTTCAGTGTCCCCCTCACCTGGACCTTTAAACACACCTGTGAAC :::::       :::	1295 700
1294 700	TCCCAGAGCCCAGTGACGGCGCGGACCC	1267 683
1266 683	CCTGCCCCATCTCCCAGTAGCTTCCTGCCCAGCCCCTCACCGCAGCCC	1219 667
1218 666	CACAGCCCAACTCCAACGTCAGCTCTGGC	1190 650
1189 650	GTCGATGCCCCCTCCCCCCCAGCCGTCCCCGCAGCCCGGCCAGCCA	1140 633
1139 633	CTCCCCATGCTGTCCTCGCGTCACCGGGCCAGCAGGTGCAGACCCCGCA	1090 624
1089 623	AGGCTGCCCAGATGGTGGCTCCCGGAGTCCAGGTCAGCCAGAGCAGC   :::::::     :::::::::::::::::::::::	1043
10 <b>4</b> 2 607	CCCAGTGCAGCCCCAGGTGCAGCAGCAGCAGCAGCAGCAGTACAGACAG	993 591
992 590	ACCCAACCACTGAAATTTGTCCGAGCTCCGATGGTGGTGCAGCAGCC ::::::::::::::::::::::::::::::	943 574
942 574		896 557
895 557	TCCAGTTGCTCAGAACCAACCATCACAACTCCCGCCACAGTCGCAGACCC        :::	846 544
845 543	laProThrProSerSerSerThrThrGluSerSerSerAlaProValThr	819 527
818 527	CCCAGGCTCTGCCCCAGCAGCTGCAGCAGATGCATCACACACA	770 510
510		494

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seq_name: SwissProt_39:ANP_NOTCO
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30-MAR-2000 (Rel. 39, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
ANTIFREEZE GLYCOPEPTIDE POLYPROTEIN PRECURSOR (AFGP POLYPROTEIN)
[CONTAINS: AFGP7 (AFGP 7); AFGP8 (AFGP 8)] (FRAGMENT).
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                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
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InterPro; IPR000104; Antifreeze_1
                                        EMBL; M55000; AAA49392.2; -. PIR; A38420; A38420. HSSP; P04002; 1WFA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            An antifreeze glyccpeptide gene from the antarctic cod Notothenia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBCELLULAR LOCATION: SECRETED.
TISSUE SPECIFICITY: SYNTHESIZED BY THE LIVER AND SECRETED INTO
THE BLOOD FROM WHICH THEY BECOME DISTRIBUTED TO ALMOST THE ENTIRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TO THREONINES IN AFGP8 AND AFGP7. DATABASE: NAME-Frotein Spotlight; NOTE-Issue 5 of December 2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EXTRACELLULAR SEACE.

DOMAIN: CONTAINS 44 CODIES OF AFGD8 AND TWO CODIES OF AFGD7.

PTM: THE DISACCFARIDE GALACTOSE-N-ACETYLGALACTOSAMINE IS ATTACHED
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WWW-"http://www.expasy.org/spotlight/articles/sptlt005.html".
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alignment_block:
US-09-668-119-1 x ANP_NOTCO
                                                                                                                   alignment_scores:
                                                         Align seg 1/1 to: ANP_NOTCO from: 1 to: 790
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236 oAlaThrAlaAlaCysAsnPheAlaAlaThrAlaAlaThrProAlaThrA 253
                             220 AlaThrAlaAlaLeuAsnPheAlaAlaThrAlaAlaThrAlaAlaThrPr 236
                                          285 GCCAATGTCTCTCAGGGCAGCCGCCTCCTGGGACCTCGGGGATGGCCC 334
                                                                                                                                        SEQUENCE
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                                                                                              1.460
56.784
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71265 MW;
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Glycoprotein; Polyprotein; Repeat;
                                                                                            Percent Identity: 33.166
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1086 CAGCCTCCCCATGCTGTCCTCGCCGTCACCGGGCCAGCAGGTGCAGACCC 1135
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                                                                                                                                                                                                                                                                                                                                                                            a \verb|AlaLeuAsnPheAlaAlaThrAlaAlaThrProAlaThrAlaAlaThr.
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oAlaThrAlaAlaPheAsnPheAlaAlaThrAlaAlaThrAlaAlaThrP 525
                                                             CGCAGTCGATGCCCCCCCCCCCCCCAGCCGTCCCCGCAGCCCGGCCAGCCC 1185
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seq_name: SwissProt_39:GALY_KLULA
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                                                                                                      alignment_block:
                                                                                     US-09-668-119-1 x GALY_KLULA
                                                                                                                                  Percent Similarity:
                                                       Align seg 1/1 to: GALY_KLULA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1286
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01-oCT-1993 (Rel. 27, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
TRANSCRIPTION REGULATORY PROTEIN GAL11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Kluyveromyces. NCBI_TaxID=28985;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     525 roAlaThrAlaAlaLeuAsnPheAlaAla.....
                                                                                                                                                                                                                                                                                                                                  entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GALY_KLULA
                                                                                                                                                                                                                       DOMAIN
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Dickson R.C., Hopper J., Mylin L.M., Gerardot C.J.; "Sequence conservation in the Saccharomyces and Kluveromyces GAL11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. MEDLINE=92020226; PubMed=1923818;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kluyveromyces lactis (Yeast).
                                                                                                                                                                                                                                                                                                               EMBL; M68870; AAA35254.1;
234 MetAsnThrSerValGlnGlnPro.......GlyMetGlyValGl 246
                           289 ATGTCTCTCAGGGCAGCCGCCTCCTGGGACCTCGGGGATGGCCCCTCA 338
                                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                                                                                               Transcription
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 laAlaThrAlaAlaThrAlaAlaThrProAlaThrAlaAlaLeuAsnPhe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CGCGGACCCCACAGAACTTCAGTGTCCCCTCACCTGGACCTTTAAAC... 1332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ....ACACCTGTGAACCCCAGCTCTGTCATGAGCCCAGCT 1368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ...ThrAlaAlaThrProAlaThrAlaAlaThrPro.AlaLeuIlePheA 550
                                                                                                                                                            Quality:
                                                                                                                                               Ratio:
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                                                                                                                                                                                                                          AA;
                                                                                                                                  327.50
1.157
41.254
                                                                                                                                                                                                                                     84
287
411
464
                                                                                                                                                                                                                           114831 MW;
                                                                                                                                                                                                                                                                                                   Activator; Galactose metabolism
                                                                                                                                   Percent
                                                            from: 1
                                                                                                                                                                                                                                                                    POLY-GLN.
GLN-RICH.
                                                                                                                                                                                                                                        POLY-GLN.
                                                                                                                                                                                                                                                         GLN-RICH.
                                                                                                                                                                                                                             436D1EBAEA17F7DB CRC64;
                                                                                                                                Length: 686
Gaps: 24
Identity: 23.178
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                                                          to: 1008
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339	TCCACAGACCCAGCTGCAGCTC	88
389	GGTGGCGCTGC&GCAGCAGCAGCAACAGCAGTTCCAGCA	38
0.0	inGinValProGinGinGinGinValArgGinGinGinGinGinGi	72
439	CGCTACAGCAGCAGCAGCAGCAGCAGCAGCAGC	88
273	lnGlnGlnGlnGlnGlnHisLysGlnGlnProGl	86
189	GGCTCAGCAGAGTGCCATGCAGCAGCAGTTCCAAGCAGTAGTGC	38
286	lnGluProProAlaValLeuGlyArgLeu	03
539	GCAGCAGCTCCA3CAGCAG	61
303	luGlnLysMetLeaTyrGluAlaGlyLysLysMetIleGl	19
562	CAGCAGCAGCAGCATCT 5	81
320	euAspSerGlnGlnGlnLeuLe 3	36
82	AT DAAAATCAGCAACAGATACAGCAGCAGCAACAG. 6	30
36	etAsnGlnMetValLeuLysLysMetGlnGlnL 3	<b>5</b> 1
31	CAGCTGCAGCGAATAGCACAGCTG 6	54
53	etProGlySerAlaGlnGlnSerGlnLeu 3	69
55	AACAACAGCAACAGCAGCAGCAGCAGCAGCAGCAGCAGCA	04
170	LeuGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnArgGl 3	86
05	AGGCTTTGGAGGCC/AGCCACCAATTCAGCAGCCACCGATGCAGCAGC 7	54
86	GlnGlnIleProGlnValGlnGlnAlaProLeuGlnGlnP 4	00
55	CA7	71
00	oGlnValGlnProProGlnSerGlnGlnAlaGlnSerArgArgGlnAla 4	16
71	77	71
17	MetGlyMetLysProTlwProValIleProAsnAlaGlyValMetLysPr 43	$\tilde{\omega}$
72	GCTGCAGCAGATGCATCACACAG	4
S	lnGlnThrProGlnAsnIleGlnGlnProMetMetGlnGl	0
15	ACCLCAGCCCCAGCAGCCTCCAGTTGCTCAGAACCAA 8	
	CARGARA CARGAR	ç
67		5 2
9		
5	α	
Ö	uAsnAlaGiuValTnriysAsnProValLysLeuAsnAspIleThrAsnA 50	ŏ
92	ACC 89	4
00	rgLeuThrAsnAspGlnLysGlnGlnIleArgSerLysLeuHisAlaAsn 51	6
95	TGGTGTCACAGG	U
17	InGlnLeuPheSerS	ω

1531	CCTGAGTAAGATGAAGAGCCTTCTGGACATTCTGACAGACCCCCT 1	1488	
329	heLeuSerThrPheAlaAspCysLeuAspIleLysAspAspAlaVal	ü	
1487	AAGAACGAAGAAAAAAAAAAAAAAAAAAAAAAAA	1465	
1464 812	GCCGCATGATCAACAAGATCGAC1	1442 796	
1441 796	ACCTGGACAAGCTGAAGCAGCTGTCGAAGTACATCGAGCCCCTGC     	1392 779	
1391 779	AACCCCAGCTCTGTCATGAGCCCCAGCTGAGCCAGCCAGGCTGAGGAGCA::::::::::	1342 763	
1341 762	CTTTAAACACACCTGTG	1325 746	
1324 746	SAC E::	1275 729	
1274 729	AGCTTCCTGCCCAGCCCCTCACCGCAGCCCTCCCAGAG	1237 713	
712	snlysaspLysLysAsnProAlaThrArgAlaValLysGlyLysLysAsn	9	
, ס	eLeuAsnSerProGluPheSerAlaIleSerProAlaValProSerProA	679	
ν .	CCTGCCCCATCTCCCA	1219	
679	AspSerSerLeuAsnAlaThrSerArgSerGlyThrAsnThrMetGluPh	663	
J c	THE AUTHOR	1218	
121	GCCAGCCCAGCTCACAGCCCCAACTCCAACGTCAGCTCTGGC	1178 646	
117 <sup>.</sup>	GCAGTCGATGCCCCCTCCCCCCCAGCCGTCCCCCGCAGCCCG	113 <b>7</b> 633	
113 633	7 AGCCTCCCCATGCTGTCCTCGCCGTCACCGGGCCAGCAGGTGCAGACCCC :::   ::: ::: :::	1087	
108 616		1049	
104 600	O .CAGCCCCAGGTGCAGCAGCAGCAGACAGCAGTACAGACAG	1000 583	
583	AsnValValAspLysValIlePheArgTyrGlnLysTyrTyrGluTyrT	567	
999	CCC	991	
990	1 ATACCCAACCACCACTGAAATTTGTCCGAGCTCCGATGGTGGTGGAGCAG :::                       :: ::::      ::: 0 hrargGluIleMetGluLysAlaValArgGlyValPheLeuValGluPro	941 550	
550	IleArg	53	
940	·····CAAGCTCTCCC	916	

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seq_name: SwissProt_39:FSH_DROME
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EMBL; M23222; AAA28541.1; ALT_TERM.
EMBL; M15762; AAA70424.1; --
EMBL; M15763; AAA70423.1; --
EMBL; M15764; AAA70422.1; --
EMBL; M15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/
PROSITE; PS00633; BROMODOMAIN_1; 2.
PROSITE; PS50014; BROMODOMAIN_2; 2.
Developmental protein; Bromodomain;
DOMAIN 51 123 BROMODO
DOMAIN 495 567 BROMODO
DOMAIN 945 1106 ET DOMP
                                                                                                                                                                                                                                                        HSSP; P04002; 1WFA.
FlyBase; FBgn0004656; fs(1)h.
InterPro; IPR001487; Bromodomain.
Pfam; PF00439; bromodomain; 2.
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                                                                                                                                                                                                  PRINTS; PR00503; BROMODOMAIN. SMART; SM00297; BROMO; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Haynes S.R., Mozer B.A., Bhatia-Dey N., Dawid I.B.; "The Drosophila fsh locus, a maternal effect homeotic gene, encodes apparent membrane proteins."; Dev. Biol. 134:246-257(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. MEDLINE=89276730; PubMed=2567251;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEMALE STERILE HOMEOTIC PROTEIN (FRAGILE-CHORION MEMBRANE PROTEIN). FS(1)H OR FSH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P13709; P13710;
01-JAN-1990 (Rel. 13, Created)
01-JAN-1990 (Rel. 13, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation updat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            829
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Drosophila melanogaster (Fruit fly)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  896 heLysPro 898
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FUNCTION: REQUIRED MATERNALLY FOR PROPER EXPRESSION OF OTHER HOMEOTIC GENES INVOLVED IN PATTERN FORMATION, SUCH AS UBX. SIMILARITY: HIGH, TO HUMAN RINGS PROTEIN. SIMILARITY: CONTAINS 2 BROMODOMAINS. SIMILARITY: CONTAINS 1 ET DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ...GAGATCGCCCTG......GA 1580
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GAAACTCAAGAATGACATGCGGTGCCCACTCCCCCACCGCCCCCGGTGCC 1630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ValGluIleSerValArgAsnAsnLysLeuLeuMetProSerLysSerGl 879
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         lyLysLysLeuSerLysAlaAlaGlnLysAlaArgAspGlnAspPro 862
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BROMODOMAIN 1.
BROMODOMAIN 2.
ET DOMAIN.
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                                                                                        Transmembrane;
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alignment_scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Percent Similarity:
                                     1403
                                                                                              1386
                                                                                                                                                       1370
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1259 alAlaThrSerGlnSerSerGlyGlyIleArgIleAlaSerAsnLeuHis 1275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1242 oIleAsnAlaAlaLeuProProHisSerPheAlaGlyGlyThrAlaThrV 1259
547 CAGCTCCAGCAGCAGCAGCAGCAGCAGCATCTA.....ATTAA
                                                                  497
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          130 CATAACAAGAAA......TCTCAAGCTTCCGTCAGTGATCC
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VARIANT
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                                                                                        aGlyProGlnGlnGlnGlnGlnGlnGlnGlnGlnProPheGlyHisG
                                                                                                                                                    SerGlyLeuThrAspAsnPheLeuMetGlnGlnHisLeuMetGlnProAl 1386
                              AGCAGAGTGCCATGCAGCAGCAGTTCCAAGCAGTAGTGCAGCAGCAGCAG 546
                                                                                                                      GGCGCTACAGCAGCAGCAGCAGCAGCAGCAGCAGCTTCCAGGCTC
                                                                                                                                                                           ......CAGCAG.....CAGCAGCAGGC 446
                                                                                                                                                                                                             alGluGlnSerLeuAlaSerLeuGluPheSerAlaGlySerThrGlyLys 1369
                                                                                                                                                                                                                                       TGCAGCAGCAGCAACAGCAGCAGTTC......429
                                                                                                                                                                                                                                                                      uAlaSerLeuAlaSerGlyLeuLysGlnIleProGlnPheAspAspProV 1353
                                                                                                                                                                                                                                                                                                   CGTGTCTACGGCAACTCCACAGACCCAGCTGCAGCTCCAGCAGGTGGCGC 400
                                                                                                                                                                                                                                                                                                                                 AlaAsnProLeuGlyGlySerHisGlyAspAlaMetValAsnAlaSerLe 1336
                                                                                                                                                                                                                                                                                                                                                             ...CAGCCGCCTCCTGGGACCTCGGGGATGGCCCCTCACAGCATGGCTGT 350
                                                                                                                                                                                                                                                                                                                                                                                        hrGlyThrAlaGlyGlyGlyIleAsnAsnAsnGlyGlySerAsnAsnAsn 1319
                                                                                                                                                                                                                                                                                                                                                                                                                       TTGGTGCCATGGGACAGCCAATGTCTCTCTCAGGG.......
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     yGluHisHisAlaAlaLeuAlaAlaAlaLeuThrSerGlyIleAsnSerT 1303
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874
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471
770
810
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3 AA; 2'
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1.269
46.154
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Gaps: 20
Percent Identity: 26.834
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H -> RKPYY.
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                                 1409
                                                                                           1403
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410	GlnGlnGlnGlnGlnGlnGlnGlnHisMetAspTyrValThrGl 1	426
588 426	ATTGCATCAAAAATCAAGAAAAAAATAAAGAGAAGAACAGCAACAGCAACAGCAACAGCA 	37 443
638	GAATAGCACAGCTCCAGCTCCAACAACAGCAACAGCAGCAGCA	87
443	mAspM	459
889		05
460	lnGlnGlnGlnGlnG.:nAlaHisAsnAsnGlyPheAsnValAlaAspP	476
706	CAGGCTTT	15
.476	:AlaGlyPhe.\spGlyLeuAsnMetThrAlaAlaSerPheLeu	
716	GGCCCAGCCAAT"PCAGCAGCCACCGATGCAGCAGCCACAC : :::    :::	
493	luProSerLe iGlnGlnGlnMetGlnGln	.505
766	AGCAGCTGCAGCAGATGCATCACA	15
506	GlnLeuGlnGlnGlnHisHisGlnGlnG	.516
816	CACCAGCCGCCACCACAGCGCCCCAGCAGCCCT	365
1516	lnGlnThrHis 3lnGlnGlnGln	525
966	ATCACAACTCCCGCC \CAGTCGCAGACCCAGCCTTTGGTGTC	15
1526	lnHisGlnGlnGlnHisHisGlnGlnGl	1536
916	CTCTCCCTGGAC AAATGTTGTATACCCAACCA	65
س ۱	lnGlnLeuThrGlnGlnGlnLeuGlnGlnGlnGln	548
1549		1559
1016	GCAGCAGACAGCAGTACAGACAGCTCAGGCTGCCCAGATG	1065
1559	HisGlnGlnHisHisGlnAlaAlaAsnLysLe	1575
1066	GGTCAGCCAGAGCAGCCTCCCCATGCTGTCCT	1115
1576	roSerPr	1589
1116	AGCAGGTGCAGACCCCGCAGTCGATGCCCCCTCCCCC	1162
1589	lnLeuGlnGlnHisGlnLysValLeuProProGlnGlnSer	1606
1163	CGTCCCCGGAGCCCGGCCAGCCCAGCTCACAGCCCAACCTCCAACGTCAGC	121
1213	CTGGCCCTGCCCCATCTCCCAGTAGCTTCCTGCCCAGCCCC	126
1623	aLysIeuValGlnThrPh	1639
1263	CCCAGAGCCCAGTGACGGCGCGGACCCCACAG	1300
1639	nAlaSerSerTrpSerSerLeuAlaSerAlaAsnSerProGl	165
0	GTCCCCTCACCTGGACCTTTAAACACACCTGTGAACCCCAG	1350
1 2 7 7		
1665	::       ::       ::       ::       ::       ::       ::        ::        ::	168.

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seq_documentation_block:
ID SNF5_YEAST STAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1695 ysGluLysLysAsnGlnLysGluAlaAlaGluLysGluGlnGlnArgLys 1711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1433 AGCCCCTGCGCCGCATGATCAACAAGATCGACAAGAACGAAGACAGAAAA 1482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1681 aLysGluArg......AspArgLeuLysLeuLeuGluAlaAlaGluL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1383 TGAGGAGCAGCAGTACCTGGACAAGCTGAAGCAGCTGTCGAAGTACATCG 1432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (TRANSCRIPTION FACTOR TYE4).

SNF5 OR TYE4 OR SWI10 OR YBR289W OR YBR2036.
Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
NCBI_TaxID=4932;
                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Holmstroem K., Brandt T., Kallesoe T.,
"The sequence of a 32,420 bp segment located on the right arm of
chromosome II from Saccharomyces cerevisiae.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=91042489; PubMed=2233708; Laurent B.C., Treitel M.A., Carlson M.; Laurent B.C., Treitel A., Carlson M.; "The SNF5 protein of Saccharomyces cerevisiae is a glutamine- and proline-rich transcriptional activator that affects expression of broad spectrum of genes."; Mol. cell. Biol. 10:5616-5625(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1990 (Rel. 16, Created)
01-OCT-1994 (Rel. 30, Last sequence update)
01-OCT-1994 (Rel. 40, Last annotation update)
20-AUG-2001 (Rel. 40, Last annotation update)
TRANSCRIPTION REGULATORY PROTEIN SNF5 (SWI/SNF COMPLEX COMPONENT SNF5)
DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Yeast 10:547-562(1994).

11 FRANSCRIPTIONAL ACTIVATION. THE SWI/SNF COMPLEX IS REQUIRED FOR THE INDUCED EXPRESSION OF A LARGE NUMBER OF GENES. THIS COMPLEX ALTERS CHROMATIN STRUCTURE TO FACILITATE BINDING OF GENES-SPECIFIC DEDICATED TRANSCRIPTION FACTORS.

11 SUBUNIT: COMPONENT OF THE SWI/SNF GLOBAL TRANSCRIPTION ACTIVATOR
                                                                                                                                                                     EMBL; M36482; AAA35062.1; -. EMBL; X76053; CAA53652.1; -. EMBL; Z36158; CAA85254.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=94378722; PubMed=8091861;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-S288C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
  Transcription regulation; Activator; Nuclear protein.
DOMAIN
31 270 GLN-RICH.
DOMAIN
72 132 PRO-RICH.
DOMAIN 272 324 PRO-RICH.
DOMAIN 272 324 PRO-RICH (ACIDIC).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                              -!- SIMILARITY: BELONGS TO THE SNF5 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUBCELLULAR LOCATION: NUCLEAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPLEX
                                                                                                                         S44551; RGBYS5
S39145; S39145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               905 AA.
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SETT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Align seg 1/1 to: SNF5_YEAST from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-668-119-1 x SNF5_YEAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                422
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       136 AAGAAATCTCAAGCTTCCGTCAGTGATCCTATGAATGCACTCCAGAGCCT 185
                                                                                                                                                                                                                                                                                                                                                            186
                                                                                                                                                                                                                                                                                                                                                                                                                                       169 lnIleGluGlnGlnLysGlyGlnGlnThrAlaGlnThrGlnLeuGluGln 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             236 GCCCGGGACAGTCTCTGGGCGGGATGGGTAGCTTTGGTGCCATGGGACAG 285
                                                            636 GCAGCGAATAGCACAGCTGCAGCTCCAACAACAGCAACAGCAGCAGCAGC 685
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                286 CCAATG.....TCTCTCTCAGGGCAGCCGCCTCCTGGGACCTCGGG 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        89 ProIleAlaAsnGlnSerAlaThrSerThrProProProProPro.... 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        83 roProGlnGlnSer.....Gln
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                80 .....ProProProP 83
                                     64 GlnGlnGlnGlnGlnThrSerProProGlnThrHisGlnSer..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GATGGCCCCTCACAGCATG......
                                                                                                                                                                                                                                                                                                                                                          GlnArgGlnLeuLeuValGlnGlnGlnGlnGlnGlnGlnLeuArgAsnG1 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AGCAGCAGCAGCAGCTCCAGCAGCAGCAGCAGCAGCAGCATCTAATT 585
                                                                                                                                                                                                                                                                              nIleGlnArgGlnGln......GlnGlnGlnPheArgHisHisValG
                                                                                                                                                                                                                                                                                                                      GTTCCAGGCTCAGCAGAGTGCCATGCAGCAGCAGTTCCAAGCAGTAGTGC 535
                                                                                                                                                                                                                                                                                                                                                                                                   CAGCAGCAGGCGGCGCTACAGCAGCAGCAGCAGCAGCAGCAACAGCAGCA 485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      n \verb|ProGlnValValAsnAlaIleThrValAlaGlnGlnValGlnArgG|
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GlnGlnGlnValLeuAsnLysLeuArgGlnGlnAlaIleAlaLysAsnAs 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                roAlaProIleAsnLeuProProGlnIleAlaGlnLeuProLeuAlaThr 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ....AlaProHisAsnLeuHisProGlnIleGlyGlnValProLeuAlaP 119
                                                                                                                                                          AAATTGCATCAAAAATCAGCAACAGATACAGCAGCAGCAACAGCAGCT 635
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .....gcrgrcgrgrcracggcaacr 366
AGCAGCAGCAGCAGCAGCAGCCTTTGGAGGCCCAGCCACCAATTCAG
                                                                                                                    lnIleGlnGlnGlnGlnLysGlnGlnGlnGlnGlnGln.....
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        905 AA;
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755
564
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2.191
48.534
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798
564
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102557 MW; A287B4A648DD1A35 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ARG/LYS-RICH (BASIC).
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16
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seq_name: SwissProt_39:GLT4_WHEAT
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alignment_scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P08489;
01-AUG-1988 (Rel. 08, Created)
01-AUG-1988 (Rel. 08, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
GLUTENIN, HIGH MOLECULAR WEIGHT SUBUNIT PW212 PRECURSOR.
Triticum aestivum (Wheat).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             836
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nucleic Acids Res. 13:8729-8737(1985).

-i- FUNCTION: GLUTENINS ARE THE HIGH MOLECULAR WEIGHT SEED STORAGI PROTEIN OF WHEAT ENDOSPERM: THOUGHT TO BE RESPONSIBLE FOR THE VISCO-ELASTIC PROPERTY OF WHEAT DOUGH.

-i- SUBUNIT: DISCLEIDE-BRIDGE LINKED AGGREGATES.
                                                                                                                                                                                                                                                                                                   the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for commodified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sugiyama T., Rafalski A., Peterson D., Soll D.G.;
"A wheat HMW glutenin subunit gene reveals a highly repeated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-CV. YAMHILL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Spermatophyta; Magnoliophyta; Liliopsida; Poales; Triticeae; Triticum.
                                                                                                                                                                                                                                                             entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                  GROUP 1 CHROMOSOMES OF WHEAT:
-!- MISCELLANEOUS: THE MATURE PROTEIN IS CHARACTERIZED BY A LARGE NUMBER OF WELL PRESERVED REPEATS OF THE TWO MOTIFS: GQQPGQ AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- MISCELLANEOUS: GLUTENINS ARE CODED BY SEVERAL GENES ON EACH OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            structure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=86093674; PubMed=3001648;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=4565;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GLT4_WHEAT
                                                         SEQUENCE
                                                                                                              CHAIN
                                                                                                                                  Seed storage protein; Repeat; Multigene family; Signal. SIGNAL 1 \hspace{1cm} 21
                                                                                                                                                                      InterPro; IPR001419; Glutenin.
PRINTS; PR00210; GLUTENIN.
                                                                                                                                                                                                            PIR; A24107; EEWTHW.
                                                                                                                                                                                                                             EMBL; X03346; CAA27052.1; -.
                                                                           DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        snValGlnProThrIle.....GlyGlnLeuProGlnLeuProLysLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CCCAGCAGCCTCCAGTTGCTCAGAACCAACCATCACAACTCCCG..... 879
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GCAGCTGCAGCAGATGCATCACACACAGCACCACCAGCCGCCACCACAGC 835
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CAGCCACCGATGCAGCAGCCACAGCCTCCGCCCTCCCAGGCTCTGCCCCA 785
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                                                                                                                                                                                                                                                                                                                                                                                                                    GQQPGQGQQGYYPTS.
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                                                       838 AA;
                                                                             130
                                                                                                                22
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                                                                             799
                                                                                                                838
                                                           89174 MW;
                                                                           REPEATS
                                                                                                              GLUTENIN, HIGH MOLECULAR WEIGHT SUBUNIT
                                                                                                   PW212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                             71D715B7BDF0722D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       838
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pooideae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STORAGE
                                                                                                                                                                                                                                                                                                               commercial
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Quality:

317.50

Length:

2	CTGAAGACCTTGCAAAAGTGTGAGATCGCCCTGGAGAAACTCAAGAA 159:	1546
15 <b>4</b> 620	AGATGAAGAGCCTTCTGGACATTCTGACAGACCCCTCGAAGCGGTGTCCC ::::::	606
1 <b>4</b> 9 605	TGATCAACAAGATCGACAAGAACGAAGAACAAAAAAGGACCTGAGTA :             :::     :::::	1446 592
144 591	TACCTGGACAAGCTGAAGCAGCTGTCGAAGTACATCGAGCCCCTGCGCCG	1396 576
139 576	TGTCATGAGCCCAGCTGGCTCCAGCCAGGCTGAGGAGCAGCAG ::::::::::       ::::::       nLeuGlnGlnProAlaGlnGlyGlnGlnGlnGlnLeuAlaGlnGlyG	1353 559
135 559	TGAACCCCAGCTC :::   ::::: lnGlnProGlyGl	1303 5 <b>4</b> 3
130 542	CCTCCCAGAGCCCAGTGACGGCGCGGACCCCACAGAAC	N 6
126 526	TGGCCCTGCCCATCTCCCAGTAGCTTCCTGCCCAGCCCTCACCGCAGC	1215 509
121 509	<pre>TCCCCGCAGCCCAGCCCAGCTCACAGCCCAACTCCAACGTCAGCTC :::</pre>	1165 495
116 494	CGGGCCAGCAGGTGCAGACCCCGCAGTCGATGCCCCCT	1115 478
111 478	CGGAGTCCAGGTCAGCCAGAGCAGGCCTCCCCATGCTGTCCTCGCCGTCAC	1065 470
106	CAGCAGCA           GlnProGl	1015
10:	TCCGAGCTCCGATGGTGGTGCAGCAGCCCCCAG :::  ThrSerProGlnG	965 444
964	5 GCAAGCTCTCCCTGGACAAATGTTGTATACCCAACCACCACTGAAATTTG :   :::       ; glnGlyGlnProGlyTyrTyrLeu	915 435
43	:::	424
91,	CCATCACAACTCCCGCCACAGTCG	865
86	ACCACCAGCCGCCACCACCAGCCCCCAGCCTCCAG	815
81 40	4CAGCAGCTGCAGGATGCATCACACACAGC	78 39
39		7
37		35 75

620 lyGln......GlnProGlyGlnGlyGlnGln 628

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Seq_documentation_block:
ID GLT5_WHEAT STANDA
AC P10388;
DT 01-MAR-1989 (Rel. 10,
DT 01-NOV-1997 (Rel. 35,
DT 15-JUL-1999 (Rel. 38,
DE GLUTENIN, HIGH MOLECU
GN GLU-ID-1-D.D OR GLU-D1-1
OS Triticum aestivum (Wh
OC Eukaryota; Viridiplan
OC Triticeae; Triticum.
OX NCBI_TAXID-4565;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-CV. CHEYENNE;
RA Anderson O.D., Greene
RA Anderson O.D., Greene
RA MALPICA-Romero J.M.;
RI "Nucleotide sequences
RT "Nucleotide sequences
RT "Nucleotide Sequences
RT "Nucleotide Sequences
RT Cheyenne.";
RL Nucleic Acids Res. 17.
RN [2]
RP REVISIONS, SEQUENCE E
REVISIONS, SEQUENCE E
RC STRAIN-CV. CHEYENNE;
RA Anderson O.D.;
RL SUBUNIT: DISULFIII
CC -1- FUNCTION: GLUTENNI
CC -1- SUBUNIT: DISULFIII
CC -1- MISCELLANEOUS: GI
CC -1- SUBUNIT: DISULFII
CC -1- SUBUNIT: DISULFII
CC -1- SUBUNIT: DISULFII
CC -1- MISCELLANEOUS: GI

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                                                                                                                                                                                                                                                                                                                    alignment_scores:
                                                                                                                                                          alignment_block:
                                                                                                                                                                                                               Quality: 316.00
Ratio: 1.141
Percent Similarity: 45.041
                                                            Align seg 1/1 to: GLT5_WHEAT
                                                                                                                        US-09-668-119-1 x GLT5_WHEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           p10388;
01-MAR-1989 (Rel. 10, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
GLUTENIN, HIGH MOLECULAR WEIGHT SUBUNIT DX5 PRECURSOR.
GLU-1D-1D OR GLU-D1-1B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Nucleotide sequences of the two high-molecular-weight glutenin genes from the D-genome of a hexaploid bread wheat, Triticum aestivum L. cv Cheyenne.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Triticum aestivum (Wheat).

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;

Triticeae; Triticum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Anderson O.D., Greene F.C., Yip R.E., Halford N.G., Shewry P.R., Malpica-Romero J.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=CV. CHEYENNE;
MEDLINE=89098419; PubMed=2563152;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nucleic Acids Res. 17:461-462(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; X12928; CAA31395.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Seed storage protein; Repeat; Multigene family; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR001419; Glutenin. PRINTS; PR00210; GLUTENIN.
39 GGATATGGAGAGCCATGTTTTCCT...GAAGGCCAAGACCCGGGACGAAT 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GROUP 1 CHROMOSOMES OF WHEAT.
MISCELLANEOUS: THE MATURE PROTEIN IS CHARACTERIZED BY A LARGE NUMBER OF WELL PRESERVED REPEATS OF THE TWO MOTIFS: GQQPGQ AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GQQPGQGQQGYYPTS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CHEYENNE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                S02262.
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                                                                                                                                                                                                                                                                                                                                                                                                                     801 F
89359 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21
839
                                                                                                                                                                                                                         Length: 615
Gaps: 30
Percent Identity: 28.780
                                                               from: 1 to: 839
                                                                                                                                                                                                                                                                                                                                                                                                                                                   REPEATS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GLUTENIN, HIGH MOLECULAR WEIGHT SUBUNIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                        OF14E1106D552643 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                839 AA
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754	731 ·	681 338	637 I	619 305	579 I	544 ( 272 (	494 ( 255 :	463 238	418 ( 222 (	368 ( 207	318 G 1 200 y	268 T	218 7 186 .	177 C	129 . 156 J	86 A	127 G
CCACAGCCTCCGCCCTCCCAGGCTCTGCCC	TTCAGCAGCCACCGATGCA	GCAGCAGCAGCAGCAGCAGCAGCAGCGCTTTGGAGGCC 	CAGCGAATAGCACAGCTGCAGCTCCAACAACAGC    ::           		TCTAATTAAATTGCATCATCAAAATCAGCAACAGATACAG 	CAGCAGCTCCAGCAGCAGCAGCAGCAGC     	TCAGCAGAGTGCCATGCAGCAGCAGTTCCAAGCAGTAGT ::	cagcagcagcagcaacagcagca              yGlnGlyGlnGlnProGlyGlnGlyGlnGlnGlnGlyGlnGlnGlyGlnGlnGlyGlnGlnGlyGlnGlnGlyGlnGlnGlyGlnGlnGlyGlnGlnGlnGlyGlnGlnGlnGlyGlnGlnGlnGlyGlnGlnGlnGlyGlnGlnGlnGlnGlyGlnGlnGlnGlyGlnGlnGlnGlyGlnGlnGlnGlyGlnGlnGlnGlyGlnGlnGlnGlnGlyGlnGlnGlyGlnGlnGlnGlyGlnGlnGlnGlyGlnGlnGlnGlyGlnGlnGlnGlyGlnGlyGlnGlyGlnGlyGlnGlyGlnGlyGlnGlyGlnGlyGlnGlyGlnGlyGlnGlyGlnGlyGlyGlnGlyGlyGlnGlyGlyGlnGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyG	CAGCAGCAGTICCAGCAGCAGCAGCAGGCGGGCGCTACAGC                GlyGlnGlnGlyGlnGlnProGlyGlnAlaGlnGlnGlyG	CACAGACCCAGCTGCAGCTCCAGCAGGTGGCGCTGCAGCA	ACCTCGGGGATGGCCCCTCACAGCATGGCTGTCGTGTCT 	<pre>FTTGGTGCCATGGGCAGCCAATGTCTCTCTCAGGGCAGC        </pre>	TTGGCATGCCTCCTCGGGGCCCGGGACAGTCTCTGGGCGGG. ::        GlnGlnProGlyGln	CCAGAGCCTGACTGGCGGACCTGCTGCGGGAG    :: 	TCATAACAAGAAATCTCAAGCTTCCGTCAGTGATCCTAT ::: ::    ::::: ::   glnTrpGluGluProGluGlnGlyGlnGlnGlyTyrTyr	CCTTTCTCTGGGGGCAGGCTCATTATCCATTTTCGAGA	::::::     lyGlnAlaSerProGlnArgProGlyGlnGlyGlnGlnP
nSerGlyG	.GCA	CAGCCACCAA          GlnGlnProG	AACAGCAGCA             	AACAGCAGCTG        roGlyGlnLeu	SerGlyTyrT	AGCAGCAGCA     	GCAGCAGCAG         yGlnGlyGln	CAGTTCCAGG    :  ProGlyGlnG	AGCAG        InGlnProGl	GCAGCAGCAA           nProAlaGln	ACGGCAACTC	CGCCTCCTGG     roGlyGlnGl	GATGGGTAGC	GCCGCTGGAA	TGAATGCACT	CAT ::: GlnGlnProG	::: roGlyGln
783	; 753 1 371	730	. 338	636	618 305	578 288	543 271	493 255	462 238	417 221	367 206	317 200	267 190	217 185	176 172	128 156	142

1604 GCCCACTCCCCCACCGCCCCCGGTGCCACCCGACCAAACAGCAG 1646

645 .ProGlyGlnGlyGlnProTrpTyrTyrProThrSerProGln 658

75	1319 CTGGACCTTTAAACACACCTGTGAACCCCAGCTCTGTCATGAGC	_
13 73	ccacagaacTTcagTgTcccc ;;;;;;;;;;;;;;;;;;;;;;;;;;;;;;;	
12 71	1240 TTCCTGCCCAGCCCCTCACCGCAGCCCTCCCAGAGCCCAGTGACGCGCGCG	ъ
12 70	190 CACAG 687 alGly	₽
11 68	149 CCCTCCCCCAGCCGTCCCCGCAGCCCGGCCAGCCG             :::    	<u> </u>
11 67	122GCAGGTGCAGACCCCGCAGTCGAT :::   :::    ::: 654 roGlySerProProSerPheArgThrGlyThrProProGlyTyrArc	ь
11 65	082 AGAGCAGCCTCCCCATGCTGTCCTCGCC         ::: 641ProGlyAlaTyrLysTh	ш.
108	.032 ACAGACAGCTCAGGCTGCCCAGATGGTGGCTCCCGGAGTCCAGGTCCAGGTCCAGGTCCAGGTCCAGGTCCAGGTCCAGATGGTGCCCGGAGTCCAGGTCCAGGTCCAGATGGTGCTCCAGGTCCAGATGCCAGATGGTCAGATGATAGATA	ь
625	982 GTGCAGCAGCCCCAGTGCAGCCCCAGGTGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG	
981	932 AAATGTTGTATACCCAACCACCACTGAAATTTGTCCGAGCTCCGATGGTG	
597	882 ACAGTCGCAGACCCAGCCTTTGGTGTCACAGGCGCAAGCTCTCCCTGGAC :::         ::	
881 580	832 CAGCCCCAGCAGCCTCCAGTTGCTCAGAACCAACCATCACAACTCCCGCC ::::: ::::::          ::: :::     ::: 566 erserAsnSerSerSerSerThrSerGlnGlySerTyrProCys	
831 566	795 GCAGATGCATCACACACAGCACCACCAGCCAGCCACCA :   ::::::   :   ::::::::::::::::	
794 549	763CTGCCCCAGCCTCCCAGGCTCTGCCCCCAGCAGCTGCA       ::         :: 533 SerLeuArgProTyrProProGlyProAlaHisLeuProProProHisSe	
532	${\tt is AlaHisProTyrAlaMetSerProSerLeuGly}$	
762		
762 516	GCAGCCACCGATGCAGCAGCCACAGCCT	
719 502	670 CAACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC	
669 485	644 TAGGACAGGTGCAGCTCCAACAACAG (	

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seq_documentation_block
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                                           MEDLINE-90348718; PubMed-2200963;

KC C., Smith C.K. II. McDonell M.;

"Identification and pharacterization of a target antigen of a monoclonal antibody directed against Eimeria tenella merozoites.";

MOI. Biochem. Parasicol. 41:53-64(1990).

MOI. Biochem. Parasicol. 41:53-64(1990).

MOI. Biochem. Parasicol. THE GLN-RICH TANDEM REPEATS MAY BE IMPORTANT FOR AN UNKNOWN A SPECT OF THE PARASITIC LIFE CYCLE. MAY BE AN IMPORTANT IMMUNOJEN.

-i- SUBGUNT: MAY BE CONALENTLY LINKED BY DISULFIDE BONDS TO OTHER POLYPEPTIDES TO COMM THE 80 KDA ANTIGEN.

-i- SUBGUNT: MAY BE CONALENTLY LINKED BY DISULFIDE BONDS TO OTHER POLYPEPTIDES TO COMM THE 80 KDA ANTIGEN.

-i- DEVELOPMENTAL STAGE: PRESENT IN ALL STAGES THROUGHOUT THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
01-FEB-1994 (Rel. 28, Last annotation update)
ANTIGEN LPMC-61 (FRA3MENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1684 ACATCCGCTCACCTGTCTTCAACCATTCCCTGTACCGCACATTCGTTCC 1732
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1634 GACCAAACAGCAGTACCTATGCCAGCCGCTCCTGGATGCCGTCCTGGCCA 1683
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1596 CATGCGGTGC........CCACTCCCCCACCGCCCCCGGTGCCACC 1633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1546 CTGAAGACCTTGCAA!AGTGTGAGATCGCCCTGGAGAAACTCAAGAATGA 1595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1496 AGATGAAGAGCCTTCTGGACATTCTGACAGACCCCTCGAAGCGGTGTCCC 1545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1449 ... GATCAACAAGAT(GACAAGAACGAAGACAGAAAAAAAGGACCTGAGTA 1495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1408 .....CTGAAGCAGCTGTCGAAGTACATCGAGCCCCTGCGCCGCAT. 1448
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        875 rProAlaLeuArgThrLeuSerGluTyrAlaArgProHisValMetSer 891
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida; Eimeriidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P15714;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         846 ......CysProSerLeuGlyProValProHisArgProPro...PheG 859
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     818 gGluLysGluArgGluArgGluLysGluArgGluLeuGlu.Arg...Ser 833
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   802 AlaGluGlnArgAlaLrgGluGluLysGluArgGluArgGluArgGluAr 818
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=5802;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LP61_EIMTE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  752 ProSerHisAlaSerGlnSerAlaArgPheAsnLysHisLeuAspArgGl 768
EXCYSTATION.
                              SPORULATION OF THE OCCYSTS AND IN THE SPOROZOITES FOLLOWING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
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alignment_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-668-119-1 x LP61_EIMTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Percent Similarity:
                                                                                                                                                                                                                                                                                568 ..CAGCAGCAGCATCTAATTAAATTGCATCATCAAAATCAGCAACAGATA 615
||||||||||
105 roGlnGlnGlnHis.....ArgArgGlnHisGlyGlnGlnGlnGlnGlnCys 119
170 GlnGlnGlnTrpSerAspGlnAsnGlnGlnGlnGlnAlaGlnGlnTrpGl 186
                             754 CCACAGCCTCCGCCCTCCCAGGCTCTGCCCCAGCAGCTGCAGCAGCAGATGCA 803
                                                                    153 rpProGluGlnProGluGlnGlnGlnGlnGlnTrpProGluGlnGln 169
                                                                                                    136 nLeuGlnGlnTrpSerGluGlnGlnGlnGlnGlnGlnGlnGlnT 153
                                                                                                                                                                               666 A...CAGCAACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCCTT 712
                                                                                                                                                                                                                120 MetAsnSerGlnGlnGlnLeuGlnGlnCysGlyGlnGlnGlnGlnGlnGl 136
                                                                                                                                                                                                                                                   616 CAGCAGCAGCAACAGCAGCTGCAGCGAATAGCACAGCTGCAGCTCCAACA 665
                                                                                                                                                                                                                                                                                                                                                                                             522 CCAAGCAGTAGTGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG.... 567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  472 CAGCAACAGCAGTTCCAGGCTCAGCAGAGTGCCATGCAGCAGCAGTT 521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        433 .....CAGCAGCAGCAGCGGCGCGCTACAGCAGCAGCAGCAGCAG 471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         367 CCACAGACCCAGCTGCAGCTCCAGCAGGTGGCGCTGCAGCAGCAGCAGCA 416
                                                                                                                                                                                                                                                                                                                                                           89 .GluGlnTrpProGlnGlnGlnProGlnValGlnGlnGlnGlnTrpP 105
                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     57 euTrpProGluGlnGlnGlnGlnTrpProGluGlnHisGlnGlnAla 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          40 sAsnGlnGlnLeuGlnLysGlnGlnTrpProGluGlyGlnArgGlnGlnL 57
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27 ProGlnProTrpLeuAspArgGlnGln.......GlnGlnGlnHi 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REPEAT
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Ratio:
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2.719
60.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Percent Identity: 46.842
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Seq_documentation_block:
ID VGIX_HSVEB STANDA
AC P28968;
PT 01-DEC-1992 (Rel. 24,
PT N (I)
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US-09-668-119-1 x VGLX_HSVEB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             lignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Align seg 1/1 to: VGLX_HSVEB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                             554 AGCAGCAGCAGCAGCAGCAGCATCTAATTAAATTGCATCATCAAAAT 603
                                                                                                                                                                                                   504
                                                                                                                                                                                                                                                                                            454 CAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGTTCCAGGCTCAGGAGAG 503
                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.

MEDLINE=92295566; PubMed=1318606;

METHOR E.A.R., Watson M.S., McBride K., Davison A.J.;

"The DNA sequence of equine herpesvirus-1.";

Virology 189:304-316(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Equine herpesvirus type 1 (strain Ab4p) (EHV-1). Viruses; dsDNA viruses, no RNA stage; Herpesviridae; Alphaherpesvirinae; Varicellovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-DEC-1992 (Rel. 24, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
01-DEC-1992 (Rel. 24, Last annotation update)
GLYCOPROTEIN X PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                804 TCACACACAGCACCAGCCGCACCAGCCCAGCCAGCCTCCAGTTG 853
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       854 CTCAGAACCAACCATCACAA 873
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; M86664; AAB02506.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         203 lnGlnGlnGlnGlnGln 209
      73
                                                                                                                                  57
                                                                                                                                                                                                                                                                                                                                                                                             24 ThrThrGluThrThrThrSerSerSerThrSerGlySerGlyGl 40
roProThrThrSerSerSerProPro...ThrSerThrHisThrSerSer 72
                                                                                                                                                                                            TGCCATGCAGCAGCAGTTCCAAGCAGTAGTGCAGCAGCAGCAGCAGCTCC
                                                                                                                                                                                                                                                              nSerThrSerSerGlyThrThrAsnSerSerSerSerProThrThrSerP 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SwissProt_39:VGLX_HSVEB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             310.00
1.225
58.295
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797
465
790
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length: 434
Gaps: 11
Percent Identity: 26.728
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL.
N-LINKED (GLCNAC. . .) (POTENTIAL).
50C9ED9211F5E5B2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GLYCOPROTEIN X. SER/THR-RICH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Signal.
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
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   89
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378	SerSerThrGlySerThrSerThrAlaGluProSerSer	366
1455	GCTGAAGCAGCTGTCGAAGTACATCGAGCCCCTGCGCCGCATGATCAAC	1406
1405 365	CATGAGCCCAGCTGGCTCCAGCCAGGCTGAGGAGCAGCAGTACCTGGACA::::::::::	1356 349
1355 349	AGTGTCCCCTCACCTGGACCTTTAAACACACCTGTGAACCCCAGCTCTGT::::: :::	1306 333
1305 332	CGCAGCCCTCCCAGAGCCCAGTGACGGCGCGGACCCCACAGAACTTC	1259 316
1258 316	CCCTGCCCCATCTCCCAGTAGCTTCCTGCCCAGCCCTCAC :::   :::   :::   ::: rSerThrProThrProThrSerAlaAlaThrSerAlaGluSerThrThrG	1218 299
1217 299	hr	1168 283
1167 282	GCCAGCAGGTGCAGACCCCGCAGTCGATGCCCCCCCCCC	1118 266
1117 266	AGTCCAGGTCAGCCAGAGCAGCCTCCCCATGCTGTCCTCGCCGTCACCGG ::: ::::: ::::: :::: ::::::::::::::	1068 249
1067 249	CAGCAGACAGCAGTACAGACAGCTCAGGCTGCCCAGATGGTGGCTGCCCGG:::::      :::    :::    :::  :    hrThr.ThrAlaAlaThrThrAlaAlaThrThrThrAlaAlaThrTh	1018 233
1017 233	ATC hr1	968 216
967 216	AGCTCTCCCTGGACAAATGTTGTATACCCAACCACCACCACTGAAATTTGTCC::::::::::	918 202
917 201	TCACAACTCCCGCCACAGTCGCAGACCCAGCCTTTGGTGTCACAGGCGCA       : : : :       : : : : :       : : : : : :       : : :       : : :       : : :         : : :         : :         : :         : :           : :	868 185
867 185	A - 6	818 168
817 168	CTCCCAGGCTCTGCCCCAGCAGCAGCAGATGCATCACACACA	768 155
767 154	GCCCAGCCAATTCAGCAGCCACCGATGCAGCAGCCACAGCCTCCGCC::::!  :::::            :::          :::	718 139
717 139	AGCAGCAGCAGCAGC ::::::      :::: oThrThrAlaAlaThrTh	668 122
667 122	hrThrThrThrProThrAla	106
653 105	GCAACAGATACAGCAGCAGCAACAGCAGCTG     :::      :::::   :::::  AlaProSerThrAlaSerSerThrThrSerI	8 0

1606 397	390	1556	379	1506	378	1456
1606 CCACTCCCCCACCGCCCCCCGGTGCCACCCAACCAACAGCAGTACCT 1651 : ::     :::       ::::::::	SerThrAspGlnPheThrGlySe 397	1556 TGCAAAAGTGTGAGATC3CCCTGGAGAAACTCAAGAATGACATGCGGTGC 1605	ThrPheThrLeuThrProSerThrAlaThrPro 389	1506 CCTTCTGGACATTCTGACAGACCCCTCGAAGCGGTGTCCCCTGAAGACCT 1555		1456 AAGATCGACAAGAACGAAGACAGAAAAAAAGGACCTGAGTAAGATGAAGAG 1505
	97	605	89	555	78	505

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Database sequences: 473505
Database length: 146272329
Search time (sec): 141.200000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               score_list:
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Command line parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Database: SPTREMBL_17:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query length: 1740
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -MODEL=frame+_n2p.model -DEV=xlp
-Q=/Cgn2_1/USPTO_spool/US09668119/runat_28022002_084717_19384/app_query.fasta_1.1824
-Q=/Cgn2_1/USPTO_spool/US09668119/runat_28022002_084717_19384/app_query.fasta_1.1824
-DB=SPTREMBL_17 - QFMT-fastan -SUFFIX=rspt -GAPOP=12.000
-GAPEXT=4.000 -MINANTCH=0.100 -LOOPCL=0.000 -LOOPEXT=0.000
-QGAPOP=4.500 -MINANTCH=0.100 -XGAPOP=10.000 -XGAPEXT=0.500
-TGAPOP=6.000 -TGAPEXT=7.000 -XGAPOP=10.000 -XGAPEXT=0.500
-TGAPOP=6.000 -FGAPEXT=7.000 -XGAPOP=10.000 -XGAPEXT=0.500
-DELOP=6.000 -DELEXT=7.000 -XGAPOP=10.000 -XGAPEXT=0.500
-DELOP=6.000 -DELEXT=7.000 -XGAPOP=10.000 -XGAPEXT=0.500
-TRANS-human40.cdi -LIST=45 -DOCALIGN=20 -THR_SCORE-pct
-THR_MAX=100 -THR_MIN-0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pfs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -NORM=ext -MINLEN=0 -MAXLEN=2000000000
-USER=US09668119_@CGN1_1_171 -NCPU=6 -ICPU=3 -LONGLOG -NO_XLPXY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Feb 28, 2002 7:35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Results were produced by the GenCore software, Copyright (c) 1993-2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-668-119-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -THREADS=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sp_plant:Q9SYQ6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  alignment_block:
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                                                                                                                                                                                                       201
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                                                                         101
                                                                                                                                                      251
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sp_invertebrate:Q9NF31 + 379.00
sp_invertebrate:Q9NF32 + 379.00
sp_invertebrate:Q9NF37 + 378.00
sp_invertebrate:Q9NF37 + 378.00
sp_plant:Q9SYQ6 + 374.00 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               seq_name: sp_human:Q9P1T3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Align seg 1/1 to: Q9P1T3 from: 1 to: 579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-668-119-1 x Q9P1T3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-OCT-2000 (TrEMBLrel. 15, 01-OCT-2000 (TrEMBLrel. 15, 01-JUN-2001 (TrEMBLrel. 17,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR002965; P_rich_extensn. PRINTS; PR01217; PRICHEXTENSN. SEQUENCE 579 AA; 63879 MW; CCC9E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "A novel glutamine rich putative transcriptional adaptor preferentially expressed in placenta and bone marrow tiss Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AF056191; AAC12944.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TPA INDUCIBLE PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                              151 TCCGTCAGTGATCCTATGAATGCACTCCAGAGCCTGACTGGCGGACCTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            101 CCAGGCTCATTATCCATTTTCGAGACATTCATAACAAGAAATCTCAAGCT 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17 rHisValPheLeuLysAlaLysThrArgAspGluTyrLeuSerLeuValA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       51 CCATGTTTTCCTGAAGGCCAAGACCCGGGGACGAATACCTTTCTCTCGTGG 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 ATGAGGAAAGCTGGTGGCACACAGTAAATCCAGCAAGGATATGGAGAG
                                                                                                                    GGGCAGCCGCCTCCTGGGACCTCGGGGATGGCCCCTCACAGCCATGGCTGT
                                                                                                                                                                                                                                                                                      CGTGTCTACGGCAACTCCACAGACCCAGCTGCAGCTCCAGCAGGTGGCGC 400
                                                                                                                                                                                                                                           laArgLeuIleIleHisPheArgAspIleHisAsnLysLysSerGlnAla
GlyGlnProProGlyThrSerGlyMetAlaProHisSerMetAlaVa
                                                                                                                                                                                           \verb"euGlyGlyMetGlySerPheGlyAlaMetGlyGlnProMetSerLeuSer"
                                                                                                                                                                                                                                                                                                                                        TGCGGGAGCCGCTGGAATTGGCATGCCTCCTCGGGGCCCGGGACAGTCTC
                                                                                                                                                                                                                                                                                                                                                                                      SerValSerAspProMetAsnAlaLeuGlnSerLeuThrGlyGlyProAl 67
                                                                                                                                                                                                                                                                                                                                                                                                            Quality: 3010.00
Ratio: 5.199
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Solomon W.B.;
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00 383.47 2.6e-14
00 382.58 3.0e-14
00 380.35 2.7e-14
380.36 5.4e-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                579 AA
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1624 i Q9w523 drosophila melanog
1589 i Q46097 drosophila melanog
2309 i Q9w2u7 drosophila melanog
1164 i Q9syq6 arabidopsis thaliana
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       134
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1301 ACTICAGIGICCCCTCACCIGGACCITTAAACACACCIGIGAACCCCAGC 1350
                                     1151 CTCCCCCCAGCCGTCCCCGCAGCCCAGCCCAGCCCAGCTCACAGCCCAAC 1200
                                                                                                                                                                                                                                                                                                                           1201 TCCAACGTCAGCTCTG3CCCTGCCCCATCTCCCCAGTAGCTTCCTGCCCAG 1250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1051 CAGATGGTGGCTCCCGGAGTCCAGGTCAGCCAGAGCAGCCTCCCCATGCT 1100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1001 AGCCCCAGGTGCAGCAGCAGCAGCAGCAGTACAGACAGCTCAGGCTGCC 1050
                                                                                                                                         401 SerAsnValSerSerGlyProAlaProSerProSerSerPheLeuProSe 417
                                                                                                                                                                                                                                          384
                                                                                                                                                                                                                                                                                                                                                                                                                         351 GlnMetValAlaProGlyValGlnValSerGlnSerSerLeuProMetLe 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              317 oProLeuLysPheValArgAlaProMetValValGlnGlnProProValG 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  334 lnProGlnValGlnGlnGlnGlnThrAlaValGlnThrAlaGlnAlaAla 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            951 ACCACTGAAATTTGTCCGAGCTCCGATGGTGGTGCAGCAGCCCCCAGTGC 1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       301 LeuValSerGlnAlaClnAlaLeuProGlyGlnMetLeuTyrThrGlnPr 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     901 TTGGTGTCACAGGCGCAAGCTCTCCCTGGACAAATGTTGTATACCCAACC 950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              851 TTGCTCAGAACCAACCATCACAACTCCCGCCACAGTCGCAGACCCAGCCT 900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    801 GCATCACACACAGCAC CACCAGCCGCCACCACCAGCCCCCAGCAGCCTCCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              234 lnGlnGlnAlaLeuGluAlaGlnProProIleGlnGlnProProMetGln
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            217 nLeuGlnLeuGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnG 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          601 AATCAGCAACAGATAKAGCAGCAGCAACAGCAGCTGCAGCGAATAGCACA 650
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      451 CTACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGTTCCAGGCTCAGCA 500
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              701 AGCAGCAGGCTTTGGLGGCCCAGCCACCAATTCAGCAGCCACCGATGCAG 750
                                                                                                                                                                                                                                  roProProGlnProSerProGlnProGlyGlnProSerSerGlnProAsn 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                alAlaGlnAsnGlnProSerGlnLeuProProGlnSerGlnThrGlnPro 300
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alignment_scores:
Quality: 1780.00
                                                                                                                                seq_documentation_block:
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Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1401 GGACAAGCTGAAGCAGCTGTCGAAGTACATCGAGCCCCTGCGCCGCATGA 1450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1701 TTCAACCATTCCCTGTACCGCACATTCGTTCCAGCCA 1737
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1601 GGTGCCCACTCCCCCACCGCCCCCGGTGCCACCGACCAAACAGCAGTACC 1650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1451 TCAACAAGATCGACAAGAACGAAGAACAGAAAAAAGGACCTGAGTAAGATG 1500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1351 TCTGTCATGAGCCCAGCTGGCTCCAGCCAGGCTGAGGAGCAGCAGTACCT 1400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1551 GACCTTGCAAAAGTGTGAGATCGCCCTGGAGAAACTCAAGAATGACATGC 1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1501 AAGAGCCTTCTGGACATTCTGACAGACCCCTCGAAGCGGTGTCCCCTGAA 1550
                                                                                                                           NON_TER 349
SEQUENCE 349 AA;
                                                                                                                                                                                Margolis R.L., Abraham M.R., Gatchell S.B., Li S.H., Kidwai A.S., Bresschel T.S., Stine O.C., Callahan C., Mcinnis M.G., Ross C.A.; "cDNAs with long CAG trinucleotide repeats from human brain."; Hum. Genet. 100:114-122(1997).
EMBL; U80745; AAB91443.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   534 rgCysProLeuProH1sArgProArgCysH1sArgProAsnSerSerThr 550
                                                                                                                                                                                                                                                                                         MEDLINE=97369492; PubMed=9225980;
                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      567 rSerThrIleProCysThrAlaHisSerPheGlnPro 579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  517 sThrLeuGlnLysCysGluIleAlaLeuGluLysLeuLysAsnAspMetA 534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     501 LysSerLeuLeuAspIleLeuThrAspProSerLysArgCysProLeuLy 517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    484 leAsnLysIleAspLysAsnGluAspArgLysLysAspLeuSerLysMet 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   467 uAspLysLeuLysGlnLeuSerLysTyrIleGluProLeuArgArgMetI 484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 451 SerValMetSerProAlaGlySerSerGlnAlaGluGluGlnGlnTyrLe 467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE-CEREBRAL CORTEX;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CTG7A (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    015413;
                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                      349
; 38853 MW; D073F67E22B70533 CRC64;
Percent Identity: 99.710
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                          Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  349 AA
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alignment\_block: US-09-668-119-1 x O15413

Align seg 1/1 to: 015413 from: 1 to:

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1231
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              981
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      781
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    731
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             481 CAGCAGTTCCAGGCTCAGCAGAGTGCCATGCAGCAGCAGTTCCAAGCAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           69
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TTCAGCAGCCACCGATGCAGCAGCCACAGCCTCCCGCCCTCCCAGGCTCTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GlnGlnPheGlnAlaGlnGln***AlaMetGlnGlnFheGlnAlaVa
                                                                                                                                                                                                                                                                                                  CCCAGTAGCTTCCTGCCCAGCCCCTCACCGCAGCCCTCCCAGAGCCCAGT 1280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   alGlnThrAlaGlnAlaAlaGlnMetValAlaProGlyValGlnValSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CAAATGTTGTATACCCAACCACCACTGAAATTTGTCCGAGCTCCGATGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACAGCCCCAGCAGCCTCCAGTTGCTCAGAACCAACCATCACAACTCCCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           nGlnGlnGlnGlnGlnGlnGlnGlnAlaLeuGluAlaGlnProProI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GlnLeuGlnArgIleAlaGlnLeuGlnLeuGlnGlnGlnGlnGlnGlnGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    lValGlnGlnGlnGlnLeuGlnGlnGlnGlnGlnGlnGlnHisL
                                                                                                                                                                                 GACGGCGCGGACCCCACAGAACTTCAGTGTCCCCTCACCTGGACCTTTAA 1330
                                                                                                                                                                                                                                                                                                                                                                                                                      AGCCCAGCTCACAGCCCAACTCCAACGTCAGCTCTGGCCCCTGCCCCATCT 1230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             nThrProGlnSerMetProProProGlnProSerProGlnProGlyG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GACCCCGCAGTCGATGCCCCCCCCCCCCCCCGCAGCCCGCAGCCCGGCC 1180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GlnSerSerLeuProMetLeuSerSerProSerProGlyGlnGlnValGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CAGAGCAGCCTCCCCATGCTGTCCTCGCCGTCACCGGGCCAGCAGGTGCA 1130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TACAGACAGCTCAGGCTGCCCAGATGGTGGCTCCCGGAGTCCAGGTCAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    lValGlnGlnProValGlnProGlnValGlnGlnGlnGlnThrAlaV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GGTGCAGCAGCCCCAGTGCAGCCCCAGGTGCAGCAGCAGCAGCAGCAG 1030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         roGlnSerGlnThrGlnProLeuValSerGlnAlaGlnAlaLeuProGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          oGlnProGlnGlnProProValAlaGlnAsnGlnProSerGlnLeuProP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ProGlnGlnLeuGlnGlnMetHisHisThrGlnHisHisGlnProProPr 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CCCCAGCAGCTGCAGCAGATGCATCACACACCAGCCACCAGCCGCCACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             leGlnGlnProProMetGlnGlnProGlnProProProSerGlnAlaLeu 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                euIleLysLeuHisHisGlnAsnGlnGlnGlnIleGlnGlnGlnGln
ProSerSerPheLeuProSerProSerProGlnProSerGlnSerProVa
                                                                                                                                                                                                                                                                                                                                                            lnProSerSerGlnProAsnSerAsnValSerSerGlyProAlaProSer
                                                                                                                                                                                                                                                                                                                                                                                        236
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GCTGAGGAGCAGCAGTACCTGGACAAGCTGAAGCAGCTGTCGAAGTACAT 1430

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RX MEDLINE 2019(06; PubMed=10731132; RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., RA Adams M.D., Celniker S.E., Holt R.M., Hoskins R.A., Galle R.F., RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., RA Amanatides P.G., Scherer S.E., Richards S., Ashburner M., Henderson S.N., RA Sutton G.G., Wortman J.R., Yaneell M.D., Zhang Q., Chen L.X., RA Brandon R.C., Rogers Y.H.C., Blazej R.G., Champe M., Pfeiffer B.D., RA Brandon R.C., Rogers Y.H.C., Blazej R.G., Champe M., Pfeiffer B.D., RA Brandon R.C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G., RA Abril J.F., Agbayani A., An H.J., Andrews Pfannkoch C. Baldwin D., RA Becson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S., RA Berkova D., Botchan M.R., Bouck J., Byraktargulu L., Beasley E.M., RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P., RA Borkova D., Botchan A.E., Butler H., Cadleu E., Center A., Chandra I., RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., RA Dodson K., Doup L.E., Downes M., Dugain Rocha S., Dunkov B.C., Dunn P., RA Gerbiel J.M., S., Galbart W.M., Glasser K., RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M., RA Harris M.L., Harvey D., Helman T.J., Hernandez J.R., Houck J., RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibeywan C., RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibeywan C., RA Kinmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z., Liang Y., Lin X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.L., Ra Markilov G., Mishina N.V., Moharry C., Worris J., Moshrefi A., Ra Mount S.M., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M., Ra Harris M.P., Pathen G.S., Pan S., Pollard J., Puri Y., Reese M.G., RA Ra Herris M., Weissarman D.A., Weinstock G.M., Weissenbach J., Ra Abne B.C., Stapleton M., Strong R., Sun E., Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang S., Yao Q.A., Pan M., Thang G., Zhao Q., Zheng L., Pathen M., Smith H.O., Zhang S., Zhao Q., Zheng L., Pathen M., Smith H.O., Zhang S., Zhao Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        seq_name: sp_invertebrate:Q9Y149
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Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1999 (TrEMBLrel 12, Created)
01-NOV-1999 (TrEMBLrel 12, Last seq
01-JUN-2001 (TrEMBLrel 17, Last ann
BCDNA:GH03922 PROTEIN.
SEQUENCE FROM N.A.

Rubin G.M., Wan K.H., Harvey D., Lewis S.E., Brokstein P., Tsan Agbayani A., Arcaina T.T., Baxter E., Blazej R.G., Butenhoff C. Champe M., Chavez C., Chew M., Doyle C.M., Farfan D.E., Frise E
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  eGluProLeuArgArgMetIleAsnLysIleAspLysAsnGluAspArgL 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CGAGCCCCTGCGCCGCATGATCAACAAGATCGACAAGAACGAAGACAGAA 1480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
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Last annotation updat
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alignment_scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-668-119-1 x Q9Y149
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                                                                                                                                                                                                                                                                                        462 GCAGCAGCAGCAACAGCAGCAGTTCCAGGCTCAGCAGAGTGCCATGC 511
                                                                                                                                                                                                                               | 152 tSerAsnIleArgGlyGlnMetProMetGlyAlaGlyGlyAlaGlyAlaG 169
184 ProGlyValMetAsnValMetGlyAlaGlyGlyGlyGlnAsnGlnGlyGl 200
                                                                                                                                                                          512 AGCAGCAGTTCCAAGCAGTAGTGCAGCAGCAGCAGCAGCAGCAGCAGCAG
                                                                                                                                                                                                                                                                                                                                             140 AsnGlnGlnArgProGlyGlnGlnGln......MetGlnProMe 152
                                                                                                                                                                                                                                                                                                                                                                                                      412 CAGCAACAGCAGCAGTTCCAGCAGCAGCAGCAGCGGCGCCTACAGCAGCA 461
                                                                                                                                                                                                                                                                                                                                                                                                                                                        135 ......LeuLeuGlnSerLeu 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Galle R., George R.A., Harris N.L., Hoskins R.A., Evans-Holm M.,
Houston K.A., Hummasti S.R., Kim E., Li P., Moshrefi M., Pacleb J.M.,
Park S., Sequeira A., Sethi H., Snir E., Svirskas R.R., Weinburg T.,
"Full length Drosophila melanogaster cDNA sequence.";
Submitted (APR-199) to the EMBL/GenBank/DDBJ databases.
EMBL, APR003589; AAF11490.1;
EMBL; AF1003589; AAF11490.1;
EMBL; AF145620; AAD:8595.1;
ENBBL; AF145620; AAD:8595.1;
ENBBL; AF145620; AAD:8595.1;
ENBBL; AF145620; AAD:8595.1;
ENBBL; AF145620; AAD:80526 MW; 42375AEB7C13A1DF CRC64;
                                                        562 CAGCAGCAGCAGCATCTAATTAAATTGCATCATCAAAATCAGCAACA 611
                                                                                                                 169 lnGlnMetMetGln.....ValGlnGlnMetGlnGlnGlyGlyAsnAla 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    362 CAACTCCACAGACCCAGCTGCAGCTCCAGCAGGTGGCGCTGCAGCAGCAG 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  312 TCCTGGGACCTCGGGGATGGCCCCTCACAGCATGGCTGTCGTGTCTACGG 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 ......GlyGlyAlaProVa 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   262 GGTAGCTTTGGTGCCATGGGACAGCCAATGTCTCTCTCAGGGCAGCCGCC 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        110 rgAsnProGlnMetMetProMetGlyAlaGly...... 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    162 TCCTATGAATGCACTCCAGAGCCTGACTGGCGGACCTGCTGCGGGAGCCG 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           212 CTGGAATTGGCATGCCTCCTCGGGGCCCCGGGACAGTCTCTGGGCGGGATG 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                154 ......GTCAGTGA 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      96 pProLeuAsnAlaLeuGlnAsnLeuAla.....SerGlnGlyAsnA 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        80 GlyProProAsnAlaGluMetGlyGlyGlyGlnAsnMetMetGlnAs 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         63 spMetSerArgLysSerGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGly 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    46 rLysAspGluTyrLeuGlyLeuValAlaLysLeuPheMetHisTyrLysA 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30 ThrLysasnalaGlyValMetGluAsnHisIlePheArgLysSerArgTh 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  75 CCGGGACGAATACCTTTCTCTCGTGGCCAGGCTCATTATCCATTTTCGAG 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25 AGTAAATCCAGCAAGCATATGGAGAGCCATGTTTTCCTGAAGGCCAAGAC 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Quality: 517.00
Ratio: 1.548
milarity: 50.915
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Percent Identity: 29.268
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1331 475	GGGACCCCACAGAACTTCAGTGTCCCCTCACCTGGACCTTTAAA 1 ::::::    :::    :::	1288 460
1287 459	GCTTCCTGCCCAGCCCCTCACCGCAGCCCTCCCAGAGCCCAGTGACGGCG 1	1238 443
1237 443	CTCACAGCCCAACTCCAACGTCAGCTCTGGGCCCTGCCCCATCTCCCAGTA 1 :::   :::      :::      :::	1188 428
427		N
		. o t
4 O F		386
- 60	GlyGlyValGlyValGlyGlyGlnGlnproGlyGlnProPheMetArgSe	7
110	CTCCCGGAGTCCAGGTCAGCCAGAGCAGCCTCCCCATGCTGTC	1060
105 369	AGACAGCAGTACAGACAGCTCAGGCTGCCCAGATGGTG: :: ::!      :::       ysProAsnMetProMetGlyGlnAlaGlyGlnMetPheProGlyAsnArg	1022 353
102 353	CCCCAGGTGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG	1003 336
100 336	CAGGTGCAGGTGCAG	988 320
987 319	CCCAACCACCACTGAAATTTGTCCGAGCTCCGATGGTGGTGCAG :::           ::       ::	944 303
943 303	GGCGCAAGCTCTCCCTGGACAAATGTTGTATA  :::    ::::         nGlyAsnGlyMetGlyGlyProGlnGlyMetProGlyGlnGlyMetGlnG	
911 286	CAACCATCACAACTCCCGCCACAGTCGCAGACCCAGCCTTTGGTGTCACA     :::            GlnGlnAsnGlnLeuGlyMetGlyMetAsnProMetMetArgMetGlyGl	862 270
861 269	AGCACCACCAGCGCCACCACGCGCCAGCAGCCTCCAGTTGCTCAGAAC	812 262
811 261	TCCGCCCTCCCAGGCTCTGCCCCAGCAGCTGCAGCAGATGCATCACACAC	762 247
761 247	TTGGAGGCCCAGCCACTTCAGCAGCCACCGATGCAGCCAGC	712 233
711 233	AACAACAGCAACAGCAGCAGCAGCAGCAGCAGCAGCAGCA	216
661 216	GATACAGCAGCAGCAACAGCAGCTGCAGCGAATAGCACAGCTGCAGCTCC	612 200

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seq_name: sp_invertebrate:Q9VF64
Adams N.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams N.D., Celniker S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA Adams N.D., Celniker S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards G., Change M., Henderson S.N.,
RA George R.A., Doyle C., Baxer E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Maril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
Beeson K.Y., Benos P. V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Glory D., Mary R., Bouck J., Brokstein P., Brottier R.,
RA Gerry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Gerry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Dodson K.J., Evangelista C.C., Ferraz C., Ferriæra S., Fleischmann W.,
RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.Ř., Houck J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1582
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       475 nSerProPheAsnProGln.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Musc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                587
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-BERKELEY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ephydroidea; Drosophilidae; Drosophila. NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q9VF64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9VF64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=20196006; PubMed=10731132;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TCGTTCCAGCCATG 1739
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CCTGGCCAACATCCGCTCACCTGTCTTCAACCATTCCCTGTACCGCACAT 1725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TyrSerGlyGlnGlnPheGlyLysSerSerAsnProLeuLeuGluValIl 570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CCGACCAAACAGCAGTAC....CTATGCCAGCCGCTCCTGGATGCCGT 1675
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAACTCAAGAATGACATGCGGTGCCCACTCCCCCACCGCCCCCGGTGCCA 1631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  lGluLysMetThrLysMetSerLysLeuLeuGluIleLeuCysAsnProT 531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAAGGACCTGAGTAAGATGAAGAGCCTTCTGGACATTCTGACAGACCCCT 1531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GluProLeuLysArgMetLeuAlaLysIleSerAsnAspGlyThrAsnVa 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GAGCCCCTGCGCCGCATGATCAACAAGATCGACAAGAACGAAGACAGAAA 148:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            heArgProThrLeu 591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             eAsnThrThrLeuGlnSerProValAlaAsnHisThrLeuTyrArgThrP 587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LysMet..Asp.....LeuIleSer 553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hrGlnArgValProLeuGluThrLeuLeuLysCysGluLysAlaLeuGlu 547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1069 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Brachycera; Muscomorpha;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               481
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alignment_block:
US-09-668-119-1 x Q9VF64
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RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Melson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Reminqton K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Syler E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Syler E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Syler E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Syler E., Wector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Yell, Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Yell, Zhong F.N., Zhong W., Zhou S., Zhu X., Smith H.O.,
RA Zheng X.H., Zhong F.N., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RI Science 287:2185-2195(2000).
DR Eighbase, FBgn003838; CG5166.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Align seg 1/1 to: Q9VF64 from: 1 to: 1069
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C., Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z., Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X., Liu X., Mattel B., McIntosh T.C., McLeod M.P., McPherson D., Liu X., Mattel B., McIntosh T.C., McLeod M.P., McPherson D., McCharles B., McCintosh T.C., McCleod M.P., McPherson D., McCharles B., McCintosh T.C., McCleod M.P., McCharles B., McCintosh T.C., McCle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            485 tArgGlnTyrGlnGlySerGlnSerAsnSerSerLeuAsnTyrGly....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                469 AsnGlyAspSerAsnAlaAsnThrAsnLysProLeuProGlnArgGlnMe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  133 AACAAGAAATCTCAAGCTTCCGTCAGTGATCCTATG.....AATGCACT 176
                                              526 GCAGTAGTGCAGCAG......CAGCAGCAGCTCCAGCAGCAGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             542 GlnGlnGlnGlnGlnGlnGlnFroProGlnGlnGlnGlnHisGl
                                                                                                                                           575 hrArgAspAsnGlnMetGlnGluLeuArgGlnPheGlyGlnAspPheGln
                                                                                                                                                                                                                                                                                                                                                                                                                                           GCAGCAACAGCAGCTTCCAGGCTCAGCAGAGTGCCATGCAG.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CAGCAGTTCCAGCAGCAGCAGCAGCGGGGGGGGTACAGCAGCAGCAGCAGCA 470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGTGCCATGGGACAGCCAATGTCTCTCTCAGGGCAGCCGCCTCCTGGGAC
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                                                                                                                                                                                                                                                                                                                                         nAsnIleGlnProGlnGlyGlnAsnThrGlnProAlaArgGlnValArgT 575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AGACCCAGCTGCAGCTCCAGCAGGTGGCGCTGCAGCAGCAGCAGCAACAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gly.....GlyHisProGlyGlnAsnSerAsnSerProPro.....
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CTCCTCGGGGCCCGGGACAGTCTCTGGGCGGG....ATGGGTAGCTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            lnGlnGln......GlnGlnGlnGlnGlnGlnGln
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1069 AA; 116107 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 464.50
1.569
45.053
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B9D774F4DDBCEACO CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .LeuGlnThrAlaGlyProG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length:
                                                                                                                                                                                                                                             .....CAGCAGTTCCAA 525
29.224
                                                        563
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1Prop 88 13 hepro 90 13 SerAs 91 FGAGG 13 aAlaT 93 aAcc. 14 96 CCTCG 15 lnTyr 95 AAAAA 14 96 CCTGG 15 nhrGln 98 rGACA 15::: 9 pheHi 10 16 apheT 10 3GCTC 16 ll rco 16 apheT 10 3GCTC 16 ll rco 16 serAs 9 syelopmer velopmer lbases. SySTEMS.	Submitted (MAY-1999) to the EMBL/GenBank/DDBJ da -:- SIMILARITY: THE N-TERMINAL REGION IS SIMILAR -:- REGULATORY COMPONENTS OF SENSORY TRANSDUCTIO EMBL; AF153362; AAD50121.1; HSSP: P19754: JAWK	A. ard C., Iranfar N., Loomis W.F.; lase that functions during late d	Dictyostelium discoideum (Slime mold). Eukaryota; Mycetozoa; Dictyosteliida; Dictyosteli FULL_TaxID=44689;	01-MAY-2000 (TrEMBLrel. 13, Created) 01-MAY-2000 (TrEMBLrel. 13, Last sequence update) 01-UN-2001 (TrEMBLrel. 17, Last annotation updat ADENYLYL CYCLASE.	cion_block: PRELIMINA	1665 CTGGATGCCGTCCTGGCCAAC 1685 ::::::::::           1036GlnSerLeuLeuAlaAsn 1041 seq_name: sp_invertebrate:09U9S7	620CCCCCGGTGCCACCACCAAACAGCAGTACCTATGCCAGC	1598 TGCGGTGCCCACTCCCCCACCG	1572 CGCCCTGGAGAAACT	1534 AAGGGTGTGCCCTGAAGACCTTGCAAAAGTGT ::::   :::::    970 lnMetArgValTyrProAspGlnProGlnGlnLeuGlnPheMetT	1484 AGGACCTGAGTAAGATGAAGAGCCTTCTGGACATTCTGACAGACC :::   :::	1437CCTGCGCCGCATGATCAACAAGATCGACAAGAACGAAGAACAG              953 GlyHisAlaProHisGinGlnPheGln	1388 AGCAGCAGTACCTGGACAAGCTGAAGCAGCTGTCGAAGTACATCG             936 hrGlyGlnProLeuIleThrAlaGlyProIleProGlnPheIleG	1372TCCAGCCAGGCT	1366GCTGGC        903 ProGlnThrHisProGlnAlaGlyGlnProProArgLeuArgArg	1354	:    869 rProValProMetThrAsnIleTyrThrThrThrGlyGlyHisVa
	1000	deve		re)			GCTC 1	1 .laPheT 1	ACA 1    eHi 1	TGAGAT 1	CCCTCG 1	AAAAA 1	AGCC. :: lnTyr	GAGG 1 AlaT 9	SerAs 9	1 PhePro 9	lprop 88

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alignment_block:
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                                                                                                                                                                                                                                                                                                                            1909 erGinGinSerGinTyrValGinGinProGinGinGinGinGinGinGinGin
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InterPro; IPR001054; Guanylt_cycla
InterPro; IPR001594; HATPase_c.
InterPro; IPR001596; Pyrophosphata
InterPro; IPR001789; Response_reg.
1982 nProGlnGlnGlnGlnGlnGlnIleGlnAsnGln......
                                                                                                                             1942 nGlnGlnGlnGlnGlnGlnGlnGlnGlnFroGlnGlnGlnGlnG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          429 CCAGCAGCAGCAGCAGCGGCGCGCTACAGCAGCAGCAGCAGCAGCAGCAAC 478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            379 CTGCAGCTCCAGCAGGTGGCGCTGCAGCAGCAGCAGCAGCAGCAGCAGTT 428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS50125; GUANYLATE_CYCLASES_2; PROSITE; PS00387; PPASE; UNKNOWN_1. Phosphorylation; Sensory transduction. SEQUENCE 2123 AA; 243039 MW; 744247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR001440; TPR
                                                                                                                                                                                                                                                                                             676 CAGCAGCAGCAGCAGCAGCAGCAGCAGCAGGCTTTGGAGGCCCAGCC 725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam;
                             876 CCCGCCACAGTCGCAGACCCAGCCTTTGGTGTCACAGGCGCAAGCTCTCC 925
                                                                                              CTCTGCCCCAGCAGCTGCAGCAGATGCATCACACAGCACCACCAGCCG 825
                                                                                                                                                                                                                             ACCAATTCAGCAGCCACCGATGCAGCCAGCCACAGCCTCCGCCCTCCCAGG 775
                                                                                                                                                                                                                                                              AACAGCAGCTGCAGCGAATAGCACAGCTGCAGCTCCAACAACAGCAACAG
                                                                                                                                                                                                                                                                                                                                                                                             nGlnGlnGlnGlnGlnGlnSerGlnAsnIleGlnGlnProGlnS
                                                                                                                                                                                                                                                                                                                                                                                                                                                            AGCAGCAGTTCCAGGCTCAGCAGAGTGCCATGCAGCAGCAGTTCCAAGCA 528
                                                                                                                                                                                                                                                                                                                                                                                                                            TCTAATTAAATTGCATCATCAAAATCAGCAACAGATACAGCAG...CAGC
                                                                 SerProGlnGlnGlnGlnPro...
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2.609
55.031
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Guanylt_cyclase.
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Percent Identity: 41.509
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InterPro; IPR001214; SET.
InterPro; IPR001282; Recombinase.
InterPro; IPR001965; PHD.
InterPro; IPR002965; P_rich_exten:
InterPro; IPR0039616; PostSET.
InterPro; IPR003888; FYYICh_N.
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014687 PRELIMII
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01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
InterPro; IPR003889; FYrich_C.
pfam; PF00628; PHD; 3.
pfam; PF00856; SET; 1.
PRINTS; PR01217; PRICHEXTENSN.
PROSITE; PS00398; RECOMBINASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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MEDLINE=97388474; PubMed=9247308;
Prasad R., Zhadanov A.B., Sedkov Y., Bullrich F., Druck T.
Rallapalli R., Yano T., Alder H., Croce C.M., Huebner K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      trithorax.";
Oncogene 15:549-560(1997).
EMBL; AF010404; AAC51735.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   strong homology to ALL-1 involved
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Structure and expression pattern of human ALR, a novel gene with strong homology to ALL-1 involved in acute leukemia and to Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Canaani E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AGCAGTACAGACAGCTCAGGCTGCCCAGATGGTGGCTCCCGGAGTCCAGG 1075
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        RECOMBINASES_2; UNKNOWN_1.
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DR PROSITE; PS50280; SET; 2 SMART; SM00542; FYRC; 1. DR SMART; SM00541; FYRN; 1. DR SMART; SM0039B; HMG; 1. R SMART; SM0039B; HMG; 1. R SMART; SM00249; PHD; 4. DR SMART; SM0050B; POSTSET; 1. DR SMART; SM00317; SET; 1.	1. 848 MW; 1026562E1419CE8D CRC64;
lignment_block: US-09-668-119-1 x 014687 .	•
Align seg 1/1 to: 014637 f	rom: 1 to: 4957
226 CCTCCTCGGGGCCCG;GACA	AGTCTCTGGGCGGGATGGGTAGCTTTGGTGC 275
276 CATGGGACAGCCAATGTCTCT	PCTCAGGGCAGCCGCCTCCTGGGACCTCGG 325
326 GGATGGCCCCTCACAGCATG :::::        ::: 3240 roGlnGlyProHisAngGln	GCTGTCGTGTCTACGGCAACTCCACAGACC 375 ::::::::::::::::::::::::::::::::::::
376 CAGCTGCAGCTCCAGCAG :::        3257 SerProGlnLeuAlacilnGl	GT 395
396 GGCGCTGCAGCAGCA(CAGC  :::	CAGCAACAGCAGCAGTTCCAGCAGCAGCAGCAGC 445 
446 CGGCG	
451	OMetGlySerLeuGlnGlnLeuGlnGlnGl 3323
462 GCAGCAGCAGCAGCAZCAGCA          3323 nGlnGlnLeuGlnGlnGlnGl	AGCAGTTCCAGGCTCAGCAGAGTGCCATGC 511
512 AGCAGCAGTTCCAAGCAGTAG           :::    3337 InGlnGlnLeuGlnGlnGlnG	TGCAGCAGCAGCAGCAGCTCCAGCAG 558
559 CAGCAGCAGCAGCAGCAGCAT	CTAATTAAATTGCATCATCAAAATCAGCA 608
609 ACAGATACAGCAGCAGCAGCA     :::	AGCAGCTGCAGCGAATAGCACAGCTGCAGC 658
659 TCCAACAACAGCAACA 3CAGCAGCA 	AGCAGCAGCAG690 
	CAGCAGCAGCAGCAGCAGCTTT
717 GGCCCA	CCGATGCAG

1218	1188 CTCACAGCCCAACTCCAACGTCAGCTCTGGC	ш
71		ω
9	138 CAGTCGATGCCCCCTCCCCCCCAGCCGTCCCCAGCCAGCC	<b>–</b>
3694	679 ysGlnProGlnLeuGlyGlyPheProGlyProGlnThrGlyProLeu	ω
1137	093CCCATGCTGTCCTCGCCGTCACCGGGCCAGCAGGTGCAGACCCCG	ı
1092 3679	1060GRCGCGGAGTCCAGGTCAGCCAGAGGCAGCCTC	
3662	46 LeuMetGlnArgGlnLeuGlnGlnSerGlnAlaValArgGlnThrProPr	
1059	021CAGACAGCAGTACAGACAGCTCAGGCTGCCCAGATGGTG	
3645	GlnLeuArgHisLeuSerProGinGlnGlnGlnGlnLeuGlnAlaLeu	
1020	GTGCAGCCCCAGGTGCAGCAG	
994 3629	951 ACCACTGAAATTTGTCCGAGCTCCGATGGTGGTGCAGCAGCCCCC :::           :::	
3612	98 ValLeuGlnSerGlyGlnGlyLeuProGlyValGlyIleMetPr	
950	GGTGTCACAGGCGCAAGCTCTCCCTGGACAAATGTTGTATACCCAACC	
3597	3583 roMetGlnAsnAsnThrGlyProGlnProProLysProGlyPro	
900	AGAACCAACCATCACAACTCCCGCCACAGTCGCAGACCCAG	
G (	66 ySerMetThrGlnAsnLeuLeuGlyProGlnGlnProMetLeuGluAr	
л	AGCACCAGCCGGCCACCACAGCCCCAGCAGCCAGCCTCCA	
	${\tt 'alProHisLeuLeuAlaGlnProSerValSerLeuGlyAspGlnProG}$	
804		
354	${f y}{f Ser}{f His}{f Gly}{f GlnLeu}{f Gly}{f Ser}{f Gly}{f Ser}{f Ser}{f Ser}{f Glu}{f Alas}$	
804		
353	16 gLeuProGlyGlnGlnGlnGlnGlnValSerLeuLeuHisThrA	
5 (	777 TOTGOOGAGOAGOTGOAGOAG	
776	751GC   THE HEAD OF THE PROPERTY   THE PROPERTY	
4	83 lyGluValLysProSerLeuSerGlyAspSerGlnLeuLeuLeuValGl	
750	750	
348	${\tt OLeuAlaIleGlyThrThrProGluSerMetAlaThrGlu}$	
750	750	
346	$\mathtt{.laValSerSerGluAlaThrGluGlyProSerThrHisGl}$	
750	750	
344	euGlyProThrLeuLeuLeuThrGlyLysGluGln1	
750	:	
343	3416 aLeuGlyProGlyMetProAlaLysProLeuGlnHisPheSerSerProG	

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seq_documentation_block:
ID 014686
AC 014686;
DT 01-JAN-1998 (TTEMBLre
DT 01-JAN-1998 (TTEMBLre
DT 01-JAN-1998 (TTEMBLre
DT 01-JAN-1998 (TTEMBLre
DT 01-JUN-2001 (TTEMBLRE
DN NCBI_TAXID-9606;
RN 11
RN MEDLINE=97388474; Pub
PAR MEDLINE=97388474; Pub
PAR ARAILBPAlli R., YANO T
RA CANABANI E., YANO T
RA CANABANI PRO01214;
DR INTERPRO; IPR001841;
DR INTERPRO; IPR003888;
DR INTERPRO; IPR003889;
DR INTERPRO; IPR003889;
DR PARMIS; PR00217; PRIC;
DR PARMIS; PR00217; PRIC;
DR SMART; SM00398; HWG;
DR SMART; SM00398; HWG;
SMART; SM00398; HWG;
DR SMART; SM00399; PHD;
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InterPro; IPRO01214; SET.
InterPro; IPRO01214; SET.
InterPro; IPRO01214; SET.
InterPro; IPRO01841; Znf_ring.
InterPro; IPRO01865; PHD.
InterPro; IPRO01965; PHD.
InterPro; IPRO03965; P_rich_extensn.
InterPro; IPRO03616; PostSET.
InterPro; IPRO03888; FYrich_N.
InterPro; IPRO03889; FYrich_C.
InterPro; IPRO03889; FYRICHEXTENSN.
INTERPROVED 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1414 CAGCTGTCGAAGTA...CATCGAGCCCCTGCGCCCCCATGATCAACAAGAT 1460
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3802 AsnLeuAlaGluThrGlnLys.....ProGluGlnSerSerLeuValPr 3816
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1264 CCCTCCCAGAGCCCAGTGACGGCGCGGGACCCCACAGAACTTCAGTGTCCC 1313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3726 isProThrProProProSerSer..ProGlnGluProLysArgProSerG 3742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1219 ..CCTGCCCCATCTCCCAGTAGCTTCCTGCCCAGCCC...CTCACCGCAG 1263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1511 TGGACATTCTGACAGACCCCTCGAAGCGGTGTCCCCTGAA 1550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1461 CGACAAGAACGAAGACAGAAAAAAGGACCTGAGTAAGATGAAGAGCCTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1364 CAGCTGGCTCCAGCCAGGCTGAGGAGCAGCAGCTACCTGGACAAGCTGAAG 1413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1314 CTCACCTGGACCTTTAAACACACCTGTGAACCCCAGCTCTGTCATGAGCC 1363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JAN-1998 (TrEMBLrel.
01-JAN-1998 (TrEMBLrel.
01-JUN-2001 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.

MEDLINE=97388474; PubMed=9247308;

Prasad R., Zhadanov A.B., Sedkov Y., Bullrich F., Druck T.,

Prasad R., Yano T., Alder H., Croce C.M., Huebner K., Mazo A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Oncogene 15:549-560(1997).
EMBL; AF010403; AAC51734.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Structure and expression pattern of human ALR, a novel gene with "Structure and expression pattern of human ALR, a novel gene with strong homology to ALL-1 involved in acute leukemia and to Drosophila trithorax.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               euAlaAspThrLeuPheSerLysGlyLeuGlyProTrpAspProProAsp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       oThr...LeuGluProProProGlyArgValSerProAlaAlaAlaGlnL 3785
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pro.....ThrHisProGlyThrProLysProGln.......GlyPr 3769
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  05,
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Last sequence update)
Last annotation update)
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0		
aLeuGlyProGlyMetProAlaLysProLeuGln	LeuGl	
GGCCCAGCCACCAATTCAGCAGCCACCGAT	GCCC	
Character   Char	lnSer	
TuGInGInPheGInGInGInGInGInGInGInMeTGILGInGInMeTGILGInGInMeTGILGInGInMeTGILGINGINMETGILGINGINGINMETGILGINGINGINMETGILGINGINMETGILGINGINGINGINGINGINGINGINGINGINGINGINGING	88 InGinG	
TCCAACAACAGCAACAGCAGCAGCAGCAGCAGCAGCAGCAG	659 TCCAAC	
9 ACAGATACAGCAGCAGCAGCAGCAGCTGCAGCGAATAGCACAGCTGCAGC 658      :::	609 ACAGATA     :::: 3671 nGlnLeu	
CAGCAGCAGCAGCAGCATCTAATTAAATTGCATCAAAATCAGCA 60	AGC 	
2 AGCAGCAGTTCCAAGCAGTAGTGCAGCAGCAGCAGCAGCTCCAGCAG 558         :::	512 AGCAGCA         3642 lnGlnGl	
2 GCAGCAGCAGCAGCAGCAGCAGCAGTTCCAGGCTCAGCAGAGTGCCATGC 511	AGCAG        nglr	
CTACAGCAGCA 461 	roLys	
etAlaGlyLeuSerHisLeuGlnGlnSerLeuMetSerHisSerGlyGln 36	      5 etAlaGl	
Cache	4.6 CGGCG	
5 GGCGCTGCAGCAGCAGCAGCAACAGCAGCAGCAGCAGCAGCAGCAG	GCGCT	
CAGCTGCAGCTCCAGC:::          SerProGlnLeuAlac	AGCT	
GGATGGCCCCTCACAGCATGGCTGTCGTGTCTACGGCAACTCCACAGACC 375 :::::       ::::::::::::::::::::::::::	GATGGC ::::: oGlnGl	
.ProAlaGlnValAlaValLeuGlnGlnGlnHisProGlyAlaLeuGl	ProAla	
CATGGGACAGCCAATGTCTCTCTCAGGGC	ATGGG	
ccrccrcgggccccgggacAgrcrcrgggcgggArgggrAgcrrrggrGc 275	CTCCTC	
eg 1/1 to: 014686 from: 1 to: 5262	g 1/1	
it_block: i68-119-1 x 014686	_block 8-119-	ω
t_scores: 647 Quality: 447.50 Length: 647 Ratio: 1.587 Gaps: 30 Similarity: 43.586 Percent Identity: 29.675	_scores Qual Ra Similar	ש
RT; SM00508; POSTSET; 1. RT; SM00184; RING; 3. RT; SM00317; SET; 1. UENCE 5202 AA; 564181 MW; 26B7C74CAD417E44 CRC64;	SMART; SM00 SMART; SM00 SMART; SM00 SEQUENCE	DR DR DR SQ

1263	9CCTGCCCCATCTCCCAGTAGCTTCCTGCCCAGCCCCTCACCGCAG :::	219
4 U.S.L	C COMPANY THE TOTAL THE CONTRACT THE CONTRACT OF THE CONTRACT	
	8 CTCACAGCCCAACTCC/ACGTCAGCTCTGGC	188
1187 4016	88 CAGTCGATGCCCCCTCCCCCCAGCCGTCCCCGCAGCCGGGCCGGCC	138
1137 3999	<pre>33CCCATGCTGTC/TCGCCGTCACCGGGCCAGCAGGTGCAGACCCGG</pre>	984
3984	7 offreding the control of the contr	967
	1 LeumetGlnArgGlnL::    ::::::::::::::::::::::::::::::::	951
1059	1CAGACAGCAG FACAGACAGCTCAGGCTGCCCAGATGG	02]
1020 3950	95 CAGT3CAGCCCCAGGTGCAGCAGCAG 	999
994 3934	1 ACCACTGAAATTTGTCCGAGCTCCGATGGTGGTGCAGCAGCAGCCCCC	95:
950 3917	01 TTGGTGTCACAGGCGCAAGCTCTCCCTGGACAAATGTTGTATACCCAACC ::::::::::::::::::::::::::::	90:
900 3902	51 TTGCTCAGAACCAACCATCACAACTCCCGCCACAGTCGCAGACCCAGCCT	88
850 3888	05CACACACAGCACCACCACCACCACCAGCCCAGCAGCCGCAGCA	87
3871	ValProHisLeuLeuA	85
804	04	0.8
3854	38 lyGlySerHisGlyGlnLeuGlySerGlySerSerSerGluAlaSerSer	83
804	04	08
3838		82
804	TGCCCCAGCAGCTCCAGCAGATGC	77
3821	ProGlnProClnProSe	80
776	AGCCACAGCCTC CGCCCTCCCA	75
3804	88 lyGluValLysProSerLeuSerGlyAspSerGlnLeuLeuLeuValGln	178
750	50	75
3788	71 yGlyProLeuAlaIl&GlyThrThrProGluSerMetAlaThrGluProG	177
750	50	75
3771	55 AspProAlaValSers'erGluAlaThrGluGlyProSerThrHisGlnGl	375
750	50	75
3754	38 lyAlaLeuGlyProThrLeuLeuLeuThrGlyLysGluGlnAsnThrVal	373

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RP SEQUENCE FROM N.A.

RP SEQUENCE PROMING F.A.

RP SEQUENCE PROM N.A.

RP SEQUENCE FROM N.
                                                          alignment_block:
                                                                                                                                                                                                                                                                                                                        alignment_scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    seq_name: sp_invertebrate:045322
                                                                                                                                                                  Quality: 447.00
Ratio: 1.781
Percent Similarity: 49.312
US-09-668-119-1 x O45322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4121 oGlyHisLeuAspGlnValAsnGlyGlnValValProGlu 4134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1511 TGGACATTCTGACAGACCCCTCGAAGCGGTGTCCCCTGAA 1550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4107 AsnLeuAlaGluThrGlnLys.....ProGluGlnSerSerLeuValPr 4121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1461 CGACAAGAACGAAGACAGAAAAAAGGACCTGAGTAAGATGAAGAGCCTTC 1510
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4090 euAlaAspThrLeuPheSerLysGlyLeuGlyProTrpAspProProAsp 4106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1414 CAGCTGTCGAAGTA...CATCGAGCCCCTGCGCCGCATGATCAACAAGAT 1460
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Caenorhabditis elegans.

Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4031 isProThrProProProSerSer..ProGlnGluProLysArgProSerG 4047
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01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-JAN-1999 (TrEMBLrel. 09, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DY3.5 PROTEIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lennard N.
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                                                                                                                                                     Length: 509
Gaps: 24
Percent Identity: 32.024
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
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Align seg 1/1 to: 045322 from: 1 to: 796

966	ACCACTGAAATTT
925 552	901TTGGTGTCACAGGCGCAAGCTCTCC ::::::   :::::::: 535 rTyrLysAsnAsnTyrGlnThrAlaAlaLeuGlyGlnValAsnThrTyrS
535	56 CAGANCCARCCATCACCACTCCCGCCACAGTCGCAGACCCAGGCT                :::
نسزر	
504 855	WINGINFTOAIAFTOGINGINFTOMETASNFNELEUFTOAIAF
	68 CTCCCAGGCTCTGCCCCAGCAGCTGCAGCAGATCACACACA
767 489	718 GCCCAGCCACTATTCAGCAGCCACCGATGCAGCAGCCACAGCCTCCGCC
717 475	677 AGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCA
676 459	7, ACAGCAGCTGCAGCGAATAGCACAGCTGCAGCTCCAACAACAACAGCAACAGC
626 442	ATTAAATTGCATCAAAATCAGCAACAGATACAGGAGCAGCA :::    :::    ::
576 425	GCAGCAGCAGCAGCAG         aGlnGlnAlaGlnGlnArg
526 411	4// ACAGCAGCAGTTCCAGGCTCAGCAGAGTGCCATGCAGCAGCAGTTCCAAG
	TTCCAGCAGCAGCAGCAGCGGGGGCGCTACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG
426 386	CAGCAGCAACAGCAGCAG               GlnGlnGlnGln
376 375	CACAGACCC
326 367	280 GGACAGCCAATGTCTCTCAGGGCAGCCGCCTCCTGGGACCTCGGG     ::                 ::
279 350	TTTGGTGCCATG ::: nGlnGlnGlnValAlaAsnGlnVal
247 334	198 TGCTGCGGGAGCCGCTGGAATTGGCATGCCTCCTCGGGGCCCCGGGACAGT
197 319	148 GCTTCCGTCAGTGATCCTATGAATGCACTCCAGAGCCTGACTGGCGGACC

ਹ <b>ਹ</b> ਜ `	lyne J.	FROM N.A.  ERKELEY;  20196006; PubMed-10731132;  D., Celniker S.E., Holt R.A., Evans C.A., Goca	
; comorpha;	nsecta a; Mus		
		i <sup>a</sup>	
		seq_name: sp_invertebrate:Q9VK09	
		1474 GACAGAAAAAGGACCTGAGTAAGATG 1500 ::::::::   :::::::::::::::::::::::::	
	1473 732	1447ATGATCAACAAGATCGACAAGAACAA ::::::	
	1446 716	1404 CAAGCTGAAGCAGCTGTCGAAGTACATCGAGCCCCTGCGCCCGC  ::: :::::: !::                    699 pSerLysAsnGluSerThrLysLysThrGluThrLeuLeuArgAspThrT	
	1403 699	GAGC :::  GlnG	
	1374 682	1325 CTTTAAACACACCTGTGAACCCCAGCTCTGTCATGAGCCCAGCTGGCTCCC	
	1324 671	1278 AGTGACGGCGCGGACCCCACAGAACTTCAGTGTCCCCTCACCTGGAC :::	
	1277 654	1228 TCTCCCAGTAGCTTCCTGCCCAGCCCCTCACCGCAGCCCTCCCAGAGCCC :::	
	1227 640	1184 CCAGCTCACAGCCCAACTCCAACGTCAGCTCTGGCCCTGCCCCA	
	1183 626	1134 CCCGCAGTCGATGCCCCCTCCCCCCAGCCGTCCCCGGCAGCCGGCCAGC	
	1133 615	1084 AGCAGCCTCCCCATGCTGTCCTCGCCGTCACCGGGCCAGCAGGTGCAGAC	
	1083	1034 AGACAGCTCAGGCTGCCCAGATGGTGGCTCCCGGAGTCCAGGTCAGCCAG	
	1033 598	84 GCAGCAGCCCCAGTGCAGCCCC ::::::     85 eGluGluGluProHisGlySer\	
	983 585	AGCTCCG :     nIleProThrHisSerTh	

					A	alig US-	p al	_	DR	D R R R	RA	RA A	RR	RA	RA	RA RA	RA A	RA A	RA	RA :	RA RA	RA RA	RA RA	RA A	RAR	RA	R	RA RA
213 TGGAAFTGGCATGCCTCCTCGGGGCCCGGGACAGTCTCTGGGCG 256  :::::	178 CAGAGGCTGACTGGCGGACCTGCTGCGGGAGCCGC 212             220 TyrSerSerThrThrSsrAspAlaValAspGlyProArgProSerAlaAl 236	iu P	78 GGACGAATACCTTTCTCTCGTGGCCAGGCTCATTATCCATTTTCGAGACA 127	28 AAATCCAGCAAGGATAIGGAGAGGCCATGTTTTCCTGAAGGCCCAAGACCCG 77     :::	lign seg 1/1 to: Q9VK09 from: 1 to: 900	gnment_block: 3-09-668-119-1 x Q9VK09	lignment_scores: Quality: 434.00 Length: 744 Ratio: 1.373 Gaps: 32 Percent Similarity: 42.473 Percent Identity: 27.151		RE Interpro; IPRO02965; P_rich_extensn.  RE PRINTS; PRO1217; PRICHEXTENSN.  Q SEQUENCE 900 AA; 98948 MW; DD99C0057CDA5E44 CRC64;	Science 287:2185-2195(2000).  EMBL; AE003639; AAF53374.1; FIVEAse: FBGn0032497 - CG6043	Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;	Ye J., Yeh RF., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L., Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,	Wang ZY., Wassarman D.A., Weinstock G.M., Weissenbach J., Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,	Spier E., Spradling A.C., Stapleton M., Strong R., Sun E., Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,	Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H., Shue B.C., Siden Kiamos I., Simpson M., Skupski M.P., Smith T.,	Welson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M., Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,	Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A., Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,	Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X., Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,	Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,	Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J., Hostin D., Houston K.A., Howland T.J., Wei MH., Thegwam C.,	Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K., Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.	Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,	Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,	Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P., Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,	Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,	wan K.H., DOYTE C., BAXTET E.G., HEIT G., NEISON C.K., MIKLOS G.L.G., Abril J.F., Agbayani A., An HJ., Andrews-Pfannkoch C., Baldwin D.,	Brandon R.C., Rogers YH.C., Blazej R.G., Champe M., Pfeiffer B.D.,	George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Sutton G.G., Wortman J.R., Yandell M.D., Zhang O., Chen L.X.,

936	CGCAGACCCAGCCTTTGGTGTCACAGGCGCAAGCTCTCCCCTGGACAAATG	887
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886	CAGCAGCCTCCAGTTGCTCAGAACCAACCATCACA	837
	 	499
836		823
9	::::::      laAlaAsnThrPheAsnSerGlnGlnGlnGlnAsnGlnPheGlyGlyA	œ
822	· · · · · · · · ATGCATCACACACAGCACCAG · · · · · · · · · · · · · · · · · · ·	799
482	   nGlnGlnArgSerArgAspValPheSerProAlaArgAsnGluThrSe	465
798	GCAGCAG	792
465	  GlnGlnGlnAspSerHisProGlnProIleTyrAsnAsnVa	449
791	CAGCCACAGCCTCCGCCCTCCCAGGCTCTGCCCCAGC	751
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S.	ADDRADDSSABRETTTDRADRADRADRADRADRADRADRADRADRADRADRADRAD	7
₽ .	:::::      LeuGlnGlnGlnPheGlnGlnGl	0 1
677	CAGCAGCTGCAGCGAATAGCACAGCTGCAGCTCCAACAACAGCAACAG	628
401	lnLeu	391
627	ATCTAATTAAATTGCATCATCAAAATCAGCAACAGATACAGCAGCAGCAGC	578
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577	AGTAGTGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG	528
376	GlnGlnGlnLeuGlnGlnGlnGl	363
527	CAGCAGCAGTTCCAGGCTCAGCAGAGTGCCATGCAGCAGCAGTTCCAA	478
362	lnArgProProThrAlaIleSerProL	346
477	AGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC	458
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426	CAGCAGCAGCAGCAACAGCAGCAG	403
312	hr Ser ProAlaValAsnValTyrThrArgGlnSerAspSerProArg	296
402		402
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1514	AAGAACGAAGACAGAAAAAAAGGACCTGAGTAAGATGAAGAGCCTTCTGGA	1465
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1418	CT	1417
1416 786	GCCAGGCTGAAGGAGCAGCAGTACCTGGACAAGCTGAAGCAG ::::::::::::::       :::::: !yasnGlyAspSerArgGlnAspLeuGlnGlnThrProGlnGluAlaGlu	1376 770
1375 770	CTCTGTCATGAGCCCAGCTGGCTCCA :   :   sSerPheArgIleLeuGlnLysIleThrAspThrValAspAspGlySerG	1350 753
1349 753	ARCITICAGITGICCCCICACCITGIAACCAACCCGAGGIGIGAACCCCAG     :::    :::::: :: 	743
29 42	CCTCACCGCAGCCCTCCCACAGCCCACTACGCCGCGGCGCGCACACACA	1250 729
1249 729	CTCCAACGTCAGCTCTGGCCCTGCCCCATCTCCCCAGTAGCTTCCTGCCCA   :::::::::::::::::::::::::::::::::	1200 712
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1149 695	CGCAGTCGATGCCC	1136 679
1135 679		662
662	${\tt ArgLeuGlnIleAsnLeuAsnThrAsnGlyAsnSerSerAsnAsnThrAs}$	646
1119		1119
1119 645	<pre>TCCCCATGCTGTCCTCGCCGTCACCGGGC    :::    :::   ::    laProIleSerLeuGlnAsnPheGlySerAsnProGlnProGlyGlyLeu</pre>	1091 629
629	CAGCCAGAGCAGCC	612
, N	roGlnGlnGlnGlnProGlnGlnGlnGlnProThrPheTyrGl	9
1076	TACAGACAGCTCAGGCTGCCCAGATGGTGG	1027
1026 595	ZAGCCCCAGGTGCAGCAGCAGACA             nproglnValValProglnGlnGln	977 579
579	aProTrpAlaArgLeuGluGluAsnGlyAsnValLeuProS	562
976	GA	973
ō,	:::     :::::::::::::::::::::::::	Ā (
545 972	gAspSerProMetArgGlnLeuProGlnGlnGln	529

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alignment_scores:
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RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Yell R., Shen M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
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Wang S., Yao Q.A.,
Wang S., Yao Q.A.,
Wang 
                                                                                                           Quality: 427.50
Ratio: 1.469
Percent Similarity: 46.935
Align seg 1/1 to: Q9VUB6 from: 1 to: 1798
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InterPro; IPR001357; BRCT.
Pfam; PF00533; BRCT; 4.
SMARF; SM00292; BRCT; 4.
PROSITE; PS50172; BRCT; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Drosophila melanogaster (Fruit fly).

Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9VUB6;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
CG8797 PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CG8797
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                             1798 AA;
                                                                                                                                                                                                                                  BRCT; 2,
A; 205695 MW; 64E4963B1181B6E9 CRC64;
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                                                                                                                                                              Length:
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		873
TTGCTCAGAACCAACCATCACAA ::        euAlaGlnAsnProGlnSerGlnAsnValTyr	CCCCAGCAGCCTCCAC	835 586
CAGCACCACCAGCCGC         ::    SerGlnGlnHisPheAsnGlnLeuS	ATCACACA: ::     !nLysThrPheIleIle	803 569
AGGCT ::: lyValGln	CTCCGCCC7	756 552
CCAATTCAGC!          ProGlnGlnG:	CTTTGGAGGC::::::::::::::::::::::::::::::	ωo
GCAGO        nGlno	ProThrAsnV	673 519
lyGlnValArgIleIleGlnGlnThrIleG	laLeuGlyAlaGl	0
		672
CACAGCTGCAGC'     :::   :  InGlnValGlnP	TGCAGCO	631 486
CAGCAACAGATACAGO             	ATCAT	593 469
CAGCAGCAGCAGCAG                	CTCCAG     AlaGln	543 452
TGCAGCAGCAGTTCCAAGCAGTAGT    :::     ::::  aLeuGlnLysGlnGlnGlnLeuLe	GCTCAGCAGAGTGCCA ::::::::    SerHisMetSerLeuA	493 436
	ArgHisValIle	478 419
CAGCAGCAGCAA            ProGlnProGlyGlnGlnGlnGlnValIleTh	CAGCAGCA           GlnGlnGl	450 402
AACAGCAGCAGTTCCAGCAGCAGCAGCA 	In I AG	400 386
CAGCTGCAGCTCCAGCAGC    ::           nAsnAlaGlnGlnIleGlnGlnGlnGlnG	nProAsnGlr	376 369
GlnGlnGlnProThrThrProThrLeuG	::::::  OArgGlnSerPr	
3lnGlnProGlnGlnGlnHisTh	InProGInGL	336

1685 940	CCAAACAGCAGTACCTATGCCAGCCGCTCCTGGATGCCGTCCTGGCCAAC	1636 923
923	Pro.ArgProGlyAlaProGlySerIleVa	<u>ب</u>
1635	CCCCGGTGC	1586
1585 913	GCGGTGTCCCCTGAAGACCTTGCAAAAGTGTGAGATCGCCCTGGAGAAAC:::: nGlnAsnLysProArgValMetLeuArgGlnGlnValAlaTyrGln	1536 898
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1485 882	CCCTGCGCCGCATGATCAACAAGATCGACAAGAACAGAAGACAGAAAAAAG	1436 866
1435 866	GGAGCAGCAGTACCTGGACAAGCTGAAGCAGCTGTCGAAGTACATCGAGC::::      :::    ::: ::        :::        :::	1386 850
1385 850	GTGAACCCCAGCTCTGTCATGAGCCCAGCTGGCTCCAGCCAG	1339 834
1338 833	ACTTCAGTGTCCCCTCACCTGGACCTTTAAACACACCT ::	1301 817
1300 817	CCCCTCACCGCAGCCCTCCCAGAGCCCAGTGACGGCGCGGACCCCACAGA :	1251 800
1250 800	TCTCCCAGTAGCTTCCTGCCCAG :::   :::    :::   :::    ThrProThrSerValGlyMetGlnSerProLeuProGlyGlyProThrTh	1228 784
1227 783	CCCAGCTCACAGCCCAACTCCAACGTCAGCTCTGGCCCTGCCCCA	1183 767
1182 767	nGlnGlnGlnSerProGlnHisHisProGlnMetGlnGlnGlnHisT	1156 750
1155 750	CAGTCGATGCCCCCTCCC.	1138 734
1137 733	CGTCACCGGGCCAGCAGGTG	1109 717
1108 717	GAGCAGCCTCCCCATG	1083 700
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1041 683	CCCCAGTGCAGCCCCAGGTGCAGCAGCAGCAGCAGCAGCAGCAGCAGCCT	992 667
991 667	<pre> ProGlnArgLeuGlnTyrLeuGlnGlnGlnLeuMetGlnLysGlnG ProGlnArgLeuGlnTyrLeuGlnGlnGlnLeuMetGlnLysGlnG ProGlnArgLeuGlnTyrLeuGlnGlnGlnLeuMetGlnLysGlnG ProGlnArgLeuGlnTyrLeuGlnGlnGlnGlnLeuMetGlnLysGlnG ProGlnArgLeuGlnTyrLeuGlnGlnGlnGlnLeuMetGlnLysGlnG ProGlnArgLeuGlnTyrLeuGlnGlnGlnGlnLeuMetGlnLysGlnG ProGlnArgLeuGlnTyrLeuGlnGlnGlnGlnLeuMetGlnLysGlnG ProGlnArgLeuGlnTyrLeuGlnGlnGlnGlnLeuMetGlnLysGlnG ProGlnArgLeuGlnTyrLeuGlnGlnGlnGlnGlnLeuMetGlnLysGlnG ProGlnArgLeuGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnG</pre>	949 650
650	${\tt MetGlnGlnFroGlnGlnIleValValAsnGlnGlnIleLeuSen}$	634

1686 ATCCGCTC 1693

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seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          seq_name: sp_rodent:Q6222)
                                                                                                                                                                                                                                                                                                                                                                                                                                                     alignment_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-668-119-1/rev x Q62220
                                                                                                                                                                                                                                                                                                                                                                                           Align seg 1/1 to: Q62220 from: 1 to: 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                     1016 TGCTGCACCTGGGGCTGCACTGGGGGCTGCTGCACCATCGGAGCTCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1996 (TrEMBLrsl. 01, Created)
01-NOV-1996 (TrEMBLrsl. 01, Last sequence update)
01-JUN-2001 (TrEMBLrsl. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   940 isGlnMet 942
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MGD; MGI:1354758; Krtap5-4.
InterPro; IPR001450; 4FE4S_ferrdxin.
InterPro; IPR001007; VWFC.
PROSITE; PS00198; 4FE4S_FERREDOXIN; UNKNOWN_2.
PROSITE; PS01208; VWFC; UNKNOWN_2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=BALB/C;
MEDLINE=91154184; PubMed=1840598;
Wood L., Mills M., Hatzenbuhler N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wood L., Mills M., Hatzenbuhler N., Vogeli G.; "Serine-rich ultra high sulfur protein gene expression in murine hair and skin during the hair cycle."; J. Biol. Chem. 265:21375-21380(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=91065960; PubMed=2250030;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SERINE 2 ULTRA HIGH SULFUR PROTEIN.
                                                                                                                                                                                             916 GCGCCTGTGACACCAAAGGCTGGGGTCTGCGACTGTGGCGGGAGTTGTGAT 867
                                                                                                                                                                                                                                                                          966 GACAAATTTCAGTGGTGGTTGGGTATACAACATTTGTCCAGGGAGAGCTT 917
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; M37760; AAA40107.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Wood L., Mills M., Hatzenbuhler N., Vogeli G.;
"Serine-rich ultra high sulfur protein gene expression in murine hair
and skin during the hair cycle.";
J. Biol. Chem. 266;4024-4024(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse)
                                     816 GTGCTGTGTGATGCATCTGCTGCAGCTGCTGGGGCAGAGCCTGGGAGG 767
                                                                                                                866 GGTTGGTTCTGAGCAACTGGAGGCTGCTGGGGGGTGTGGTGGCGGCTGGTG 817
54 .....CysGlySerCysGlyGlyCysLys.....
                                                                          39 GlyCysLysGlyGlyCysGlySerCysGlyGlyCysLysGlyGly.... 53
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                                                                                                                                                                                                                                                                                                              3 CysCys.....GlyCysSerGlyGlyCysGlySerSerCysGlyGly.. 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           223 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                   .....CysGlySerSerCysCysLysProValC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        427.00
3.389
49.219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21442 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length: 256
Gaps: 24
Percent Identity: 37.891
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C654BDB9FD08C59A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        223 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Murinae; Mus.
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seq_documentation_block:
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Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D., Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G., Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D., Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 553 GGAGCTGCTGC.....TGCTGCACTACT...GCTTGGAACTGCTGC 513
                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   512 TGCATGGCACTCTGCTGAGCCTGGAACTGC.....TGCTGTTGC..... 474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                152 lnSerSerCysCysLysProCysCysSerSerGlyCysGlySerSerCys 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         109 ysProCysCysCysGlnSerSerCysCysLysProCysCysSerSerGly 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              716 TCCAAAGCCTGCTGC.....TGCTGCTGC.....TGCTGCTGCTG 682
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 766 GCGGAGGCTGTGGCTGCATCGGTGGCTGCTGAATTGGTGGCTGGGCC 717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CG6026 PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           214 ...CysAlaProValCys 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  386 AGCTGCAGCTGGGTCTGT 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       181 rSerCysCysLysProCysCysCysGlnSerSerCysCysLysProCysC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           126 CysGlySerSerCysCysGlnSerSerCysCys........................ 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   661 GGAGCTGCAGCTGTGCTATTCGCTGC.....AGCTGCTGT...... 627
                                                                                                                                                                                                                                                             MEDLINE=20196006; PubMed=10731132;
                                                                                                                                                                                                                                                                                           STRAIN-BERKELEY;
                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Drosophila melanogaster (Fruit fly)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   62 ..GlyGlyCysGlySerCys...GlyGlyCys...LysGlyGlyCysCys 75
                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       92 oCysCysSerSerGlyCysGlySerSerCysCysGlnSerSerCysCysL 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     76 GlnSerSerCysCysLysProCysCysCysGlnSerSerCysCysLysPr 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ....LysProCysCysGlnSerSerCysCysLysProCysCysCysG 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TTTAATTAGATGCTGCCTGC.....TGCTGC.....TGCTGCTGCT 554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GCTGCTGGAACTGCTGCTGTTGCTGCTGCTGCAGCGCCACCTGCTGG 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ....TGCTGCTGCTGCTGCTGTAGCGCCCGCCTGC......TGCT 437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CysGlnSerSerCys......CysLysProCysCysCysGlnSe 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .........TGCTGCTGCTGTATCTGTTGCTGATTTTGATGATGCAA 589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ysCysGlnSerSerCysCysLysProCysCysCysGlnSerSerCys...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1542 AA
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RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,

RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,

RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

RA Cherry J.M., Delcher A., Deng Z., Mays A.D., Dew I., Dletz S.M.,

RA Glodson K., Doup L.E., Downes M., Dugan-Roha S., Dunkov B.C., Dunn P.,

RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,

RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,

RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,

RA Harris N.L., Harvey D., Heiman T.J., Wei M.-H., Ibegwam C.,

RA Harris N.L., Harvey D., Heiman T.J., Wei M.-H., Ibegwam C.,

RA Harris N.L., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,

RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,

RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,

RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.L.,

RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,

Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,

RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,

RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,

RA Shue B.C., Siden Kiamos I., Simpson M., Skupski M.P., Sinth T.,

RA Spier E., Spradling A.C., Stapleton M., Skupski M.P., Sinth T.,

RA Spier E., Spradling A.C., Stapleton M., Skupski M.P., Sinth T.,

RA Wang Z.-Y., Wassarman D.A., Weinstcok G.M., Weissenbach J.,

RA Wang Z.-Y., Wassarman D.A., Weinstcok G.M., Weissenbach J.,

RA Wang Z.-Y., Wassarman D.A., Weinstcok G.M., Weissenbach J.,

RA Wang Z.-Y., Wassarman D.A., Weinstcok G.M., Weissenbach J.,

RA Shens S.M., Moodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,

RA Shens S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,

RA Shens S.M., Woodage T., Worley K.C., Wu D., Yang S., Zhu X., Smith H.O.,

RA Shens S.M., Shens S.M., Woodage T., Shen M., Zahou X., S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           alignment_block:
US-09-668-119-1 x Q9VE07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Align seg 1/1 to: Q9VE07 from: 1 to: 1542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               130 CATAACAAGAAATCTCAAGCTTCCGTC....AGTGATCCTATGAATGC 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              338 luGlyProThrProProPro..... 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        212 CTGGAATTGGCATGCCTCCTCGGGGCCCGGGACAGTCTCTGGGCGGGATG 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       174 ACTCCAG.....AGCCTGACTGGCGGACCTGCTGCGGGAGCCG 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  305 HisHisAlaThrProGlnAlaAlaIlePheProThrGluProValThrTh 321
                                                                                      lnLysAsnThrGlnAlaGluGluGlnGlnGlnLeuGlnLeu.....
                                                                                                                                                                                                                                                                                                                                                                                                                                TCCTGGGACCTCGGGGATGGCCCCT.....CACAGCATGGCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          rThrLysMetTyrThrThrSerSerThrSerAlaProValValPheThrG 338
                                                                                                                                                                                                                                                             TCGTGTCTACG...GCAACTCCACAGACCCAGCTGCAGCTCCAGCAGGTG 396
                                                                                                                                                                                                                                                                                                                                                   yThrGlyIleProAsnLeuAspProAlaAspValTyrHisThrLeuGlyG 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGTAGCTTTGGTGCCATGGGACAGCCAATGTCTCTCTCAGGGCAGCCGCC 311
.....GluLysGlnGlnGlnMetGlnLysGlnGlnGlnIl 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1542 AA; 168644 MW; 27C06E61A73FF016 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1.284
48.820
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                425.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps:
Percent Identity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          678
32
26.844
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679	CCCCCTTCCCCCCAGCCGTCCCCGCCAGCCCAGCCCAGC	664
4 63	yGlnValIleAsnGluAspIleGlyAsnIleLysArgProLeuLysGl	6.4
	GTGCAGACCCCGCAGTCGA	1126
1125 647	CCCATGCTGTCCTCGCCGTCACCGGGCCAGCAG	1093 630
30		0 0
613	AsnAsnValVallleSerProGlyGlnGlnSerAl	1054
1053	GGTGCAGCAGCAGCAGACAGCAGTACAGACAGCTCAGGCTGC	1004
1003 599	GAAATTTGTCCGAGCTCCGATGGTGGTGCAGCAGCCCCCAGTGCAGC :::::::    :::	957 582
582	luGlnLysValIleSerGlySerGlnGluAsnTyrSerAsnGluTyrV	566
956	GCTCTCCCTGGACAAATGTTGTATACCCA	910
565	::: :::    	4
909	AACCATCACAACTCCCGCCACAGTCGCAGACCCAGCCTTTGGTGTC	860
859 549	CCGCCACCACAGCCCCAGCAGCCTCCAGTTGCTCAGA	823 532
532	yrGlnGlnAsnGlnGlyPheAspAlaGlnGlyAsnLeuIleGlnProIl	516
822	CCAG	817
816	GCAGCAGATGCATCACACACAGCAC : ::::: ::: :::   ::: eAsnSerLeuAlaGluGluGluSerAsnValAlaGlnAsn	782 499
781	GCAGCCACCGATGCAGCCACAGCCTCCGCCCTCCCAGGCTCTGC	735 485
00	isGlnHisGlnGlnHisGlnProLeuProProThrLe	472
734	GCAGCAGCAGCAGGCTTTGGAGGCCCAGCCACCAATTCA	685
684 471	TGCAGCGAATAGCACAGCTGCAGCTCCAACAGCAACAGCAGCAGCAGCAGCAGCAG	635 460
460	:::           :::	42
634	AAATTGCATCAAAAATCAGCAACAGATACAGCAGCAGCAACAGCAGC	œ
443	CAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC	541 427
N	GlnTyrGlnLeuGlnLeuGluLysGlnHisLeuAspLysGlnLysHis	410
540	AGAGTGCCATGCAGCAGCAGTTCCAAGCAGTAGTGCAGCAG	497
410	eGlnHisGlnGlnTyrGlnGluGlnGlnGlnGlnLeuTyrGluGlnG	393
496	AGGCTC	447

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seq_documentation_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1667 ......GGATGCCGTCCTGGCCAACATCCGCTCACCTGTCTTCAAC 1706
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1599 GCGGTGCCCACTCCCCCACCGCCCCCGGTGCCACCGACCAAACAGCAGTA 1648
Q9VP17;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2001 (TrEMBLrel. 13, Last sequence on June-2001 (TrEMBLrel. 17, Last anno CG7177 PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                          1707 CATTCCCTGTACCGCACATTCGTTCCAGCCAT 1738
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1549 AAGACCTTGCAAAAGTGTGAGATCGCCCTGGAGAAACTCAAGAATGACAT 1598
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1453 ....AACAAGATCGACAAGAACGAAGACAGAAAAAAGGACCTGAGTAAGA 1498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1423 AAG......1452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1373 CCAGCCAGGCTGAGGIGCAGCAGCTACCTGGACAAGCTGAAGCAGCTGTCG 1422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1329 AAACACACCTGTGAACCCCAGCTCTGTCATGAGC.....CCAGCTGGCT 1372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1295 CACAG...... 1299
                                                                                                                                                                                                                                                                                                                                   920 heArgProAsnAlaLysIleSerSerGlyHis 930
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         887 ProLeuGlyThrSerProProSerAsnPheTyrAsnGluTyrAsnArgLy 903
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          828 ySerAlaSerValGlrIleGlnGlnHisGluValLeuAsnLeuSerGlnG 845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1300 .....AACTTCAGTGTCCCCTCACCTGGACCTTT 1328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1240 TTCCTGCCC..... AGCCCCTCACCGCAGCCCTCCCAGAGCCCAGTGAC 1283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1222 ......GCCCCATCTCCCAGTAGC 1239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1197 CAACTCCAAC..... 1221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    903 sProGlnAsnGlyProArgProSerAsnLeuProAsnIleLeuProGlnP 920
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               858 uGlnProSerLeuGluMetGluProProProArgTyrProThrThrValP 875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   845 lnLysGlnProLeu.IysPhe......ProAlaGlnGlnProGlyGl 858
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         812 AsnSerAsnProValValPheProLysProMetAspGluValValProG1 828
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          796 roAsnIleAsnGlyHisAlaGlnProLeu...SerLeuGlnGlnIleGln 811
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          779 uSerLeuGluProPrcSerSerAlaValMetGlnGlyProProAlaGlyP 796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    746 roGlnLysProGlnProThrProProValLeuMetGlnGlyGluAspThr 762
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               763 LysGluLeuLeuValSerThrAsnIleArgPheProAlaGlnGlyGluGl 779
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        729 rLysProGluGlnProSerHisSerTyrProProGlnGlnSerSerThrP 746
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             713 GlnLeuProLeuIleClySerAsnLysArgProSerLysLysProValTh 729
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  696 lyThrIleSerTyrGinGluProProGluAlaProThrProTyrGln 712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   679 nAsnSerAsnPheH1::GlnAsnGlyAsnValAlaThrSerGlyAlaProG 696
                           Last sequence update)
Last annotation update)
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alignment_scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RA Adams N.D., Cehriker S.E., Holt R.A., Evans C.A., Gocayne J.D., RA Madams M.D., Cehriker S.E., Holt R.A., Evans C.A., Gocayne J.D., RA Adams M.D., Cehriker S.E., Holt R.A., Hoskins R.A., Galle R.F., RA George R.A., Lewis S.E., Kinhards S., Ashburner M., Henderson S.M., Ra Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Ra Baradon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D., RA Man K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G., RA Man K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G., RA Ballew R.M., Basu A., Baxendale J., Bayraktaroju L., Besseley E.M., Ra Beeson K.Y., Benos P.V., Berman B.P., Bhandarid D., Botkohan W.R., Bouck J., Brokstein P., Botter A., Chandra I., Charler M., Cawley S., Dahlke C., Davenport L.B., Davies P., RA Dodson K., Doup L.E., Downes M., Dugan Rocha S., Dunber S., Dowles M., Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W., Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K., RA de Pablos B., Houston K.A., Heinan T.J., Hernandez J.R., Houck J., Lavitsky R.A., Howland T.J., Wei M.-H., Ibewam C., Jalai M., Kalush F., Karpen G.H., Ke Z., Kannson J.A., Ketchum K.A., Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z., Man Merkulov G., Milshina N.V., Moharry C., Morris J., Moshrefi A., Nelson D.L., Ra Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L., Ra Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L., Ra Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L., Ra Maris M., Moharry C., Morris J., Moshrefi A., Nelson D.L., Stong R., Sunders R.D.C., Stapleton M., Strong R., Smith T., Shen H., Strong R., Smith T., Ra Shue B.C., Stapleton K.A., Nisskern D.R., Pacleb J.M., Nelson D.L., Ra Shue B.C., Siden Films S., Pan S., Pollard J., Purl Y., Resee M.G., Ra Maris M., Wolffer R., Weinstock G.M., Weissenbach J., Ra Maris M., Wolffer J., Weinstock G.M., Weissenbach J., Ra Maris M., Wolffer J., Pacleb J.M., Smith H.O., Pacle M., Weinstock G.M., 
                                                                                                                                                                                                                                         Align seg 1/1 to: Q9VP17 from: 1 to: 2285
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336 TCACAGCATGGCTGTCGTGTCTACGGCAACTCCACAGACCCAGCTGCAGC 385
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                                                                                                                                                            286 CCAATGTCTCTCAGGGCAGCCGCCTCCTGGGACCTCGGGGATGGCCCC 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CG7177.
Drosophila melanogaster (Fruit fly).
Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Euterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=20196006; PubMed=10731132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=7227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ratio:
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1.484
47.185
                                                                                                                                                                                                                                                                                                                                                                                                                                     Length: 604
Gaps: 33
Percent Identity: 29.967
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951 1220	9 GACAAATGTTGTATACCCAACCA	92 120
928 1204	8CCTTTGGTGTCACAGGCGCAAGCTCTCCCTG        :::      1 nProIleGlnLeuSerMetProLeuGlnGlnGlnLeuGln	89 119
897 1191	5CATCACAACTCCCGCCACAGTCGCAGACCCAG	86 117
864 1174	3GCTCAGAACCAA	115 115
852 1158	6 .CCACCACAGCCCCAGCAGCCTCCAGTT	82 114
825 1141	2 CATCACACAGCAGCACCAGCCG	80 112
801 1124	6 CTCTGCCCCAGCAGCTGCAGCAGATG   :::	77 110
775 1108	2 TCAGCAGCCACCGATGCAGCAGCACAGCCTCCGCCCTCCCAGG:	73 109
731 1091	2 CAGCAGCAGCAGCAGCAGCAGCAGCGTTTGGAGGCCCAGCCACCAAT	108
681 1082	2 AGCTGCAGCGAATAGCACAGCTGCAGCTCCAACAACAGCAACAGCAGCAGCAGCAGCAGCAGCAGCAG	63 106
631 1066	8 ATTGCATCATAAATCAGCAACAGATACAGCAGCAGCAACAGC :::	58 105
587 1050	8 CAGCAGCAGCAGCCAGCAGCAGCAGCAGCAGCAGCAGCATCTAATTAA          :::            9 IleGlnGlnIleLeuGlnGlnGlnGlnValAl	53 103
537 1038	8 TCCAGGCTCAGCAGAGTGCCATGCAGCAGCAGTTCCAAGCAGTAGTGCAG::	48 102
487 1022	CAGCAGCAGT          AlaValAsnMetGlnGlnAlaT	100
452 1005	09CAGCAGCAACAGCAGCAGTTCCAGCAGCAGCAGCAGCAGGCGGCGCT	98
988	2 roLeuGlnGlnGlnLeuGlnGlnLeuM	
972	isGluGln	ي پ

	CTGTCTTCAACC 1707	1696 1483
1482	erThrProProThrThrThrSerThrMet	1473
1695	GTACCTATGCCAGCCGCTCCTGGATGCCGTCCTGGCCAACATCCGCTCAC	1646
1645 1473	GTGCCCACTCCCCCACCGCCCCCGGTGCCACCACCAAACAGCA	1456
1		1600
1456	GlnSerAsnCysAsnLeuThrLeuGluAlaAr	4
1601	ACCTTGCAAAAGTGTGAGATCGCCCTGGAGAAACTCAAGAATGACATGCG	1552
1445	:::	1429
1551	AGAGCCTTCTGGACATTCTGACAGACCCCTCGAAGCGGTGTCCCCTGAAG	1502
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1379	${\tt rGlyThrGlyThrArgSerGlnLysProArgArgSerAsnArgSerGlyA}$	1362
1395		1395
1362	LysThrGluProGlnAsnSerAlaAspAlaGluLysGlnGlnLysGlnTh	1346
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1290	oGlnAsnGlnProGlnProGlnThrGlnGl	1273
1162	GCAGTCGATGCCCCCTCCCCCC	1137
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1136		1087
1260	1 isGlnGln	1251
1086		1037

PRT; 926 AA.

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RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
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RA Brandon R.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Wan K.H., Doyle C., Haxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           O9W3Gi,
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Ærthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CG10555 PROTEIN.
                             148 GCTTCCGTCAGTGATCCTATGAATGCACTCCAGAGCCTGACTGGCGGACC 197
                                                                                                                                                                                                                                                                                                                                                                  EMBL, AE003443; AAF43366.1; -
FlyBase; FBgn030034 - GG10555.
InterPro; IPR002965; P_rich_extensn.
PRINTS; PR01217; PRICHEXTENSN.
189 AlaGlnLeuAlaAspProAlaMetAsnIleSerGlnIleLeuProProPr 205
                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                  926 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Drosophilidae; Drosophila
                                                                                                                                                                                                                                                                                                                                               )3004 MW; 6FD5B9F77C36C006 CRC64;
                                                                                                                                                                                                         Percent Identity: 28.883
                                                                                                                                                                                                                                                        Length:
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5 AGCAGCAGCAGCCTTTGGAGGCCCAGCCAACCAATTCAGCAG            1	408
5 G     nArgProAsnA	675 391
TAGC	625 375
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CAGCAGCAGCAA	406 278
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GCCTCCTGGGACCTCGGGGATGGCCCCTCACAGCATGGCTG          yProProGlnMetGlyMetGlnGlnHisGly	251
ATGGGTAGCTTTGGTGCATGGGACAGCCAATGTCTCTCTC	ωισ
CTCGGGGCCCGGACAGTCTCTGGGCGG	230 222
TGCTGCGGGAGCCGCTGGAATTGGCATGCCTC 22	198 205

1474	AGTACAT	424
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1385 7 <b>4</b> 7	CTGGCTCCAGCCAGCCTGA	367 731
731	${\tt ProProProGlnGlyGlyAlaGlyGlyGlyAlaGlyProSerGly}$	<u> </u>
1366	- ≫	363
1362 714	TTAAACACACCTGTGAACCCCAGCTCTGTCATGAGC    :::    :::   ::::: :::    AlaGlyGlyGlyAsnAsnAsnProAsnGlyProAsnAlaGlnGlnSerTh	327 698
697	yr Ser Thr Thr Ala Pro Ser Gln Thr Pro Pro Pro Gln Gly	681
1326		326
681	roProProProPr	664
1326	CACAGAACTTCAGTGTCCCCTCACCTGGAC	288
664	er	648
1287		287
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1287	CCCAGAGCCCAGTGACGGC	265
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N		193
1192 581	GCCGTCCCCGCAGCCCGGCCAGCCCAGCTCAC	161 564
1160 564	TCACCGGGCCAGCAGGTGCAGACCCCGCAGTCGATGCCCCCCCC	111 549
1110 548	CCAGGTCAGCCAGAGCAGCCTCCCCATGCTGTCCTCGCCG	532
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943	CTGGACAAATG	894

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Query length: 579
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gb_pr:BC007529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gb_pr:AF328769
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Command line parameters:
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174 | AF010404 Homo sapiens ALR mRN

189 | AF010403 Homo sapiens ALR mRN

1838 | AC011603 Homo sapiens chromo

1940 | AC02556 Homo sapiens chromo

1940 | AC025256 Homo sapiens chromo

1940 | AC025256 Homo sapiens chromo

1940 | AC091616 Rattus norvegicus chromo

1940 | AC017582 Drosophila melanoga

1941 | AC017582 Drosophila melanoga

1951 | AC017581 Drosophila melanoga

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1951 | AC017581 Drosophila melanoga
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315 | AC068137 Homo sapiens Chromo
1 | AK00003 Homo sapiens Chromo
356 | AC004033 Homo sapiens Chromo
908 | AC007030 Homo sapiens Chromo
908 | AL358856 Homo sapiens chromo
1 | AC087802 Mus musculus chromo
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316 | AC079044 Mus musculus chromo
317 | AL359452 Homo sapiens chromo
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1 AF145620 Drosophila melanogas

5 1 AC074221 Mus musculus chromo

1 AC014160 Drosophila melanogas
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AF388769 Homo sapiens PC2-glut
AF328870 Mus musculus PC2-glut
U80745 Homo sapiens CTG7a mRNA
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                           AC090886
AC090004
                                                                           AC007891 Drosophila melanoga
AC007814 Drosophila melanoga
AE003724 Drosophila melanoga
AE093645 Homo sapiens chromo
AC021022 Homo sapiens chromo
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AE003594 Drosophila melanoga
AC090437 Mus musculus clone
4200 Boreogadus saida antifr
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Submitted (30-MAR-1998) Microbiology, State University of New York
Health Science Center at Brooklyn, 450 Clarkson Ave., Brooklyn, NY
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Abraham, S. and Solomon, W.B.
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TPA inducible gene; TIG-1"
                                  SSTIPCTAHSFQP"
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/db_xref="taxon:9606"
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1015 TIGCTCAGAACCATCACAACTCCCGCCACAGTCGCAGACCCAGCCT 1064
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seq_documentation_block:
LOCUS AF328769
                                                                                                                                                                                                                                                    seq_name: gb_pr:AF328769
                                                                     KEYWORDS
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                                                                                                                Homo sapiens PC2-glutamine-rich-associated protein (PCQAP) mRNA, aF328769
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                          Homo sapiens
                                                                                        AF328769.1 GI:14276856
                                                human.
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REFERENCE
AUTHORS
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laArgLeuIleIleHisPheArgAspIleHisAsnLysLysSerGlnAla 50
                                                                             CCAGGCTCATTATCCATTTTCGAGACATTCATAACAAGAAATCTCAAGCT
                                                                                                                                                              CCATGTTTTCCTGAAGGCCAAGACCCGGGACGAATACCTTTCTCTCGTGG
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Ratio: 5.142
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novelli,G. and Meisterernst,M. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 (bases 1 to 3170)
Berti,L., Mittler,G., Przemeck,G.K.H., Stelzer,G., Guenzle
Amati,F., Conti,E., Dallapiccola,B., Hrabe' de Angelis,M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Isolation and characterization of a novel gene from the digeorge chromosomal region that encodes for a mediator subunit Genomics 74 (3), 320-332 (2001)
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PRGPGQSLGGMGSLGAMGQPMSLSGQPPPGTSGMAPHSMAVVSTATPQTQLQLQQVAL
QQQQQQQFQAQQAALQQQQQQQQQQQQQAAQQSAMQQQFQAVVQQQQQQQQQQQQQQ
HLIKLHHQNQQQIQQQQQQLQRIAQLQQQQQQQQQQQQQQQALQAQPFIQQPPMQQP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product-"PC2-glutamine-rich-associated protein"
/protein_id="AAK58423.1"
/db_xref="Gi:14276857"
/translation="MDVSGQETDWRSTAFRQKLVSQIEDAMRKAGVAHSKSSKDMESH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
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REFERENCE
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JOURNAL
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Berti, L., Mittler, G., Przemeck, G.K.H., Stelzer, G., Guenzler, B., Amati, F., Conti, E., Dallapiccola, B., Hrabe' de Angelis, M., Novelli, G. and Meisterernst, M.
Isolation and characterization of a novel gene from the digeorge chromosomal region that encodes for a mediator subunit Genomics 74 (3), 320-332 (2001)
                                                                                                                                                                                                 Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
1 (bases 1 to 3395)
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                                                                                                    329 TGGGTGGGATGGGTGGCCTTGGCGCTATGGGACAACCACTGCCCCTCTCC 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    179 CCCGACTCATTATCCATTTCCGAGATATTCATAACAAGAAATCCCAAGCT 228
101 GlyGlnProProProGlyThrSerGlyMetAlaProHisSerMetAlaVa 117
                                                                                                                                                                                                                                                                                                   279 CCCAGGAGCAGCTGGGATTGGCATGCCTCCTCGGGGCCCAGGACAGTCCC 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 229 TCTGTCAGTGACCCCATGAATGCACTGCAGAGCCTTACTGGTGGACCCCAC 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   129 TCATGTGTTCCTGAAGGCCAAGACCCGGGATGAGTATCTTTCCCTTGTGG 178
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                                                                                                                                                 84 euGlyGlyMetGlySerPheGlyAlaMetGlyGlnProMetSerLeuSer 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   51 SerValSerAspProMetAsnAlaLeuGlnSerLeuThrGlyGlyProAl 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17 rHisValPheLeuLysAlaLysThrArgAspGluTyrLeuSerLeuValA 34
                                                                                                                                                                                                                                                                                                                                                                                 67 aAlaGlyAlaAlaGlyIleGlyMetProProArgGlyProGlyGlnSerL 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        34 laArgLeuIleIleHisPheArgAspIleHisAsnLysLysSerGlnAla 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           79 ATGAGGAAAGCTGGTGTGGCCCACAGTAAATCTAGCAAGGATATGGAGAG 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MetArgLysAlaGlyValAlaHisSerLysSerSerLysAspMetGluSe 17
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Ratio: 4.636
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Submitted (14-DEC-2000) Department of Protein Biochemistry,
Institute of Molecular Immunology-GSF, Marchionini Str. 25, Munich
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Berti,L., Mittler,G., Przemeck,G.K.H., Stelzer,G., Guenzler,B., Amati,F., Conti,E., Dallapiccola,B., Hrabe' de Angelis,M., Novelli,G. and Melsterernst,M.
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//BICTURE AKT SHA
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364	GlnValSerGlnSerSerLe	358
1251	TAAGAGCCCGGTTCCCGCCCACCTCCACCATGTCTGCTGGCCCCGTCAAGC	1202
357		357
357	ProGlyVal	354
354 1151	GlnGlnGlnThrAlaValGlnThrAlaGlnAlaAlaGlnMetValAl	339
	GGTCCAGCAGCCGCAAGTGCAGCCCCCAGGTGCAGCAGCAGCTGCAGCCC	
338	alValGlnGlnProProValGlnProGlnValGln	327
1051	CTGCCCAACAGCAGCTGAAATTTGTCCGTGCTCCGATG	.002
327	etLeuTyrThrGlnProProLeuLysPheValArgAlaProMe	311
1001		Ū
311	lnSerGlnThrGlnProLeuValSerGlnAlaGlnAlaLeuProGl	295
951	:::	Ō
294	${\tt nProGlnGlnProProValAlaGlnAsnGlnProSerGlnLeuProPr}$	278
901	CCAGCAGCTGTCACAGCTGCATCATCCACAGCATCACCAGCCACCACCTC	852
278	GlnGlnLeuGlnGlnMetHisHisThrGlnHisHisGlnProProPro	261
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4	Jordon Carlor   Striet   Arien   Striet   Stri	<b>J</b>
228 751	nGlnGln	211 720
719	TTAAGTTGCATCAAAGCCAGCAACAACAGATACAACAGCAGC	673
211	sLeuHisHisGlnAsnGlnGlnGlnIleGlnGl	195
672	CAGCAGCAGCT	629
194		178
628	TCCAGGCACAACAG	579
178	GlnHheGlnAlaGlnGlnSerAlaMetGlnGlnGlnPheGlnAlaVal	161
	ACAGCAGCAACAGCAGCAGCA	N i
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528	eugingingingingingingingheginGingingingingingingingingingingingingingi	134 479
		) i
134 478	lValSerThrAlaThrProGlnThrGlnLeuGlnLeuGlnGlnValAlaL          :::	117 429
428	GGCAACCACCCCTGGAACCTCTGGAATGGCCCCTCATGGCATGGCTGT	379

AUTHORS TITLE JOURNAL MEDLINE REFERENCE	SOURCE ORGANISM	seq_documer LOCUS DEFINITION ACCESSION VERSION	seq_name:	564 l : 1893 T	547 n   1843 C	531 s 1793 A	514 s   1743 T	498 S       1693 A	481 r 1 1643 G	464 n   1593 G	448 A     1543 A	431 h:     1493 C	414 el 1 1443 C	398 G:     1393 C:	381 ej       1352 CC	364 up       1302 CA	1252 TCC
Margolis,R.L., Abraham,M.R., Gatchell,S.B., Li,S.H., Kidwai,A.S., Margolis,R.L., Stine,O.C., Callahan,C., McInnis,M.G. and Ross,C.A. cDNAs with long CAG trinucleotide repeats from human brain Hum. Genet. 100 (1), 114-122 (1997) 97369492 (bases 1 to 1048)	human. Homo sapiens Eukaryota; Met. Mammalia; Euth	ntation_block: 1048 bp mRNA PRI 18-DEC-1997 HSU80745 1048 bp mRNA, partial cds. U80745 U80745.1 GI:2565064	gb_pr:HSU80745	aHisLeuSerSerThrIleProCysThrAlaHisSerPheGlnPro 579 :	SerSerThTTyralaSerArgSerTrpMetProSerTrpProThrSerA 564                ::::::	nAspMet.ArgCysProLeuProHisArgProArgCysHisArgProAs 547         :::            :::    ::: TGACATGGCAGTGCCCACACCCCCACCACCCCCAGTTCTTCCAACCAA	ProLeuLysThrLeuGlnLysCysGluIleAlaLeuGluLysLeuLysA 531 	erlysMetlysSerLeuLeuAspIleLeuThrAspProSerLysArgCy 514 	'gArgMetlleAsnLysIleAspLysAsnGluAspArgLysLysAspLeu 497 	GlnTyrLeuAspLysLeuLysGlnLeuSerLysTyrIleGluProLeuA 481 	AsnProSerSerValMetSerProAlaGlySerSerGlnAlaGluGluGl 464	rProGlnAsnPheSerValProSerProGlyProLeuAsnThrProVal 447 	LeuProSerProSerProGlnProSerGlnSerProValThrAlaArgT 431 	lnProAsnSerAsnValSerSerGlyProAlaProSerProSerSerPh 414 	rMetProProProProGlnProSerProGlnProGlyGlnProSerSer 397 	ProMetLeuSerSerProSerProGlyGlnGlnValGlnThrProGlnS 381 	CATCTCTTTGGGCGGACAGCCCACAACACAGGTCAGCCAAAGCAGCCT 1301

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alignment_scores:
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                                                                                                                                                                         207 GCAGCAGCAGCAGCAGCAGCAGCAGCCAGCCACCAA 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          211 GlnLeuGlnArgIlek.laGlnLeuGlnLeuGlnGlnGlnGlnGlnGlnGlnGl 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       177 lValGlnGlnGlnGlnGlnLeuGlnGlnGlnGlnGlnGlnGlnGlnHist 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 repeat_region
307 CCCCAGCAGCTGCAGCAGATGCATCACACACAGCACCACCAGCCGCCACC 356
                                         261 ProGlnGlnLeuGlnClnMetHisHisThrGlnHisHisGlnProProPr 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                    227 nGlnGlnGlnGlnGlnGlnGlnAlaLeuGluAlaGlnProProI 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          107 TAATTAAATTGCATCITCAAAATCAGCAACAGATACAGCAGCAGCAACAG 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            194 euIleLysLeuHisHisGlnAsnGlnGlnGlnIleGlnGlnGlnGlnGln 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    57 AGTGCAGCAGCACCACCTCCAGCAGCAGCAGCAGCAGCAGCAGCATC 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              source
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Ratio: 5.159
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
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/rp:_unit=CAG
388 c 251
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/no:e="glutamine rich"
/codon_start=1
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<1. .>1048
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<1. .>1048
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/db_xref="taxon:9606"
/ch:omosome="20"
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seq_documentation_block:
LOCUS BC007529
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                                                                                                                                                                                                                                                              KEYWORDS
                                                                                                                                                                                                         ORGANISM
                                 JOURNAL
                                                                                         AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      957 CGAGCCCCTGCGCCGCATGATCAACAAGATCGACAAGAACGAAGACAGAA 1006
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                607 CAGAGCAGCCTCCCCATGCTGTCCTCGCCGTCACCGGGCCAGCAGGTGCA 656
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 361 GlnSerSerLeuProMetLeuSerSerProSerProGlyGlnGlnValGl 377
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAAAGGACCTGAGTAAGATGAAGAGCCTTCTGGAC 1041
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AGCCCAGCTCACAGCCCAACTCCAACGTCAGCTCTGGCCCTGCCCCATCT 756
Gene Collection (MGC), Cancer Genomics Office, National Cancer
                   Direct Submission Submitted (10-MAY-2001) National Institutes of Health, Mammalian
                                                                                     Strausberg, R
                                                                                                             Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

[] (bases 1 to 2106)
                                                                                                                                                                                                         Homo sapiens
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                                                                                                                                                                                                                                       human.
                                                                                                                                                                                                                                                                                                                                                                           2106 bp
                                                                                                                                                                                                                                                                                                                                                                                  mRNA
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COMMENT
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ORIGIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                51 CCCATGGCACAGGTCAGCCAGAGCAGCCTCCCCCATGCTGTCCTCGCCGTC 100
SerGlyProAlaProSerProSerSerPheLeuProSerProSerProGl 421
                                                                                                      #ProGlyGlnGlnValGlnThrProGlnSerMetProProProProProGlnP 388
                                                                                                                                                                                                       roSerProGlnProGlyGlnProSerSerGlnProAsnSerAsnValSer 404
                                                                                                                                                                                                                                                                                                             Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAL Plate: 22 Row: n Column: 21
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 7209306.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield, Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin, Letticia Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven Ness, Pawan Pandoh, Anna-Liisa Prabhu, Parvaneh Saeedi, Jacqueline Schein, Duane Smailus, Michael Smith, Lorraine Spence, Jeff Stott, Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy, Recent Parker, Miranada Tsai, Natasja van den Bosch, Jill Vardy, Recent Parker, Miranada Tsai, Natasja van den Bosch, Jill Vardy, Recent Parker, Miranada Tsai, Natasja van den Bosch, Jill Vardy, Recent Parker, Miranada Tsai, Natasja van den Bosch, Jill Vardy, Recent Parker, Miranada Tsai, Natasja van den Bosch, Jill Vardy, Recent Parker, Miranada Tsai, Natasja van den Bosch, Jill Vardy, Recent Parker, Miranada Tsai, Natasja van den Bosch, Jill Vardy, Recent Parker, Miranada Tsai, Natasja van den Bosch, Jill Vardy, Recent Parker, Miranada Tsai, Natasja van den Bosch, Jill Vardy, Recent Parker, R
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cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Quality: 1174.00
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       George Yang, Scott Zuyderduyn, Marco Marra.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 info@bcgsc.bc.ca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: MGC help desk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NIH-MGC Project URL: http://mgc.nci.nih.gov
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PPPQPSPQPSQVMSPAGSSQAEEQQYLDKLKQLSKYIEPLRHMINKLDKNEDRKKDLS
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DAVLANIRSPVFNHSLYRTFVPAMTAIHGPPITAPVVCTRKRRLEDDERQSIPSVLQG
EVARLDPKFLVNLDPSHCSNNGTVHLICKLDDKDLPSVPPLELSVPADY PAQSPLWID
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/tissue_type="Eye, retinoblastoma"
/clone_lib="NIH_MGC_16"
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719 c 553 g 378 t
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/db_xref="taxon:9606"
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99.115
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seq_name: gb_htg:AC068137
                                          COMMENT
                                                                                                                                                              REFERENCE
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                                                                                                                                                                                                                                                                                                       SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                               KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                     VERSION
                                                                                                                                                                                                                                                                                                                                                                                        ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                              DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                    seq_documentation_block:
LOCUS AC068137 1
                                                                                                                                                                                 TITLE
JOURNAL
                                                                                                                                      AUTHORS
                                                                                                    JOURNAL
                                                                                                                       TITLE
                                                                                                                                                                                                                          AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    421 nProSerGlnSerProValThrAlaArgThrProGlnAsnPheSerValP 438
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       455 ProAlaGlySerSerGlnAlaGluGluGlnGlnTyrLeuAspLysLeuLy 471
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     651 CTCCTGGATGCCGTCCTGGCCAACATCCGCTCACCTGTCTTCAACCATTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CCCCACCGCCCCGGTGCCACCGACCAAACAGCAGTACCTATGCCAGCCG
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                                                                                                                                                                                                                                                                                                                                                                                 HTG 10-Homo sapiens chromosome 2 clone RP11-803A13, WORKING SEQUENCE, 6 unordered pieces.
                                        9n M
                                                                        Submitted (28-APR-2000) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis,
                                                                                                                     Waterston, R.H.
Direct Submission
                                                                                                                                                                             Unpublished
                                                                                                                                                                                                  The sequence of Homo sapiens clone
                                                                                                                                                                                                                          Waterston, R.H.
                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                             HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN
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                                      ) 63108, U
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                                        USA
, 2001 this sequence version replaced gi:13431262
---- Genome Center -----
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Center: Washington University Genome Sequencing Center code: WUSSC
Web site:http://genome.wustl.edu/gsc/index.shtml
Project Information

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alignment_block:
US-09-668-119-3 x AC068137/rev
                                                                                                                                                                                                                                                                                                                             alignment_scores:
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ORIGIN
                                                                                                                                                                                                                                      Quality: 911.00 Length: 425
Ratio: 2.930 Gaps: 17
Percent Similarity: 73.412 Percent Identity: 57.412
                                                                                                     Align seg 1/1 to reverse of: AC068137 from: 1 to: 156315
154498 AAGCAAGAATCCGTCTCAAAAACAAAACAAAACAAAATCAGAACAGAAATG 154449
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                                                 166 GlnGlnSerAlaMetGinGlnGlnPheGlnAlaValValGlnGlnGlnGl 182
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Sequencing vector: Ml3; 38%
Sequencing vector: Ml3; 38%
Sequencing vector: Ml3; 38%
Sequencing vector: Plasmid; 22%
Chemistry: Dye-terminator Big Dye; 58% of reads
Chemistry: Dye-terminator Big Dye; 58% of reads
Assembly program: Phrap; version 0.9903l9
Consensus quality: 153264 bases at least Q40
Consensus quality: 153105 bases at least Q30
Consensus quality: 155105 bases at least Q20
Insert size: 168000; agarose-fp
Insert size: 168000; sum-of-contigs
Quality coverage: 9.85 in Q20 bases; sqarose-fp
Quality coverage: 9.86 in Q20 bases; sum-of-contigs
Quality coverage: 9.86 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                              Quality:
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                                                                                                                                                                                                                                                                                                                                                                                                                                     42538 a
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1 35745 c 36389 g 41139 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1. .156315
/organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /not == "assembly_name:Contig68"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone="RP11-803A13"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9172: contig of 9172 bp in length
9272: gap of unknown length
17587: contig of 8315 bp in length
17687: gap of unknown length
39085: contig of 21398 bp in length
39185: gap of unknown length
61924: contig of 22739 bp in length
62024: gap of unknown length
107416: contig of 45392 bp in length
107516: gap of unknown length
107515: contig of 46799 bp in length
156315: contig of 48799 bp in length
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                                                                                                                                                                                                                                                                                                                                                                                                                               504 others
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182	lnLeuGlnGlnGlnGlnGlnGln.GlnHisLeuIleLysLeu	198
154448	GAGACTAAAAAAATACAAAAGACCAATAAAATTTCCAGTTATATTGAAT	154399
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455 153656	OAlaGlySerSerGlnAlaGluGluGlnGlnTyrLeuAspLysLeuLysG 4               :::      :::	72

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REFERENCE
AUTHORS
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SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                    FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      seq_name:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     153556 GGGAACCAAGACAGCAAAAGGGCTGCGGTAAGACG....AGCCTTCTGGA 153511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           153360 TCCTGGACACAGTCCTGGCCGGCATCTGCTCGCAG.TCCTGAACCATT 153312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        153460 CTGAGATCGCCCTGGAGAAACGCAAGCATGACCTGGAGGTGCCCAAGCCC 153411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   571 ProCysThrAla 574
                                                                                                                     CDS
                                                                                                                                                                                                                                                                                                                                                                             source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CGCTCTGACAGTCGGCTCCCAGCTGTGTCCCCTGGAGACCCTGTGGAAGC 153461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CGCTGCCCAAGTACAGGGAGCCCCTGCGCCCCTGAGCAACGGGATCCAC 153557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CCCTGCACCGCG 153300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ysGluIleAlaLeuGluLysLeuLysAsnAspMet.ArgCysProLeuPr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       pIleLeuThrAspProSerLysArgCysProLeuLysThrLeuGlnLysC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SerTrp..MetProSerTrpProThrSerAlaHisLeuSerSerThrIle 570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gb_pr:AK000003
                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (14 FEB-2000) to the DDBJ/EMBL/GenBank databases. Osamu Ohara, Kazusa DNA Research Institute, Department of Human Gene Research; 153-3 Yana, Kisarazu, Chiba 292-0812, Japan (E-mail:cdnainfo@kazusa or.jp, URL:http://www.kazusa.or.jp, Tel:81-438-52-3913, Fax:81-438-52-3914)

NEDO human cDNA sequencing project supported by Ministry of International Trade and Industry of Japan; CDNA full insert sequencing: Research Association for Biotechnology; cDNA library construction, 5'-& 3'-end one pass sequencing and clone selection: Kazusa DNA Research Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Published Only in DataBase (2000) In press 2 (bases 1 to 4701)
Ohara,O., Kikuno,R., Nagase,T. and Okumura,K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 (bases 1 to 4701) Ohara,O., Kikuno,R., Nagase,T. and Okumura,K. The nucleotide sequence of a long cDNA clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AK000003.1 GI:7209306
FLJ00003 protein; fis (full insert sequence).
Homo sapiens adult spleen cDNA to mRNA, clone:as00003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sapiens mRNA
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                                                                                                                                                                          /note="vector: pBluescriptII SK plus" 3081. .3788
                                                                                                                                                                                                                                  /tissue_type="spleen"
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/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                    location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         partial
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polyA_signal 'BASE COUNT 881 a
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US-09-668-119-3 x AK000003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Align seg 1/1 to: AK000003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    141 CAGAGGAGCATGTCACAGGACAGGCCAGGCGTGTCAGGGAAGGCCAGGCTA 190
                                                                                                                                                                                                                                                                                                                                                                                                                 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                               363
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                                             388
                                                                                                                                                                                                                                                                           463
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     244 eGlnGlnProProMetGlnGlnProGlnProProProSerGlnAlaLeuP 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             228 GlnGlnGlnGlnGlnGlnGlnAlaLeuGluAlaGlnProProIl 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GTGCCAGCCA.....
                       oSerProGlnProGlyGlnProSerSerGlnProAsnSerAsnVal.... 403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GlnProGlnGlnPro......ProValAlaGlnAsnGlnProSe 290
GTCCCCGCAGCCCGGCCAGCCCAGCTCACAGCCCAACTCCAACGTCAGGT
                                                                                                                     ProGlyGlnGlnValGlnThrProGlnSerMetProProProProGlnPr 388
                                                                                                                                                                                     TCCACTTCCAGGTCAGCCAGAGCAGCCTCCCCATGCTGTCCTCGCCGTCA
                                                                                                                                                                                                           GlyVal..GlnValSerGlnSerSerLeuProMetLeuSerSerProSer 371
                                                                                                                                                                                                                                                                              GGAGGCAGGCGGGCGGCGTGTG.....GCAGCGCGCCGGCTGAGCCCC
                                                                                                                                                                                                                                                                                                                       lnGlnGlnThrAlaValGlnThrAlaGlnAlaAlaGlnMetValAlaPro 355
                                                                                                                                                                                                                                                                                                                                                                  GTGAGGCTGTGCGGGAGGATGGGCCTATGCGTGCGGTGGGCAGGTGGTGT 462
                                                                                                                                                                                                                                                                                                                                                                                                                                                            GTGCCTGTGTGTATGTCCAGGTGGCATTTGGATGAAGACACAGGTGTGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GTGTGCCAGGC.....TGGGGGAGT 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                laLeuProGlyGlnMetLeuTyrThrGlnProProLeuLysPheValArg 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CTGGGCCCCCCCCCGCCAGC..
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAAGCCTGTGCCCCTGTGGGTCCCTGGCCAAGGAGCAAGGGCTGCCCTGC 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CTCCCAGACTGCCCTTTTCCTCACACTCC.....CACGACACAGCCCTC 254
                                                                                          CCGGGCCAGCAGGTGCAGACCCCGCAGTCGATGCCCCCCTCCCCCCCAGCC
                                                                                                                                                                                                                                                                                                                                                                                                        roGlnGlnLeuGlnGlnMetHisHisThrGlnHisHisGlnProProPro
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2.751
31.813
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /translation="SASWYSYQRAGTGYGKQALTAAPGLCHPSQMAQREEPTLCSRPA
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DLPSVPPLELSVPADYPAQSPLWIDRQWQYDANPFLQSVHRCMTSRLLQLPDKHSVTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product="FLJ00003 protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          accessible through http://www.kazusa.or.jp. Start codon is not identified."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .....CCCTTGGTCACCTCATGC...T 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Percent Identity: 27.144
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Gaps:
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403		403
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404	SerSerGlyPr	407
707	CCCGGCTC\CATGTTTCTCTCACTTGG	756
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757	GCCCATCTCCCAGTAGCTTCCTGCCCAGCCCCTCACCGCAGCCCCTCCCA	806
424	SerProValThrAl:(ArgThrProGlnAsnPheSerValProSerPro	441
807	GCCCAGTGACGGCGCGGA	856
441	oLeuAsnThrPio.Val	447
857	ACCTTTAAACACAC(:TGGTAAGTTGGGCCTGAGGTGCTAAGGTCACTC	906
447	:	447
907	TTTATGAGGCCTCAGCTCATACTGGGTGTGCGAGCTCTGGGGC	956
447		447
957	CAAGTTCCCCCACCCGAGGGTCGAGGGCTGTGGCCTCACCC	1006
448		459
7007	TGUAGTGLAUCCUAGCTUTGTCATGAGCCCAGCTGGCTCCA	1056
459	rGlnAlaGluGluGlrGlnTyrLeuAspLysLeuLysGlnLeuSerLysT	76
7 (	CHOOLINGS CANADATACTION CONTRACTOR TO TO TO THE CONTRACTOR TO TO THE CONTRACTOR TO T	) ⊢
 1107	ACATCGAGCCCCTGCCCCGCATGATCAACAAGATCGACAAGAACGAAGAC	1156
493	ArgLysAspLeuSerLysMetLysSerLeuLeuAspIleLeuThrAs	509
1157	.GAAAAAAGGACCTG#.GTAAGATGAAGAGCCTTCTGGACATTCTGACAG	1206
50	:	511
1207	CCCTCGAAGCGG	1256
511		511
1257	.GCC ATGGATGGGCACTTGGTGATGATGTGGGTTTA	1306
511		511
1307	GGCAGCTCTTTGGACCCTGGCCAGAGGCCTCCAAGGCTCC	1356
511		511
1357	TGCTCGGGCTTCAAGCCCAGGCTTCATCTTGGCC	1406
511		511
1407	CCTATTCCTGGCTGCTGCTGTGGCCCTCATGCTGGG	1456
511		511
1457	ACCTCATCCAGTCAGCAGCCAGGGGCCCAGCTTGCAG	1506
-		511
1507	CCTGACCATCAGCTGGCCCAGATGGGCCTGAGCCTGACCTGGAGTTCTGC	1556

534		534
2456	TGGGTGGGAACATGGGAGAAGTCACCCTCTGTCTACGGCCCCCGTGGGTG	. 2407
534		534
2406	GCCTGACCTTGGACCCTGCCCACGAGGCTTCCTGGCCAGGTCTGCTGTGC	2357
534		534
2356	GAGTGCCGCTGAGAGGGCCTTCAAGGTCAGGGCATCTGGGCGGGGGCCCG	2307
534		534
2306	GGGATGCCAGACACCCCTAGGGGAACCAGGGCTCTCCTAAGAGCTCCTGG	2257
534		534
534 2256	ysCysGluIleAlaLeuGluLysLeuLysAsnAspMet.Arg	521 2207
2206	CTCTCTGCAGGTGTCCCCTGAAGACCTTGCA	2157
521	LysArgCysProLeuLysThrLeuGlnL	512
2156	GTGGCAGTAGTTGGGATCCTGAGCCTGAGAACTGCCATGTCTTCCACTCT	2107
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2106	CTGGTCAACTGGTAGGAGCTCCTGCAGAGGTTTCTGATGGCTGAGGCCCA	2057
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511		511
2006	ACTGTCCCTTCTCTTGACCCATCACCTCACTCTGCCAACCAGGGACAAGC	1957
511		511
1956	ACTGGCCTACATGACAATGAGGCCATTCACAGCCTGATCAGGGGCCTGGCC	1907
511		511
1906	${\tt TCTTCATGGGTTGATCCTTTGTTAGGGTTATAGGGATGAGTGGGGCAGGG}$	1857
511		511
1856	GTTCTGCTTGTCTGGATAGAATGCCAGTCACTATTGGGTGGTCCTCCAGG	1807
511		511
1806	TTCACCTCAACTCAGGCTATCCCCCCAACCCCTGTCTAGAAGGGTCTCTCT	1757
511		511
1756	GAGCTCGGGCAGTACCTCCAAACTGCATGGGCATTGGCATATACCTCCCT	1707
511		511
1706	AGAAGCAGGTGGAAGGCAGGGCTGCTGGCCACAGGCTGCTGTGAGGATCA	1657
511		511
1656	TTTGTAGCCCACGTGTGTTGTCATGAAAATGAAAACAAGGTGGCGCTGGTG	1607
511		511
1606	CCCTGACTTGCTGGTGACCATGGGCAGGGGGACTGCATCTCAGTTACCCCCA	1557
511		511

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2657 GACCGTGCCCATCCTGTCTCCAGCCCACTCCCCCACCGCCCCGGTGCCA 2706
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Homo sapiens Chromosome 27
Region, complete sequence
                                                                                                  Submitted (26-JAN-1999) Department Of Chemistry And Biochemistry, The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman
                                                                                                                                                                                                                                          4 (bases 1 to 145356)
Zhang,G., Lao,V., Zhan,M., Budarf,M.L., Emanuel,B.S. and Roe,B.A.
Direct Submission
Submitted (09-DEC-1998) Department Of Chemistry And Biochemistry,
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Submitted (26-JAN-1998) Department Of Chemistry And Biochemistry,
The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
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Submitted (04-FEB-1999) Department Of Chemistry And Biochemistry,
                   Zhang,G., Lao,V., Zhan,M., Budarf,M.L.,
Direct Submission
                                                                                 OK 73019,
                                                                                                                                         5 (bases 1 to 145356)
Zhang,G., Lao,V., Zhan,M., Budarf,M.L., Emanuel,B.S. and Roe,B.A.
Direct Submission
                                                                                                                                                                                                                           The University Of Oklahoma,
                                                                                                                                                                                                                                                                                                                                                                                                             Zhang, G., Lao, V., Zhan, M., Budarf, M.L., Emanuel, B.S.
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Homo sapiens Chromosome 22q11.2 BAC Clone p_m11 In BCRL2-GGT Region
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                        Emanuel, B.S. and Roe, B.A
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                                                                                                                                                                                                                                            119672 AAAGCCTGTGCCCCTGTGGGTCCCTGGCCAAGGAGCAAGGGCTGCCCTGC 119721
                                                                                                                                                                                                                                                                                                                                                                   119628 CTCCCAGACTGCCCTTTTCCTCACACTCC.....CACGACACAGCCCTC 119671
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      119608 GTGCCAGCCA.....AGGGCATTGC
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119760 GTGTGCCAGGC......19779
                                                                                                                                                                                                                                                                                                         278 GlnProGlnGlnPro......ProValAlaGlnAsnGlnProSe 290
                                                      307 laLeuProGlyGlnMetLeuTyrThrGlnProProLeuLysPheValArg 323
                                                                                                                                                                                                                                                                                                                                                                                                                            261 roGlnGlnLeuGlnGlnMetHisHisThrGlnHisHisGlnProProPro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   244 eGlnGlnProProMetGlnGlnProGlnProProProSerGlnAlaLeuP 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             228 GlnGlnGlnGlnGlnGlnGlnAlaLeuGluAlaGlnProProIl 244
                                                                                                                      CTGGGCCCCCCCCCCCCAGC
                                                                                                                                                                            rGlnLeuProProGlnSerGlnThrGlnProLeuValSerGlnAlaGlnA 307
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OK 73019, USA
ON Apr 12, 1999 this sequence version replaced gi:4580479.
On Apr 12, 1999 this sequence version replaced gi:4580479.
Because these overlapping clones came from different libraries
Because these overlapping clones came from deletions, and single
there are numerous instances of insertions, deletions, and single
nucleotide polymorphisms in the overlapping regions below.
AC005500(p52f6) 112352 192592 (0) overlapps AC004033(p_mll) 1 78509
AC005500(p52f6) 112352 192592 (1) overlaps AC004033(p_mll) 89227 145356 (0) overlaps AC007050(bac32) 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9 (bases 1 to 145356)
2hang,G., Lao,V., Zhan,M., Budarf,M.L., Emanuel,B.S. and Roe,B.A.
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Submitted (12-APR-1999) Department Of Chemistry And Biochemistry,
The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
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Zhang,G., Lao,V., Zhan,M.,
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1. .145356
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/db_xref="taxon:9606"
/chromosome="22"
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Ñ	lVal3lnGlnProProValGlnPro	335
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336	GlnValGlnG	339
119830	  GGCTGTGCGGG.\GGATGGGCCTATGCGTGCGGTGGGCAGGTGGTGT	119879
339 119880	hralaValGlnThralaGlnAlaAlaGlnMetValAlaPro :::::       ::: :::::    CGGGCG43GCGTGTGGCAGCGCGGCCGGCTGAGCCCC	355 119923
356 119924	euProMetLeuSerSerProSer	371 119973
372 11 <b>9</b> 974	ProGlyGlnGlnValGlnThrProGlnSerMetProProProProGlnPr	388 120023
; 388 12 <sub>0</sub> 024	oSerProGlnProGlyGlnProSerSerGlnProAsnSerAsnVal	403 120073
1 403		403
120074	TGGGG::GCCCCTCCCCACCTGGCCCTCGAGGCTGGCCCTG	120123
404 120124	ACTTGGCTGCAGCTCTGGCCT	407 120173
408 120174	ProSerProSerProGlnProSerGl             CCCAGCCCCTCACCGCAGCCCTCCCA	424 120223
424	nSerProValThrAl:ArgThrProGlnAsnPheSerValProSerProG (	441 120273
441	lyProLeuAsnThrPro.Val	447 120323
. 447	4	447
120324	TCATACTGGGTGTGCGAGC	120373
447		147
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AC007050 163908 bp DNA PRI 31-MAY-2000 DEFINITION Homo sapiens chromosome 22q11 clone bac32, complete sequence. ACCESSION AC007050 VERSION AC007050.25 GI:6456174 KEYWORDS HTG. SOURCE Human. ORGANISM Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; REFERENCE 1 (bases 1 to 163908) AUTHORS Chen,F., Hu,X., Budarf,M., Emanuel,B. and Roe,B.A. TITLE Homo sapiens Chromosome 22q11 BAC Clone bac32 In BCRL2-GGT Region	274 CTTCAACCATTCCCTGTACCGCACATTCGTTCCAGCCA 122311 ame: gb_pr:AC007050 ccumentation_block:	() ()	CCTCGGGAATCTGACTGTGAGTGACCATGGGCCTGGGGTGTGAAGGCCCC 1  CTAAATGGGGAACCCTCGGGTCCCGGGCTGCTGACCATGCCCATCCTGTC 1	GAGGAGGCAGGGACTGTAGGGAGGATAGGCTGTGGGGGGTGGGGGATTATT 15 CCCAGGATCAGCCAACATTGTCTGCACAAGGGTGGAGGGCTGTGAGAGAGA	121824 CTTCAAGGTCAGGCATCTGGGCGGGGCCGGGCCTGACCTTGGACCCTG 121873  534		121574 CTCCTGCAGAGGTTTCTGATGGCTGAGGCCCAGTGGCAGTAGTTGGGATC 121623  511
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	AUTHORS TITLE JOURNAL COMMENT	Seq_documen LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM	567 e 33044 c seq_name:	535 . 32944 T 550 r 52994 C	534 . 32894 C	534 . 32844 C	534 . 32794 C
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COMMENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   75128 GCACATGCAGCCCGT3GCTCTGTCAGCAGTAGTTTCTAGGCTCTTTGGCT 75079
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       410 SerProSerSerPheleuProSer 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       393 yGlnProSerSerGlnProAsnSerAsnValSerSerGly...... 406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           377 GlnThrProGlnSerMetProProProProGlnProSerProGlnProGl 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                348 GlnAlaAlaGlnMetValAlaProGlyValGlnValSerGlnSerSerLe 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             331 roProValGlnProGlnValGlnGlnGlnThrAlaValGlnThrAla 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .....ProGlyGlnGlnVal 376
                                                                                                                                                                                                                                                                                                                                             OK 73019, USA
ON APT 23, 2001 this sequence version replaced gi:12740049.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 4 contigs. Gaps between the contigs
* lare represented as runs of N. The order of the pieces
* lare believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission
Submitted (26-JAN-2001) Department Of Chemistry And Biochemistry,
The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 187315)
Jiang, X., Sorg, L. and Roe, B.A.
r provided by the submittor.

This sequence will be replaced

This sequence will be replaced

to the finished sequence as soon as it is available and

the accession number will be preserved.

1 7408: contig of 7408 bp in length

7409 7508: gap of unknown length

7509 17332: contig of 9824 bp in length

17333 17422: gap of unknown length

17433 93194: contig of 75762 bp in length

93195 93294: gap of unknown length

93195 93294: gap of unknown length

93295 187315: contig of 94021 bp in length.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus Chromosome 16 BAC Clone rp23-472f15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HTG; HTGS_PH1.SE2; HTGS_DRAFT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AC087802 187315 bp DNA HTG 23-APR-20 Mus musculus chromosome 16 clone rp23-472f15, WORKING DRAFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 house mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AC087802.5 GI:13752732
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE, 4 ordered pieces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (bases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sorg, L. and Roe, B.A.
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alignment_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORIGIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ratio: 3.031
Percent Similarity: 49.015
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Align seg 1/1 to reverse of: AC087802 from: 1 to: 187315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-668-119-3 x AC087802/rev
                                                                                                      54653 CCATCTCCCAGCAGCTTCCTGCCTAGCCCTTCACCACAGCCTTCTCAGAG 54604
54844 GACCCCACAGTCGATGCCACCTCCCCCACAGCCGTCCCCACAACCTGGC. 54796
                                                                                                                                                                                                                     54703 TCTAGGCTCAGACCTGCTTTATTCACTTGGCTGCAGCTCCGGCCCTGCC 54654
                                                                                                                                                                                                                                                                                                                              54753 CCTTCCCTTAGCCTCCTTCACCCCATTTGGCCTTAGGGCTGGCATCGTGT 54704
                                                                                                                                                                                                                                                                                                                                                                                                                                 54795 .....TCACAGCCCAACTCTAATGTCAGGTAGGCTGCTGGGATGCAC 54754
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          54894 CAAAGCAGCCTCACCATGCTGTCCTCACCGTCACCAGGCCAGCAGGTGCA 54845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   54944 AGGGTGTGTGGAGCATGGAGCTGGCTAAGTCTCCACTTCCAGGTCAGC 54895
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         54994 AGAAATAAGGGTGGATAAGATGGGATGTCAGAGCAGTGGGGGAGTTTGTAC 54945
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      55038 .....CATGTGTTATGTGTGCCCAGAGGTAAGGCTTGTGCCTGAGTGAA 54995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               55083 .....GGAGCCAGGCTACCTACCTGGCCTTTCTAGCCCCTTGGATAC 55039
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        55129 ATCTATACCAGCCCAGAAACCTGAAATCCTTGTGGTCTCCCACCAA.... 55084
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              55179 CCGAGGCTCCCTCCTTATACACCAGTGCTTGAGGAGCAGGCCATTACCAT 55130
                        425 rProValThrAlaArgThrProGlnAsnPheSerValProSerProGlyP 442
                                                                                                                                                          409 ProSerProSerSerPheLeuProSerProSerProGlnProSerGlnSe 425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      377 nThrProGlnSerMetProProProProGlnProSerProGlnProGlyG 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        361 GlnSerSerLeuProMetLeuSerSerProSerProGlyGlnGlnValGl 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 338 nGlnGlnThrAlaValGlnThrAlaGlnAlaAlaGlnMetValAlaP 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          308 euProGlyGlnMetLeuTyrThrGlnPro......ProLeuLysPhe 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     355 roGlyVal......GlnValSer 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       322 ValArgAlaProMetValValGlnGlnProProValGlnProGlnValGl 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             292 uPro...ProGlnSerGlnThrGlnProLeuValSerGlnAlaGlnAlaL 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      276 ProProGlnProGlnGlnProProValAlaGlnAsnGlnProSerGlnLe 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                source
                                                                                                                                                                                                                                                                       .....Val.SerSerGlyProAla 408
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Ratio:
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/clone_lib="rp23"
/c44136 c 42281 g 51159 t
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1. .187315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       679.00
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/chromosome="16"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps: 15
Percent Identity: 41.357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      319 others
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VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                          seq_name:
                                                                                                                                                                                                 DEFINITION
                                                                                                                                                                                                                                               seq_documentation_block:
                                                                                 SOURCE
                                                           ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      54003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      54253
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           492
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                                                                                                                                                                                                                                                                                                                                          CACTTGTGGCTGTCATAGC 53868
                                                                                                                                                                                                                                                                                                                                                                                eProCysThrAlaHisSer 576
                                                                                                                                                                                                                                                                                                                                                                                                                                     AGGAGTTGTGGT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GGAAACTTCACCCCTCCCGGCACCTT....TCCAGCACCCACCTTTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CTCTGTGACCATGCCTGAGGCTTAGGTGACTTTACAAGTGAGGTGTGCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GGCCTGTTCTTAGTGTCCCTTTCTTTCCTAGACAGAAAAAAGGACTTAAG 54154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACAAGAATGAAGGTAGGCTAGCCAAAAGCAGGATGGGGCCGGACACCCAA 54204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GCAATTGTCCAAGTACATCGAGCCCCTGCGACGCATGATCAACAAGATCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CATGGGACCCTCACATCTCCTGTGACACCTGCTCCACAGGTTGTAGCCAT 54404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AGGTGCCTAAATCCCCTTCCCTCCCAAGGGCTCAGATTGGGTAAAGGGCT 54454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CTTTAAACACCCCTGGTAAGTTGGGCCTGGGCTGGGTAGGCAGCTTTACA 54504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             roLeuAsnThrPro.....
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sGluIleAlaLeuGluLys.....LeuLysAsnAspMetArgCysProL 537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TACTGGCCCAGGGCTTTGGGCAGGGCTGTGTTGTGCCACAGCTCACATAG 54054
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TAAGATGAAGAGCCTGCTGGACATCCTCACCGACCCCTCGAAGAGGTGAG 54104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         rLysMetLysSerLeuLeuAspIleLeuThrAspProSerLysArg.... 513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       spLysAsnGlu.....
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ArgSerTrpMetProSerTrpProThrSerAlaHisLeuSerSerThrIl 570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gb_htg:AC079044
Mus musculus
Mus musculus
Eukaryota; Metazoa; Chordata;
Eukaryota; Metazoa; Rodentia;
                                                                                                                                                                                               Mus musculus chromosome
                                                                                                    HTG; HTGS_PHASE1; HTGS_DRAFT
                                                                                                                              AC079044.14 GI:15042857
                                                                                                                                                      AC079044
                                                                                   house mouse.
                                                                                                                                                                         unordered pieces.
                                                                                                                                                                                                                     228467 bp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .....GlnLysCy 522
                                                                                                                                                                                               DNA
16 clone
         Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                               rp23-5117,
                                                                                                                                                                                                                                                                                                                                                                                                                                TCTCACACTTT 53887
                                                                                                                                                                                                 WORKING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    53954
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                                                                                                                                                                                                                     10-AUG-2001
                                                                                                                                                                                                 DRAFT SEQUENCE,
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alignment_scores:
Quality:
Ratio:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   alignment_block:
US-09-668-119-3 x AC079044/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Align seg 1/1 to reverse of: AC079044 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE
                                                                             51675
                                                                                                                                                                                                                                                                                                                                                             51819
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 51910 ATCTATACCAGCCCAGAAACCTGAAATCCTTGTGGTCTCCCACCAA.... 51865
                                                                                                                                                                     51725 AGGGTGTGTGTAGCATGGAGCTGGCTAAGTCTCTCCACTTCCAGGTCAGC 51676
                                                                                                                                                                                                                   355
                               377
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               source
nThrProGlnSerMetProProProProGlnProSerProGlnProGlyG
                                                                        GlnSerSerLeuProMetLeuSerSerProSerProGlyGlnGlnValGl 377
                                                                                                                                                                                                                roGlyVal......GlnValSer 360
                                                                                                                                                                                                                                                                 AGAAATAAGGGTGGATAAGATGGGATGTCAGAGCAGTGGGGAGTTTGTAC 51726
                                                                                                                                                                                                                                                                                                          nGlnGlnGlnThrAlaValGlnThrAlaGlnAlaAlaGlnMetValAlaP 355
                                                                                                                                                                                                                                                                                                                                                                                                      ValArgAlaProMetValValGlnGlnProProValGlnProGlnValGl 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                euProGlyGlnMetLeuTyrThrGlnPro.....ProLeuLysPhe 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            uPro...ProGlnSerGlnThrGlnProLeuValSerGlnAlaGlnAlaL 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CCGAGGCTCCCTCATACACCAGTGCTTGAGGAGCAGGCCATTACCAT 51911
                                                                                                                                                                                                                                                                                                                                                           .....CATGTGTTATGTGTGCCCAGAGGTAAGGCTTGTGCCTGAGTGAA 51776
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               on Jul 31, 2001 this sequence version replaced gi:14861748.

* NOTE: This is a 'working draft' sequence. It currently

* consists of 2 contigs. The true order of the pieces

* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence

* as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (17-AUG-2000) Department Of Chemistry And Biochemistry, The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 (bases 1 to 228467)
Yang,L., Hu,P., Wu,H.,
Mus musculus BAC Clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OK 73019, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                       .GGAGCCAGGCTACCTACCTGGCCTTTCTTCTAGCCCCCTTGGATAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              be preserved.
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/db_xref="taxon:10090"
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/clone_lib="RP23"
a 52795 c 53888 g 60257
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3.031
49.015
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41.357
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51625	${\tt GACCCCACAGTCGATGCCACCTCCCCCACAGCCGTCCCCACAACCTGGC}.$	51577
394	rGlnProAsnSerAsn	402
51576	TCACAGCCCAACTCTAATGTCAGGTAGGCTGCTGGGATGCAC	51535
402		402
51534	CCTTCCCTTAGCCTCCTTCACCCCATTTGGCCTTAGGGCTGGCATCGTGT	51485
403	Val.SerSerGlyProAla	408
51484	TTTATTCACTTGGCTGCAGCTCCGGCCCTGCC	51435
409 51434	ProSerProSerSerFheLeuProSerProSerProGlnProSerGlnSe	425 51385
425	IPTOVALThrAlaArgThrProGlnAsnPheSerValProSerProGlyP 	442
442	oLeuAsnThrPro	446
51334	GTAAGTTGGGCCTGGGCTGGGTAGGCAGCTTTACA	51285
446		446
51284	AGGTGCCTAAATCCCCTTCCCTCCCAAGGGCTCAGATTGGGTAAAGGGCT	51235
446		446
51234	CATGGGACCCTCACATCTCCTGTGACACCTGCTCCACAGGTTGTAGCCAT	51185
447	ValAsnProSerSerValMetSer	454
455	AspLysLeuLy	471
4	GlnLeuSerLysTyrIleGluProLeuArgArgMetIleAsnLysIleA	88
œ		Ĥ
488	SpLysAsnGlu	491
492	AspArgLysLysAspLeuSe	98
50984	CTAGACAGAAAAAAGGACTTAAG	50935
498 50934	rLysMetLysSerLeuLeuAspIleLeuThrAspProSerLysArg	513 50885
υī	CysProLeuLysThrLeu	519
50884	GTGTTGTGCCACAGCTCACATAG	50835
520	СУ	522
50834	GTCCAACAGCG	50785
522	sGluIleAlaLeuGluLysLeuLysAsnAspMetArgCysProL ::::::::::::::::::::::::::::::::::::	537
537	rgProArgCysHisArgProAsnSerSerThrTyrAlaSer	553
50734	CCCTCCCGGCACCTTTCCAGCACCCACCTTTCA	50691

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COMMENT
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TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Assembly program: XGAP4; version 4.5
Sequencing vector: plasmid; L08752; 100% of reads
Chemistry: Dye-terminator Hig Dye; 100% of reads
Consensus quality: 52454 bases at least Q40
Consensus quality: 57767 bases at least Q20
Consensus quality: 59753 bases at least Q20
Insert size: 62331; sum-of-contigs
Insert size: 190157; 8.2% error; agarose-fp
Quality coverage: 2.09x in Q20 bases; sum-of-contigs Quality
Coverage: 1.09x in Q20 bases; agarose-fp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (12-JUN-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Aug 27, 2000 this sequence version replaced gi:9864141.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AL359452 64231 bp DNA HTG 13-JUN-2001
Homo sapiens chromosome 1 clone Rp11-422P18, *** SEQUENCING IN
PROGRESS ***, 20 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   * NOTE: This is a 'working draft' sequence. It currently consists of 20 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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AL359452.4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AL359452.4 GI:9930964
HTG; HTGS_PHASE1; HTGS_CANCELLED.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Center code: SC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
                                                                                                                                          5237 7850: contig of 2614 bp in length
7851 7950: gap of 100 bp
7951 9976: contig of 2026 bp in length
977 10076: gap of 100 bp
10077 12531: contig of 2026 bp in length
1253 12631: gap of 100 bp
12632 14688: contig of 700 bp
14689 14770
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (bases 1 to 64231)
18057 18156: gap of 100 bp
18157 21784: contig of 3628 bp in length
21785 2184: gap of 100 bp
21865 24801: contig of 2917 bp in length
                                                                                                                                 14689 14788:
                                                                                                                                                                                                                                                                                                                                    2993 3092: gap of 100 bp
2993 3092: gap of 2044 bp in length
5137 5236: gap of 100 bp
5237 7850: contig of 2614 bp in length
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                                                                                                    14688: contig of 2057 bp in length 788: gap of 100 bp 100 bp 100 bp 18056: contig of 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Summary Statistics
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FEATURES
BASE COUNT
ORIGIN
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24902 27603: contig of 2702 bp in length
27604 27703: gap of 100 bp
27704 30911: contig of 3208 bp in length
30912 31011: gap of 100 bp
31012 35721: contig of 4710 bp in length
35722 35821: gap of 100 bp
35822 38454: contig of 633 bp in length
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38555 41225; contig of 2671 bp in length
41226 41325; gap of 100 bp
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61882. .64231
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                                                                                                                                                                                                                                                                                                                /note="assembly_fragment:00698"
52757. .54927
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27704. .30911
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18157. .21784
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="assembly_fragment:00573"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          note="assembly_fragment:00401"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            note="assembly_fragment:00120"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 note="assembly_fragment:00098"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             48166:
                                /note="assembly_fragment:00888"
15771 c 16128 g 15446 t 1
                                                                                                                                                                                                                                                                                                                                                                                                              note="assembly_fragment:00677"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'note="assembly_fragment:00450"
                                                                                                                                                                                                       note="assembly_fragment:00827"
                                                                                                                                                                                                                                                                        note="assembly_fragment:00748"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        41325: gap of 100 bp 48066: contig of 6741 bp in length 48166: gap of 100 bp 52656: contig of 4490 bp in length 52756: gap of 100 bp 52752: contig of 2171 bp in length 55027: gap of 100 bp 55027: ga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .64231
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20: gap of 100 bp
61781: contig of 4261 bp in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .9976
                                                                                                                                                                                                                                                                                                                                                                                     .52656
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                                           1912 others
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alignment_block:
US-09-668-119-3 x AL359452
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Align seg 1/1 to: AL359452
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  42454 GCACCAGCGGCCACCACAGCCCCAGCAGCCTCCAGTTGCTCAGAACC
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                                                                                                                                                                                                                                                                                                                                     42751 TCTAGCATGGCTCAGCAGGGAAGCATGTGTTTTGCATTTTGTGTTCTGAG 42800
                                                                                                                                                                                                                                                                                                                                                                                                                          42701 TCAAGTGCTGAGACTTCAGGCAGCCCCCACCCCTTGCCAGCCCTGCCGAC 42750
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42909 GAGCACTTCGACTGATGAGCACCACATGAAAGGATGTGCCAGCTCCGTCA 42958
                                                                                     42859 TCCAAGCAGTGTGGCTGATTGCAGCAGTTCTGTGGGCCCTTTCAGGGTGT 42908
                                                                                                                                                                  42842 ......GGGGCACCAAGTCGCAT 42858
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               338 lnGlnGlnGlnThrAlaValGlnThrAlaGlnAlaAlaGlnMetValAla 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           271 nHisHisGlnProProProGlnProGlnGlnProProValAlaGlnAsnG 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       205 IleGlnGlnGlnGlnGlnLeuGlnArgIleAlaGlnLeuGlnLeuGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       288 lnProSerGlnLeuProProGlnSerGlnThrGlnProLeuValSerGln 304
                                                                                                                           398 nProAsnSer.....AsnValSerSerGly.....
                                                                                                                                                                                                            382 MetProProProProGlnProSerProGlnProGlyGlnProSerSerGl 398
                                                                                                                                                                                                                                                                                             366 ..MetLeuSerSerProSerProGlyGlnGlnValGlnThrProGlnSer 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                             ProGlyValGlnValSerGlnSerSerLeuPro................. 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    eValArgAlaProMetValValGlnGlnProProValGlnProGlnValG 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AACCATCACAACTCCCGCCACAGTCGCAGACCCAGCCTTTGGTGTCACAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ProProSerGlnAlaLeuProGlnGlnLeuGlnGlnMetHisHisThrG1 271
                                                                                                                                                                                                                                                        AGCTGCTTCTGCACCCCGCACAGGGTACTGCTGCTGCTACT..... 42841
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GTCAGCAGTAGTTTCTAGGCTCTTTGGCTAGAGATAGCATATCCTATTCT 42700
                                     .....ProAlaProSer 410
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ratio:
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3.862
63.424
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Percent Identity: 55.642
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411 ProSerSerPheLeuProSer 417

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alignment_scores:
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KEYWORDS
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AUTHORS
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LOCUS AX071270
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                seq_name: gb_pat:AX071270
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          42959 GTGTCTGGTGGTTTGCCAACT 42979
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                                                                                                                                                                                                                                                                                                                                                     270 ThrGlnHisHisGlnProProProGlnProGlnGlnProProValAlaGl 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             169 GGCTTTGCAGGCCCAGCCAACTTCAGCAGCCTCCGATGCAGCAGCCAC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      170 MetGlnGlnGlnPheclnAlaValValGlnGlnGlnGlnGlnLeuGlnGl 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 236 nAlaLeuGluAlaGlnProProIleGlnGlnProProMetGlnGlnProG 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                203 lnGlnIleGlnGlnGlnGlnGlnLeuGlnArgIleAlaGlnLeuGln 219
                                                                                    286 nAsnGlnProSerGlnLeuProProGlnSer 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               269 ACCAGATACAGCAGCAGCAGCTAGCAGCTGCAGCGAATAGCACAGCTGCAG 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               319 GCAGCAGCAGCAGCACCAGCATTTAATTAAATTGCATCATCAAAATCAGC 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              186 nGlnGlnGlnGlnGlrGlnHisLeuIleLysLeuHisHisGlnAsnGlnG 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 369 ATGCAGCAGCTTCCTAGCAGTAGTGCAGCAGCAGCACTAGCTCAGCTA 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    source
19 GAAC.....TCGTGCCGAATTCG 1
                                                                                                                                                                        69 ACACAGCACCACCAGCCGCACACAGCCCAGCAGCCTCCAGTTGCTCA 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Quality:
Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human genes and gene expression products
Patent: WO 0.02568-A 1742 11-JAN-2001;
CHIRON CORPORATION (US); HYSEQ, INC. (US)
LOCALTION/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Matazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eurheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 :0 386)

Williams, L.T., Escobedo, J., Innis, M.A., Garcia, P.D., Klinger, J., Kassam, A., Rainhard, C., Randazzo, F., Kennedy, G.C., Pot, D., Milliams, C., Company, C., Company, C., Pot, D., Company, C., C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kassam,A., Reinhard,C., Randazzo,F., Kennedy,G.C., Pot,D.,
Lamson,G., D.manac,R., Crkenjakov,R., Drmanac,S., Dickson,M.,
Labat,I., Leishkowittz,D., Kita,D., Garcia,V. and Strache-Crain,B.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AX071270.1 3I:12581621
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/db_xref="taxon:9606"
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alignment_scores:
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                                                                                                                                                                                                  BASE COUNT
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Tsang,G., Agbayani,A., Arcaina,T.T., Baxter,E., Blazej,R.G.,
Butenhoff,C., Champe,M., Chavez,C., Chew,M., Doyle,C.M.,
Farfan,D.E., Frise,E., Galle,R., George,R.A., Harris,N.L.,
Hoskins,R.A., Evans-Holm,M., Houston,K.A., Hummasti,S.R., Kim,E.,
Li,P., Moshrefi,M., Patcleb,J.M., Park,S., Sequeira,A., Sethi,H.,
Snir,E., Svirskas,R.R., Weinburg,T. and Celniker,S.E.
Full length Drosophila melanogaster cDNA sequence
Unpublished
2 (bases 1 to 2500)
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Submitted (23-APR-1999) Berkeley Drosophila Genome Project,
University of California Berkeley, Berkeley, CA 94720, USA
For further information about this sequence, including its local and relationship to other sequences, please visit our web site (http://fruitfly.berkeley.edu) or send email to cdna@fruitfly.berkeley.edu
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Drosophila melanogaster clone GH03922 BcDNA.GH03922 (BcDNA.GH03922)
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RTKDEYLGLVAKLFHHYKDMSRKSOQOQOQOGGGPPINAEMGGGONMMODPLALO
NLASGGRANDOMBMGAGGGAPVPGGFGT-ASNLLOSLNOQREGOONMMODPLALO
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MVGPFGPNSGPAVGGAGGFNAAAPGAGGPGPNNVMGAGGGONGGGANLTWAMQOMPBMQOIQONOLGM
GNNPMARMGGGBGAMAGGGAPGAPGAGAGAPFONNGGAGGAPHAVVOGG
GNNPMGGMGYUNMPPNLOQKFNNEMGQAGAGMFPGORFGGAGCAPFMRSSFSPAD
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QNSQRNIRQASSSAINTPGQVTGNSPRMPGEEALYREKXKQLIKY IEPLKMLAKIS
NDGTNVEKMTKMSKLLEILCNPTGNVFLETILKCEKALEKNDLISYSGQOFGKSSNPL
LEVINTTLOSFVANHTLYRTFRETIELICETDDITAFVPAKRFRVEEKSTSFEDGAPHV
CSLAFDQTISATFTLOSTVOQALIARISKLPKNYSHSHLLDTWEMAVRQACSPQSKPRAV
CELSTILGY
CSLAFDGTSATFTLOTVQQALIARISKLPKNYSHSHLLDTWEMAVRQACSPQSKPRAV
CELSTLIGGT
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63. .2312
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/protein_id="AAD38595.1"
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/db_xref="taxon:7227"
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Quality: 471.00

593

alignment\_block: US-09-668-119-3 x AF145620 Align seg 1/1 to: AF145620 from: 1 to: 2580 Ratio: 1.529 Percent Similarity: 51.939 91 yAlaMetGlyGlnProMetSer...LeuSerGlyGlnProProPlyT 107
::: |||||||||||::: |||||| |||:
500 GCAGCAAATGCAGCCCATGTCAAATATCCGTGGCCAAATGCCCATGGGTG 549 684 172 GlnGlnPheGlnAlaValValGlnGlnGlnGlnGlnLeu.GlnGlnGlnG 188 550 CCGGAGGA..... 557 9 SerLysSerSerLysAspMetGluSerHisValPheLeuLysAlaLysTh 25 :::|||:::::|| ||||:::::|| || |||:::::|| 150 ACTAAAAATGCCGGGGTTATGGAGAACCACATATTTCGAAAGTCGCGTAC 199 834 AATGCCATGCAACAGATGCCTCCCATGCAGCAGATTCAGCAGAACCAATT 883 205 IleGlnGlnGlnGlnGlnLeuGlnArgIleAlaGln..LeuGlnLeu 220 734 GAACAGTGGACCCGCCGTTGGCGGAGCTGGCGGACCAAATGCTGCTCCAG 634 GCGCCGGCGGGCAAAATCAGGGACAGATTGTCGGTAATCCCGGGCAG 683 124 GlnThrGlnLeuGlnLeuGlnGlnValAlaLeuGlnGlnGlnGlnGlnGl 140 107 hrSerGlyMetAlaProHisSerMetAlaValValSerThrAlaThrPro 123 250 ACATGTCACGAAAGTCCCAGCAACAGCAGCAGCAGCAACAACAGCAGGGT 299 237 aLeuGluAlaGlnProProIle......GlnGlnProProMetG 250 784 GAGCAGGCGGACCCGGGCCAAATCAGATGCAGGGCGGACCAATGAACGTA 833 188 lnGlnGlnGlnHisLeuIleLysLeuHisHisGlnAsnGlnGlnGln 204 155 lnGlnGlnGlnGlnGlnPheGlnAlaGlnGlnSerAlaMetGln 171 450 GGAACTGCCTCTAACTTGCTACAATCCCTGAATCAGCAGCGCCCCTGGACA 499 400 AGATGATGCCCATGGGCGCCGGAGGAGGAGCGCCAGTGCCCGGTGGCCCC 449 300 GGCCCGCCCCAAATGCGGAAATGGGCGGCGGCAGAATATGATGCAGGA 349 81 Gly.......GlnSerLeuGlyGlyMetGlySerPheGl 91 67 ......AlaAlaGlyAlaAlaGlyIleGlyMetProProArgGlyPro 80 CAAATGGGCGTGGGCGTTGGCATGCCTAACCAAATGGTAGGACCGGGACC 733 ......GCTGGTGCCCAGCAGATGATGCAGGT 583 Gaps: 22 Percent Identity: 29.680 783

521	uAspIleLeuThrAspProSerLysArgCysProLeuLysThrLeuGlnL  :::       :::	504
6	GTAACGACGGAACCAATGTGGGAGAAGATGACAAAGATGAGCAAGTT	00 (
504	pLvsAsnGluAspArqLvsLvsAspLeuSerLvsMetLvsSerLe	488
487 1583	ysGlnLeuSerLysTyrIleGluProLeuArgArgMetIleAsnLysIle         :::                 :::       :::   AGCAGCTGACCAAGTACATTGAGCCACTGAAGCGGATGCTTGCCAAGATC	471 1534
471 1533	rProAlaGlySerSerGlnAlaGluGluGluGlnTyrLeuAspLysLeuL        :::      	454 1506
i Un	:::	. 6
454	roGlyProLeuAsnThrProValAsnProSe	440
439 1466	erGlnSerProValThrAlaArgThrProGlnAsnPheSerValProSer	423 1420
423 1419	yProAlaProSerProSerProEnProSerProGlnProS         :              :             TCCGGCACTGGTTCCCCAGTCCAGTCCGCAGATGATGCAGATGCAGAATT	406 1370
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406	ProAsnSerAsnValSerSer	390
ίω	CAGACGCCAACACAGCAACCTCGGACTCGGCAG	$\vdash$
	yGlnGlnValGlnThrProGlnSerMetProProProProGlnProS	ω 7
1310	yvalGinvalSerGinSerSerLeurrowetLeuserSerProSerProG	1310
·ω	CAACAACAGCAGCAACAGCTGGTGGTGGGCA	7
	lnAlaAlaGlnMetValAlaPrc	4
1274	AGCAGATGCTCAGCAATTACAGCAACAGGCGCA	1225
339	.laProMetValValGlnGlnProProValGlnProGlnValGlnG	324
1224	 	1175
323	lnProProLeuLysPheValAr	314
1174		1131
313	${\tt nAlaGlnAlaLeuProGlyGlnMetLe}$	303
1130	GCGGTATGGGCGTGAACATGCCACCGAATTTGCAGCAAAAACCAAATATG	1081
3		)
290 1080	GlnProProValAlaGlnAsnGlnProSer	281 1031
1030	TGCGGGTC	981
280	isThrGlnHisHisGlnProProProGlnProG	267
266 980	InGlnProGlnProProProSerGlnAlaLeuProGlnGlnLeuGlnGln	250 934
933	GGGGATGGGCATGAATCCCATGATGCGGATGGGCCAAGGCAACGGAATGG	884

1634 GGAGATTCTCTGCAATCCTACACAGGGGGGTGCCGCTGGAGACTCTACTTA 1683

521 ysCysGluIleAlaLeuGluLysLeu 529

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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 AAB69609
                 AAB69614
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1618.432 Million cell updates/sec
                                                                              Human polypeptide
Human polypeptide
Peptide #696 encod
Peptide #709 encod
Peptide #674 encod
Human polyhomeotic
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                                A tumour suppresso
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 Huntingtin accumul
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ingtin acc	*/*COMPH	ب د د	900		2/0.5	
	AAB2/901	17	, , , ,		1/7	
Human secreted	AAB27648	2 2	, 51 1 51	9.0	271	
Shrimp white sp	AAG85028	22	2293	-	271.5	
Peptide #12090	AAM38053	22	170		272	
Peptide #8172 e	AAM21738	22	170		272	
Peptide #	AAM01440	22	223		274.5	
Peptide #127	AAM26090	22	223	9.1	274.5	
Peptide #124	AAM13690	22	223		274.5	
Human polypep	AAM39667	22	576	•	277.5	
Human	AAM41453	22	388	9.2	277.5	
Mouse	AAW37153	19	802		280	
Mouse neural	AAW37152	19	787		280	
Mouse neural	AAW37151	19	783	•	281	
Huntingtin ac	AAB69611	22	123	•	282	
Mous	AAY94252	21	44	•	283	
Cellular tran	AAW40058	19	2441	9.4	283	
CREB bind	AAR79054	16	2441	9.4	283	
Amino acid se	AAB62331	22	1162		288	
HHV8 ORF	AAY58500	21	1162	9.6	288	
Kaposi's sarcoma-	AAY96255	21	1162	9.6	288	
	AAW37391	18	903	•	292.5	
Human	AAW37389	18	903	9.7	292.5	
Huntin	AAB69615	22	113	•	295	
	AAY55933	20	1326	•	296	
AFP-1 (A	AAR23963	13	2783	0	304.5	
AFP-1.	AAR23962	13	2783		304.5	
Amino ac	AAY54320	21	2023	0	310	
Mature dur	AAW62647	19	369	10.3	311.5	
Human polypeptide	AAM40064	22	2063	10.4	312	
Amino acid sequenc	846	22	3190	10.4	312.5	
	AAY54319	21	2074	10.7	322	

## ALIGNMENTS

AAM40299 RESULT 21-JAN-2000; 25-APR-2000; 09-JUL-2000; 19-JUL-2000; 03-AUG-2000; 14-SEP-2000; 19-OCT-2000; 29-NOV-2000; Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation; Human polypeptide SEQ ID NO 3444. 22-OCT-2001 AAM40299; AAM40299 standard; 26-DEC-2000; 2000WO-US34263 26-JUL-2001 WO200153312-A1. Homo sapiens. Tenkaemia. μ. 2000US-0488725. 2000US-0553317. 2000US-05598042. 2000US-0620312. 2000US-0663450. 2000US-0663191. 2000US-0663193036. 2000US-0727344. (first entry) Protein; 748 AA

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                                                                                                                                                                                                                                                                                                                                                                                                                                           Вþ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DЬ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DЬ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Qy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypep:ides (AAA38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polypucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system diseases, such as alzehimer's, parkingon's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activitities such as Immune system suppression, activing highlights, chemotractic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and or a disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                specification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 6; SEQ ID NO 3444; 10078pp; English.
                                   481 RRMINKIDKNEDRKK CLSKMKSLLDILTDPSKRCPLKTLQKCEIALEKLKNDMRCPLPHR 540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; AAI59455.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (HYSE-) HYSEQ INC
                                                                                                                                                                                                              327 lvsqaqalpgqmlytqpplkfvrapmvvqqppvqpqvqqqqtavqtaqaaqmvapgvqvs
                                                                                                                                                                                                                                                                                                                                                                                                                                61 SLTGGPAAGAAGIGWPPRGPGQSLGGMGSFGAMGQPMSLSGQPPPGTSGMAPHSMAVVST 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .N.S disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local
                                                                                                                                                              QSSLPMLSSPSPGQQVQTPQSMPPPPQPSPQPGQPSSQPNSNVSSGPAPSPSSFLPSPSP 420
                                                                                                                                                                                                                                                                                                                                                          qqqlqqqqqhlikihhqnqqqiqqqqqlqriaqlqlqqqqqqqqqqqqqqqqalqa
rrminkidknedrkkilskmkslldiltdpskrcplktlqkceialeklkndmavptppp 566
                                                                                                                                                                                                                                                                                     \tt qppiqqppmqqpqpqsqalpqqllqqmhhtqhhqppqqqppvaqnqpsqlppqsqtqp
                                                                                                                                                                                                                                                                                                          QPPIQQPPMQQPQPPSQALPQQLQQMHHTQHHQPPPQPQQPPVAQNQPSQLPPQSQTQP 300
                                                                                                          QPSQSPVTARTPQNFSVPSPGPLNTPVNPSSVMSPAGSSQAEEQQYLDKLKQLSKYIEPL 480
                                                                                                                                                                                                                                       LVSQAQALPGQMLYTQPPLKFVRAPMVVQQPPVQPQVQQQQTAQAAQAAQAAQAAGAVAAPGVQVS
                                                                        qpsqspvtartpqnf3vpspgpintpvnpssvmspagssqaeeqqyidklkqlskyiep1 506
                                                                                                                                           qsslpmlsspspqqvqtpqsmpppppqpspqpgpsqpnsnvssgpapspssflpspsp 446
                                                                                                                                                                                                                                                                                                                                                                                                 sltggpaagaagigmpprgpggslggmgslgamgqpmslsgqpppgtsgmaphsmavvst 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2001-442253/47.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       544;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       nucleic acids and polypeptides, useful for treating disorders as central nervous system injuries -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The sequence clata for this patent did not form part of the printed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Wang Z,
Zhou P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               748 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Asundi V, Chen R, Ma Y, Wehrman T, Xu C, Xue AJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Goodrich R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               91.2%; Score 2746; DB 22;
91.0%; Pred. No. 2e-161;
91.0%; Mismatches 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 22; Length 748;
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Yang Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels 28; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  J,
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AAM42085
                                                                        The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polypucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system disease, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, Activiny, inhibin activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and cassays for receptor activity, arthritis and inflammation, leukaemias and
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03-AUG-2000;
14-SEP-2000;
19-OCT-2000;
                            \overline{\text{C.N.S}} disorders. Note: The sequence data for this patent did not form part of the printed
                                                                                                                                                                                                                                                                                                            Example 2; SEQ ID NO 7016; 10078pp; English.
                                                                                                                                                                                                                                                                                                                                               Novel nucleic acids and polypeptides, useful for treating disorders such as central nervous system injuries -
                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-442253/47.
                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; AAI61241.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tang YT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29-NOV-2000;
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25-APR-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; neuropathy; central nervous system; CNS; Palzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAM42085 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26-DEC-2000; 2000WO-US34263
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                                                                                                                                                                                                                                                                                                                                                                                                                                               QA,
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Zhou P,
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2000US-0552317.

2000US-0598042.

2000US-0620312.

2000US-0653450.

2000US-0652191.

2000US-0693036.

2000US-0727344.
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Yang Y,
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Sequence

780 AA

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RESULT
ADM/1422
ID AAMI
XX AMI
AC AAMI
AC AAMI
XX 12-C
XX Pept
CXY Prok
KW CCTY
XX Home
OS Home
XX WO21
XX WO21
PN WO21
PN 09-1
PR 30--
PR 30--
PR 21--
PR 27-PR 27-PR 27-PR
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26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
                                                                                                                                                                                                                                                                                                                         AAM14262 standard; Protein;
                                                                                                                      09-AUG-2001.
                                                                                                                                                 WO200157278-A2
                                                                                                                                                                         Homo sapiens.
                                                                                                                                                                                                     cervical cancer
                                                                                                                                                                                                              Probe; human; microarray; gene expression; cervical epithelial cell;
                                                                                                                                                                                                                                         Peptide #696 encoded by probe for measuring cervical gene expression.
                                                                                                                                                                                                                                                                     12-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   178
                                                                 04-FEB-2000;
                                                                                            30-JAN-2001;
                                                                                                                                                                                                                                                                                                                                                                                         598
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        358 plvsqaqalpgqmlytqpplkfvrapmvvqqppvqpqvqqqqtavqtaqaaqmvapgvqv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Match 85.8%; Score 2583.5; DB 22; Length 780; Local Similarity 86.0%; Pred. No. 2.2e-151; nes 515; Conservative 13; Mismatches 42; Indels 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61
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                                                                                                                                                                                                                                                                                                                                                                                                                  RP-----RCHRPNSSTYASRSWMPSWPTSAH---LSSTIPCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PLVSQAQALPGQMLYTQPPLKFVRAPMVVQQPPVQPQVQQQQTAVQTAQAAQMVAPGVQV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          \verb|aqppiqqppmqqpppsqalpqqlqmhhtqhhqpppqppqqppvaqnqpsqlppqsqtq|\\
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               \verb"pqpfqspvtartpqnfsvpspgplntpvnpssvmspagssqaeeqqyldklkqlskyiep"
2000US-0180312.
2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-0236359.
                                                                                                                                                                                                                                                                     (first entry)
                                                                                            2001WO-US00670.
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                                               04-FEB-2000; 2000US-0180312.
26-MAY-2000; 2000US-0508408.
30-JUN-2000; 2000US-0532366.
21-SEP-2000; 2000US-0234687.
27-SEP-2000; 2000US-0236359.
04-OCT-2000; 2000GB-0024263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention relates to human single exon nucleic acid probes (SENP: see AAI10068-AAI28459). The present sequence is a peptide encoded by one such probe. The SENPs are derived from human HeLa cells. The SENPs can be used to produce a single exon microarray, which can be used for measuring human gene expression in a sample derived from human cervical epithelial cells. By measuring gene expression, the probes are therefore useful in grading and/or staging of diseases of the cervix, notably
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cervical cancer.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-488901/53.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 27; SEQ ID No 19088; 487pp; English.
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                                                                                                                                                                                                                                                                                                                                                                    AAM26672 standard;
                                                                                                                                                                            09-AUG-2001.
                                                                                                                                                                                                   WO200157272-A2
                                                                                                                                                                                                                                                    genetic disorder
                                                                                                                                                                                                                                                                Probe; microarray;
                                                                                                                                                                                                                                                                                        Peptide #709 encoded by probe for measuring placental gene
                                                                                                                                                                                                                                                                                                                 17-OCT-2001
                                                                                                                                                                                                                                                                                                                                          AAM26672;
                                                                                                                                                  30-JAN-2001; 2001WO-US00663
                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Penn
                         (MOLE-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                        186 QQQQQQQHLIKLHHQNQQQ 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                               SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         genome-derived single exon nucleic acid probes useful for
                       MOLECULAR DYNAMICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gene expression in human cervical epithelial cells
  Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 79 AA;
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                                                                                                                                                                                                                                                                                                                 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                  Protein; 79
                                                                                                                                                                                                                                                                  human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13.0%; Score 390; DB 22;
100.0%; Pred. No. 2.3e-17;
tive 0; Mismatches 0;
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  Chen W,
                                                                                                                                                                                                                                                                  placenta;
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  Rank DR;
                                                                                                                                                                                                                                                                   antenatal diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 79;
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                                                                                                                                                                                                                                                                                             expression.
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The present invention relates to novel single exon nucleic acid probes (see AAI00010-AAI100;7). The present sequence is a peptide encoded by one
                                          Claim 27; SEQ ID No 10732; 322pp; English.
                                                                                                                  WPI; 2001-476286/51.
                                                                                                                                               Penn
                                                                                                                                                                                                                             04-FEB-2000; 2000US-0180312.

26-MAY-2000; 2000US-0207456.

30-JUN-2000; 2000US-060846.

03-AUG-2000; 2000US-0633366.

21-SEP-2000; 2000US-0234687.
                                                                          Novel single exon nucleic acid probe used to measuring gene expression in a human breast -
                                                                                                                                                                     (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                   04-OCT-2000; 2000GB-0024263.
                                                                                                                                                                                                                                                                                                              29-JAN-2001; 2001WO-US00661.
                                                                                                                                                                                                                                                                                                                                                                                                                  Probe; human; breast disease; breast cancer; development disorder; inflammatory disease; proliferative breast disease; non-carcinoma tumour.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Peptide #674 encoded by probe for measuring human breast gene expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        09-OCT-2001 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention relates to single exon nucleic acid probes (SENP: see AAI31315-AAI575:6). The present sequence is a peptide encoded by one such probe. The projes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of human manatic diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human placenta -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-488897/53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          human genetic disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          186 QQQQQQQHLIKLHHQNQQQ 204
                                                                                                                                                                                                                                                                                                                                                                      200157270-A2
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                                                                                                                                             Hanzel DK,
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                                                                                                                                                                                                                  2000US-0236359
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 390; DB 22; ; Pred. No. 2.3e-17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                             Rank DR;
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Best Local
This polypeptide comprises a novel human polyhomeotic 1 protein encoded by the hph1 oncogene that is implicated in neoplastic disorders. Also claimed are: (1) an hph1 polypeptide consisting at least 22 contiguous amino acids; (2) an hph1 fusion protein; antibodies which specifically bind to a hph1 protein; (4) an expression construct for expressing all or a portion of hph1 protein; (5) a homologously recombinant cell; (6) a method of
                                                                                                                                                                                                                                                                                                                                                            06-FEB-1997;
23-AUG-1996;
04-DEC-1996;
                                                                                                                                    Claim 1; Page 28-30; 39pp; English.
                                                                                                                                                                   disorders, e.g. neoplasia, dysplasia or hyperplasia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   such probe. The probes are useful for measuring human gene expression in a human breast sample, where the probe hybridises at high stringency to a nucleic acid expressed in the human breast. The probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human breast, particularly those diseases with polygenic aetiology. The diseases include: breast cancer, disorders of development, inflammatory diseases of the breast, fibrocystic changes, proliferative breast disease and non-carcinoma tumours.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIFO at fifth. WiFO.int/pub/published_pct_sequences.
                                                                                                                                                                                     Isolated human polyhomeotic 1 oncogene - used to develop products for diagnosis and therapy of proliferative and developmental
                                                                                                                                                                                                                                           N-PSDB; AAV29009.
                                                                                                                                                                                                                                                        WPI; 1998-169164/15.
                                                                                                                                                                                                                                                                                           Randazzo F;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28-AUG-1998 (first entry)
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                                                                                                                                                                                                                                                                                                                         (CHIR ) CHIRON CORP
                                                                                                                                                                                                                                                                                                                                                                                                                              22-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            26-FEB-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human polyhomeotic 1 (hph1) protein
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                                                                                                                                                                                                                                                                                                                                                                                                                          97WO-US14886
                                                                                                                                                                                                                                                                                                                                                            96US-0031569
                                                                                                                                                                                                                                                                                                                                                                             96US-0024349
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Live 0;
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AAW52830
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             identifying neoplastic tissue of a human, where over-expression of the hph1 gene identifies the tissue as being neoplastic; (7) a method to aid in the diagnosis or prognosis of neoplasia, where a difference in the hph1 gene, mRNA, or protein between a first and second tissues indicates neoplasia in the first tissue; (8) a method to aid in detecting a genetic predisposition to neoplasia; (9) a method of identifying a human chromosome 12; and (10) a method of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             to suppress tumours.
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                            09-JUL-1998
                                                                                                                                                AAW52830 standard;
                                                                                      AAW52830;
                                                                                                                                                                                                                                                                                                690 ---nantpssel----val-----tpapsvp----pptlamvsrqmgdskppqa 727
                                                                                                                                                                                                                                                                                                                                                         508 TDPSKRCPLKTLQKCEIALEKLKNDMRCPLPHRPRCHRPNSSTYASRSWMPSWPTSA 564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                342 TAVQTAQAAQMVAPGVQVSQSSLPMLSSPSPGQQVQTPQSMPPPPQPSPQPGQPSSQPNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             233 QQQD----ALEAQPPIQQPPMQQPQPPPSQALPQQLQQMHHTQHHQPPPQPQQPPVAQNQ 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      378 sliqqqqihlqqkqvviqqqiaihh--qqqfqhrqsqllhtathlqlaqqqqqqqqqqq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         176 AVVQQQQQLQQQQQQ--QHLIKLHHQNQQQIQQQQQLQRIA-QLQLQQQQQQQQQQQQQQQQ 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          318 aqtvtvsqgsqteaesaaakkaeadgsgqqnvgmnltrtatpapsqtlissatytqiqph 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   260 qslnlsqagggsgnsipgsmgpggggahgglgglpssg--mgggscprkgtgvvqplpa 317
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         qapgalqecpptlapgmtlapvqgtahvvkggattsspvvaqvpaafymqs---vhlpgk 633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NVSSGPAPSPSSFLPSPSPQPSQ------SPVTARTPQNFSVPSPGPLNTPVN 448
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                                                                                                                                                                                                                                                                                                                                                                                                                   pqtl---avkrkadseeerddvstlgsmlpakaspvaespkvmdeksslgekaesvanv-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PSSVMSPAGSSQAEEQQYLDKLKQLSKYIEPLRRMINKIDKNEDRKKDL-SKMKSLLDIL 507
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                            (first entry)
                                                                                                                                                Protein; 1004 AA
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23-AUG-1996;
04-DEC-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present sequence encodes a novel human tumour suppressor gene termed polyhomeotic 1 (hph1). The hph1 gene maps to human chromosome 12pl3, a region which is frequently lost in non-small cell lung cancer and breast cancer. A method of identifying neoplastic tissue of a human comprises comparing the expression of a hph1 gene in a tissue of a human suspected of being neoplastic with the expression of a hph1 gene in a tissue of the human which is normal. Under-expression of the hph1 gene identifies the subject as having neoplastic tissue. The hph1 oncogene functions to suppress neoplastia and dysplastic or hyperplastic cell growth as well as to induce cellular differentiation. The cDNA, protein and vectors can be used as diagnostic and therapeutic tools for proliferative and developmental disorders and to identify a pl3 region of a human chromosome 12. They can be used for the detection, diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A tumour suppressor gene called polyhomeotic 1 (hph1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tumour suppressor gene; polyhomeotic 1; hph1; human chromosome 12p13; identification; neoplastic tissue; cellular differentiation; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            or prognosis of neoplasia or for detecting a genetic predisposition neoplasia. They can also be used to treat tumours.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Pages 28-30; 40pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             disorders, e.g. neoplasia, dysplasia or hyperplasia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Isolated human poly:homeotic 1 oncogene - used to develop products
for diagnosis and therapy of proliferative and developmental
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (CHIR ) CHIRON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22-AUG-1997;
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   289
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                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                       sliqqqqqihlqqkqvviqqqiaihh--qqqfqhrqsqllhtathlqlaqqqqqqqqqqq 435
                                                                                                                                                                                                                                                     qslnlsqagggsgnsipgsmgpgggggahgglgglpssg--mgggscprkgtgvvqplpa 317
                                                                                                                                                                                                                                                                            QSLTGGPAAGAGIGMP----PRGPGQSLGGMGSFGAMGQPMSLSGQPPPGTSGMAPHSM 115
 PSQLPPQSQTQPLVSQAQALPGQMLYTQPPLKFVRAPMV-----VQQPPVQPQVQQQQ 341
                                                                      QQQQ----ALEAQPPIQQPPMQQPQPPPSQALPQQLQQMHHTQHHQPPPQPQQPPVAQNQ 288
                                                                                                                                             AVVQQQQQLQQQQQQ--QHLIKLHHQNQQQIQQQQQQQQQQRIA-QLQLQQQQQQQQQQQQQQQQQ
                                                                                                                                                                                aqtvtvsqgsqteaesaaakkaeadgsgqqnvgmnltrtatpapsqtlissatytqiqph 377
                                                                                                                                                                                                                    qqqqpqattltapqppqvpptq--qvppsqs-----qqqaqtlvvq------pmlqss
                                                                                                                                                                                                                                                                                                                                                                                                                            1004 AA;
                                                                                                                                                                                                                                                                                                                                Conservative
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                                                                                                                                                                                                                                                                                                                                                 12.7%; Score 382.5;
28.1%; Pred. No. 1e
                                                                                                                                                                                                                                                                                                                                  67;
                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                   .5; DB 19;
le-15;
                                                                                                                                                                                                                                                                                                                                  218;
                                                                                                                                                                                                                                                                                                                                    Indels 101; Gaps
                                                                                                                                                                                                                                                                                                                                                                    Length 1004;
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                                        modulate polyglutamine toxicity using animal models with polyglutamine sequences that cause toxicity in the animal. The model is preferably Drosophila, and toxic polyglutamine sequences include the human and Drosophila heat shock protein 40/HDJI, tetratricopeptide repeat protein (TPR2) and myeloid leukaemia factor 1 (MLF) genes. The model is useful for identifying treatments for neurodegenerative and proliferative disorders, including Alzheimer's disease, Parkinson's disease, Creutzfeldt-Jacob's disease (CJD), bovine spongiform encephalopathy (BSE), Huntington's disease, Machado-Joseph disease, spinocerebellar ataxias, dentatorubropallidoluysian atrophy, Kennedy's disease, stroke,
                                                                                                                                                                                                                                       The present invention describes a method of screening for genes which
                                                                                                                                                                                                                                                                                                                      and Creutzfeldt-Jakob disease
                                                                                                                                                                                                                                                                                Example 2; Fig 1B; 775pp; English.
                                                                                                                                                                                                                                                                                                                                                       Identifying genes on other compounds that modulate polyglutamine
                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-147537/15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            heat shock protein 40; tetratricopeptide repeat protein 2; TPR2; stroke; myeloid leukaemia factor 1; MLF; human; fruit fly; Alzheimer's disease; Parkinson's disease; CJD; BSE; Huntington's disease; head trauma; cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB72673;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (CALY ) CALIFORNIA ENST OF TECHNOLOGY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12-AUG-1999;
12-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22-FEB-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200112238-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Animal model; polyglutamine tract; neurodegenerative disorder; HDJ1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Polyglutamine tract #2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 09-MAY-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB72673 standard; Protein; 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          634 pqtl---avkrkadseeerddvstlgsmlpakaspvaespkvmdeksslgekaesvanv- 689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               œ
                                  trauma and cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TAVQTAQAAQMVAPGVQVSQSSLPMLSSPSPGQQVQTPQSMPPPPPQPSPQPGQPSSQPNS 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ---nantpssel----val-----tpapsvp----pptlamvsrqmgdskppga 727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TDPSKRCPLKTLQK:EIALEKLKNDMRCPLPHRPRCHRPNSSTYASRSWMPSWPTSA 564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PSSVMSPAGSSQAEEQQYLDKLKQLSKYIEPLRRMINKIDKNEDRKKDL-SKMKSLLDIL 507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    qapgalqecpptlapgmtlapvqgtahvvkggattsspvvaqvpaafymqs---vhlpgk 633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NVSSGPAPSPSSFLPSPSPQPSQ------SPVTARTPQNFSVPSPGPLNTPVN 448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 vgtrqpgtaqaqaljlaqlaaavp---
                                                                                                                                                                                                                                                                                                                               useful for treating Alzheimer's disease, Parkinson's disease
                                                                                                                                                                                                                                                                                                                                                                                                                                   Kazemi-Esfarjani P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2000US-0205720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2000WO US22496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2000US:0177047
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99US-0148934.
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Sequence

149 AA;

Query Match

11.6%;

Score 350.5;

DB 22;

Length 155;

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Qy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                         used in the prevention of diseases such as Alzheimer's, Parkinson's Huntington's diseases, prion disease, frontoemporal dementia, amyotrophic lateral sclerosis, spinal and bulbar muscular atrophy, dentatorubal pallidoluysian atrophy, spinocerebellar ataxia type 1
 Sequence
                                                                                                    aggregates of certain proteins, involving contacting the protein with binding molecule known as an intrabody. Proteins to be bound include those associated with neurological disorders, and so the method can be
                                                                                                                                                    The present invention describes a method for inhibiting the formation
                                                                                                                                                                                 Disclosure; Page 99; 108pp; English.
                                                                                                                                                                                                                          Inhibiting intracellular polypeptide accumulation, useful for treating neurological disorders, e.g. Alzheimer's disease, comprises contacting
                                                                                                                                                                                                                                                                             WPI; 2001-182700/18.
                                                                                                                                                                                                                                                                                                        Huston JS,
                                                                                                                                                                                                                                                                                                                                       (MESS/) MESSER A. (LECE/) LECERF J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Neurological disorder; Huntington's disease; Alzheimer's disease; Parkinson's disease; prion disease; frontotemporal dementia; amyotrophic lateral sclerosis; spinal and bulbar muscular atrophy; amyotrophal-pailidoluysian atrophy; spinocerebellar ataxia type 1
                                                                                                                                                                                                               the polypeptide with a specific intrabody -
                                                                                                                                                                                                                                                                                                                                                                                                    21-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                   27-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                24-JUL-2000; 2000WO-US20131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200106989-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Huntingtin accumulation inhibitor peptide HD-Q104-Myc-HIS6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAB69612 standard; Protein; 155 AA
                             (SCA1), SCA2,
                                                                                                                                                                                                                                                                                                                                                                      (HUST/) HUSTON J S.
                                                                                                                                                                                                                                                                                                                                                         (MESS/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100 qqqqqqqqqqqqqqqqqqqqqqqqqqqqqqqtsrtyp 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             219 QLQQQQQQQQQQQQQQQALEAQPPIQQPPMQQPQPPPSQALP 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      159 QQQFQAQQSAMQQQFQAVVQQQQQQQQQQQQQQHLIKLHHQNQQQIQQQQQQQQQQQRIAQL 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99 LSGQPPPGTSGMAPHSMAVVSTATPQTQLQLQQVALQQQQQQQQFQQQQQAALQQQQQQQ 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 / Match 12.5%;
Local Similarity 55.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 mgggpp--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SCA3;
                                                                                                                                                                                                                                                                                                                                                       MESSER
 155 AA;
                                                                                                                                                                                                                                                                                                        Messer A,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                2000US-0620955
                             SCA3, SCA4, SCA5,
                                                                                                                                                                                                                                                                                                                                                                                                                   99US-0146047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lecerf J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SCA6; SCA7; protein accumulation; intrabody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 376.5;
Pred. No. 3.1
                           SCA6 and SCA7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3.1e-16;
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                                  Best
                                                              Query Match
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                                                                                                                                                                                                                                                                                               The present invention describes a method for inhibiting the formation of aggregates of certain proteins, involving contacting the protein with a binding molecule known as an intrabody. Proteins to be bound include those associated with neurological disorders, and so the method can be used in the prevention of diseases such as Alzheimer's, Parkinson's and
                                                                                                                                                                                         Huntington's diseases, prion disease, frontotemporal dementia, amyotrophic lateral sclerosis, spinal and bulbar muscular atrophy, dentatorubal-pallidoluysian atrophy, spinocerabellar ataxia type 1 (SCA1), SCA2, SCA3, SCA4, SCA5, SCA6 and SCA7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Parkhison's disease; prion disease; frontotemporal dementia; amyotrophic lateral sclerosis; spinal and bulsar muscular atrophy; dentatorubal-pallidoluysian atrophy; spinocerebellar ataxia type 1 SCA2; SCA3; SCA4; SCA5; SCA6; SCA7; protein accumulation; intrabod
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 100; 108pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Inhibiting intracellular polypeptide accumulation, useful for treating neurological disorders, e.g. Alzheimer's disease, comprises contacting the polypeptide with a specific intrabody -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic.
                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-182700/18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Huston JS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27-JUL-1999;
21-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24-JUL-2000; 2000WO-US20131.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Huntingtin accumulation inhibitor peptide GFP-HD-Q104.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30-APR-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (HUST/) HUSTON J S.
(MESS/) MESSER A.
(LECE/) LECERF J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Neurological disorder; Huntington's disease;
Local 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 133 ALQQQQQQQFQQQQAALQQQQQQQQQQQQFQAQQSAMQQQFQAVVQQQQQLQQQQQQQQQQQQQ192
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    253 QPPPSQALPQQLQQMHHTQHH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Messer A,
           Conservative
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                                                                                                                                              AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Protein; 145
                                  11.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         58.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lecerf
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 151
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     ω
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                               Score 345; DB 22;
Pred. No. 2.6e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. 1.3e-14; 7; Mismatches 47;
     Mismatches
                                                        DB 22;
     43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Alzheimer's disease;
                                                      Length 145;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         intrabody
     26;
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     Gaps
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     4;
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Query Match Best Local Matches

Local Similarity nes 77; Conserv

Conservative

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Indels Length 121;

7;

Gaps

1;

10.9%;

Score 328.5; DB 22; Pred. No. 2.2e-13; Pred. No. 2.2e-13;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q
                       used in the prevention of diseases such as Alzheimer's, Parkinson's Huntington's diseases, prion disease, frontotemporal dementia, amyotrophic lateral sclerosis, spinal and bulbar muscular atrophy, dentatorubal-pallidoluysian atrophy, spinocerebellar ataxia type 1 (SCA1), SCA2, SCA3, SCA4, SCA5, SCA6 and SCA7.
                                                                                                  The present invention describes a method for inhibiting the formation aggregates of certain proteins, involving contacting the protein with binding molecule known as an intrabody. Proteins to be bound include those associated with neurological disorders, and so the method can be
                                                                                                                                                                                                                                                                        WPI;
Sequence
                                                                                                                                                                              Disclosure; Page 98; 108pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Parkinson's disease; prion disease; frontotemporal dementia; amyotrophic lateral sclerosis; spinal and bulbar muscular atrophy; dentatorubal-pallidoluysian atrophy; spinocerebellar ataxia type 1 SCA2; SCA3; SCA4; SCA5; SCA6; SCA7; protein accumulation; intrabod
                                                                                                                                                                                                                       Inhibiting intracellular polypeptide accumulation, useful for treating neurological disorders, e.g. Alzheimer's disease, comprises contacting
                                                                                                                                                                                                                                                                                                    Huston JS,
                                                                                                                                                                                                                                                                                                                                 (HUST/) HUSTON J S.
(MESS/) MESSER A.
(LECE/) LECERF J.
                                                                                                                                                                                                                                                                                                                                                                                                                                        24-JUL-2000; 2000WO-US20131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-FEB-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAB69609
                                                                                                                                                                                                                                                                                                                                                                                               21-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                             27-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Neurological disorder; Huntington's disease; Alzheimer's disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Huntingtin accumulation inhibitor peptide HD-Q104-GFP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             85
                                                                                                                                                                                                          polypeptide with a specific intrabody
                                                                                                                                                                                                                                                                        2001-182700/18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OFQQQQAALQQQQQQQQQQQQQQQAQQSAMQQQFQAVVQQQQQLQQQQQQQQQQHLIKLHHQN 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gggggkg---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GGMGSFGAMGQPMSLSGQPPPGTSGMAPHS----MAVVSTATPQTQLQLQQVALQQQQQQQ 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                standard;
121 AA;
                                                                                                                                                                                                                                                                                                    Messer A,
                                                                                                                                                                                                                                                                                                                                                                                             2000US-0620955
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                                                                                                                                                                                                                                                                                                                                                                                                           99US-0146047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Protein; 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            --pvtgtgsmatleklmkafeslksfqqqqqqqqqqqqqqqqqqqq
                                                                                                                                                                                                                                                                                                    Lecerf J;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             intrabody
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                                                                                                                                                                                                                                                      The present sequence represents a murine PCTG4 protein. Polymorphisms CC in the human PCTG4 region of chromosome xq13 are associated with mental retardation, autism, depression, bipolar affective disorder or hypothyroidism. One 12 bp insertion polymorphism occurs within the C coding region of the human OPA gene, and introduces a 4 amino acid consertion in a putative OPA domain. This domain has been shown to be involved in tissue specific expression. Another polymorphism consists C of a pentanucleotide repeat approximately 7 kb upstream of the 12 bp CC oplymorphism. Another polymorphism. The CC oplymorphism. Another polymorphism consists of a dinucleotide repeat approximately 4.5 kb downstream of the 12 bp polymorphism. The CC specification describes a method for screening for polymorphisms in a CC sequences within the q13 region of the X chromosome have polymorphisms CC associated with neuropsychiatric disorders. The methods can be used to screen for the presence of a heritably linked form of mental retardation, autism, depression, bipolar affective disorder or hypothyroidism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; PCTG4 region; X chromosome; q13 region; polymorphism; mental retardation; autism; depression; bipolar affective disorder; hypothyroidism; OPA gene; neuropsychiatric disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Amino acid sequence of a murine PCTG4 protein.
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                                         1874 adptrhlqqrpsgyvhqqaptyg-hgltstqrfshqtl------qqtpm 1915
                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Identification of pclymorphisms in the PCTG4 region of Xql3 for diagnosing mental retardation or autism -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         04-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus sp.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2000-126357/11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Philibert RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 7; Page 81-{4; 100pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (USSH ) US DEPT HEALTH & HUMAN SERVICES (IOWA ) UNIV IOWA RES FOUND.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            107 TSGMAPHSMAVVSTATPOTQLQLQQVALQQQQQQQQFQQQQQAALQQQQQQQQQQQQFQAQ 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12
                                                                                                                                             Local Similarity
                                                                                 SDPMNALQSLTGG-----PAAGAAGIGMPPRGPGQSLGGMGSFGAMGQPMSLSGQPPPG 106
                                                                                                                                                                                                                             2074 AA;
                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ginns EI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98US-0083465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99WO-US09365
                                                                                                                      10.7%; Score 322; DB 21; 38.2%; Pred. No. 1.2e-11; Mismatches 70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 21; Length 2074;
                                                                                                                           Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 13
                                              The present sequence represents a CBP protein. A probe derived from the CBP protein is used to isolate a Drosophila cellular protein, designated 532. Protein 532 interacts with proteins involved in the control of cell proliferation, in particular partners of p300/CBP and Rb proteins. The cellular proteins of the invention are used for in vitro screening of compounds (including immunosuppressants) which are able to interact physically and/or functionally with them, particularly to determine sensitivity of the protein to immunosuppressants or to identify capacity to interact with Ela viral proteins. The proteins can be used to induce (or interfere with) cellular differentiation and proliferation, including formation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1916 mgtmtplsaqgvqagvrstsi-----lpeqqqqqq------qqqqqqqqqqqqq-- 1958
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Drosophila sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     malignant cell; protein 532.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cellular protein; cell proliferation; p300; CBP; Rb protein; immunosuppressant; Ela viral protein; cell differentiation;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB84634 standard; Protein; 3190 AA.
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Sequence
                                                                                                                                                                                                                                                                          Disclosure; Fig 10; 147pp; French.
                                                                                                                                                                                                                                                                                                                          New nucleic acid encoding a protein that interacts with p300/CBP and proteins, useful for identifying specific interaction partners,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             05-JUL-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200147981-A1.
                                   of malignant cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Modjtahedi N, Cavarec L;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22-DEC-2000; 2000WO-FR03677.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Amino acid sequence of CBP protein of Drosophila.
                                                                                                                                                                                                                                                                                                              including immunosuppressants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (INSR ) INST ROUSSY GUSTAVE (CNRS ) CENT NAT RECH SCI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           227 QQQQQQQQQALEAQPPIQQPPMQQPQPPPSQALPQQLQQMHHTQHHQPPPQPQQPPVAQ 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        167 QSAMQQQFQAVVQQQQQLQQQQQQQQHLIKLHHQNQQQIQQQQQLQRIAQLQQQQQQQ 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     287 NQP-SQLPPQSQTQPLVSQAQALPGQMLYTQP 317
                                                                                                                                                                                                                                                                                                                                                                                                      2001-425633/45.
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  3190 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99FR-0016432
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Query Match Best Local Si Matches 184;

Similarity

10.4%; Score 312.5; DB 22; 20.7%; Pred. No. 7.1e-11; tive 65; Mismatches 185;

Length 3190; Indels 457;

Gaps

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                                                                                                                                                                                          RESULT 14
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                                                                                                                                                                                                                                                                                                                       1309 lealnagagapgtggsasnvtvsapspspgflsngpsigtpsnnnnsssannnppsvssl 1368
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1018 ekrlkrkeqhqqmlmqqqgvanpvaggaaggagsaagvaggvvlpqqqqqqqqqqqqqqqq 1077
Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;
                                   Human polypeptide SEQ ID NO 3209.
                                                                                                                   AAM40064;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      543
                                                                             22-OCT-2001 (first entry)
                                                                                                                                                      AAM40064 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       236 QALEA--QPPIQ-----QPPMQ-QPQPPPSQALPQQ------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  958 klvqaifptsdpttmqdkrmhnlvsyaekvekdmyemaksrseyyhllaekiykiqkele 1017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   838 vnvggfgntnfggaaaggavgandkqqlkvaqvhpqshgvgaggasagagasggqvaags
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       {\tt svlmpadttgsgnagnpnqnaggvaggagggnggntgppgdnekdwresvtadlrnhlvh}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              nslhqqqqqmlqqq----qqqgqnrrrgglatmveqqqqhqqqqqqpnpaqlggnipapls
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gkqgqqvapgggqntaivlpqqqgaggapgapktpadmvqqltqqqqqqqqqqvhqqqvqq 720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GTSG--MAP---HSMAVV-----STATPQTQLQL-QQVALQQQQQQQQQFQQQQ---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          fqnanvppgggpagiggappggggagggaagaggnlqqqqqqqqqqqqqqqqnqqpnltglvvg 660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LQSLTGGPAAGAAGIGMPPRGPGQSLGGMGSFGA------MGQPMSLSGQPPP 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  vnyckamksvlahmgtckqskdctmqhcassrqillhyktcqn--sgcvicypfrqnhsv 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VAHSKSSKDMESHVFLKAKTRD---EYLSLVARLIIHFRDIHNKKSQASVSDPM----NA
                                                                                                                                                                                                                                                mqqplsnrpgtppyipaspvpatsasglaass----tpasaaatcassgs 1414
                                                                                                                                                                                                                                                                                   L-----PSPSPQPSQSPVTARTPQNFSVPSPGPLNTPVNPSSVMSPAGS 458
                                                                                                                                                                                                                                                                                                                                                                                                 snstplqqqqqqqqqqqqqqatsns---fsspmqqqqqqqqqqqqqqqkpgsvlnnmpptpts 1308
                                                                                                                                                                                                                                                                                                                                                                                                                                        ---TAVQTAQAAQMVAPGVQVSQSSLPMLSSP----SPGQQVQTPQ-----SMPPPP--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          s---pvpgqqqqqfinanggtganpqlseimkqrhihqqqqqqqqqqqqqqqqmllpqspf 1251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gnmlalqqqqrmqf--pqqqqqqppgsgagkmlvgppgpspggmvvnpalspyqttnvlt 1194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ----LQQMHHTQHHQPPPQPQQPP-----VAQNQPS-----QLPPQSQTQPLV 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ----QQQQQFQAQQSAMQQQFQ-----AVVQQQQQLQQQQQQ-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SQAQALPGQMLYTQ-------PPLKFVRAPMVVQQPPVQPQVQQQQ------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Protein;
                                                                                                                                                                                                                                                                                                                                                               --QPSPQP------GQPSSQPNSNVSSGPAPSPSSF 414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ---QQHLI- 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             199
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Qy Db Qy Db

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257

fpq----lqqqqqqqqqq---

143 FOOOQOAALOOOQOQOQOQFQAQOSAMQQQFQAVVQQQQQLQQQQQQQQQQHLIKLHHQNQ 202

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Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system diseases, such as localised neuropathies and central nervous system diseases, such as alzheiner's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tang
Wang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   09-JUL-2000;
19-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Zhao QA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            03-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25-APR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21-JAN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26-DEC-2000;
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                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C.N.S disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 5; SEQ ID NO 3209; 10078pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel nucleic acids and polypeptides, useful for treating disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-442253/47.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14-SEP-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                    specification.
        197
                                                                                                          142 nrsqdvrmngpmgagnsvrmeagfpmasgpgiirmnnpatvmippggnvss----smma 196
                                                         93
                                                                                                                                                                45 NKKSQASVSDPM----NALQSLTGGPAAGAAGI-----GMPPRGPGQSLGGMGSFGA 92
pgpnpelqprtprpasqsdamdpllsglhiqqqshpsgslapphhpmqpvsvnrqmnpan 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                as central nervous system injuries -
                                                      MG------QPMSLSGQPPPGTSGMAPHSMAVVSTATPQTQLQLQQVALQQQQQQQQ 142
                                                                                                                                                                                                                          134;
                                                                                                                                                                                                                                                                                                                                                                                                                                              The sequence data
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Wang Z,
Zhou P,
                                                                                                                                                                                                                    10.4%; Score 312; DB 22; iilarity 27.6%; Pred. No. 4.8e-11; Conservative 41; Mismatches 169;
                                                                                                                                                                                                                                                                                                                                                                 2063 AA;
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2000US-0662191.
2000US-0693036.
2000US-0727344.
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2000US-0552317
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Wehrman T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Goodrich R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                 for this patent did not form part of the printed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chen R, Ma Y,
, Xu C, Xue AJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Drmanac RT;
                                                                                                                                                                                                                               169;
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Yang Y,
                                                                                                                                                                                                                                                                             Length 2063;
                                                                                                                                                                                                                               Indels 142;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wang
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RESULT 15
AAW62647
ID AAW626
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         Matches 121;
                         Query Match
Best Local (
                                                                                                           The present sequence represents the mature glutenin protein. The DNA sequence encoding this protein is isolated from the genomic DNA of Triticum durum L. The gene codes for a low-molecular-weight glutenin protein and can be used to produce transgenic durum wheat plants with "better quality characteristics" [no details given].
                                                                                                                                                                                                                                                                                                                                                                                                            19-DEC-1996;
                                                                                      Sequence
                                                                                                                                                                                                              Claim 8; Page 14; 18pp; French.
                                                                                                                                                                                                                                                                                                 N-PSDB; AAV38816.
                                                                                                                                                                                                                                                                                                              WPI; 1998-365055/32.
                                                                                                                                                                                                                                                                                                                                            Cardelli LE, D'Ovidio R, Marchitelli C,
                                                                                                                                                                                                                                                                                                                                                                         (ITUY-) ITAL MIN UNIV RICERCA SCI & TECNOLOGICA.
                                                                                                                                                                                                                                                                                                                                                                                                                                          18-DEC-1997;
                                                                                                                                                                                                                                                 molecular weight
                                                                                                                                                                                                                                                          Durum wheat glutenin gene - coding for glutenin protein of low
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26-JUN-1998.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FR2757538-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Triticum durum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Glutenin gene; durun wheat; low-molecular-weight;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mature durum wheat glutenin protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               09-OCT-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAW62647 standard; Protein; 369 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAW62647;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     transgenic durum wheat.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    411 PSSFLPSPSPQPSQ3P-----VTARTPQNFSVPSPGP--LNTPVNPSSVMSPAGSS 459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               354 APGVQVSQSSLPMLSSPSPGQQVQTPQSMPPPPQPSPQP---GQPSSQPNSNVSSGPAPS 410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              393 msn------pgq--ftapqmkslqggpsrvptplqqphltnkspa-sspssfqqg 438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           333 gslgtmtanqgwkkaplpgpmqqqlqarpslatvqtpshppppypfgsqqasqahtnfpq 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              295 QSQTQPLVSQAQALPGQMLYTQPPLKFVR-APMVVQQPPVQPQVQQQQTAVQTAQAAQMV 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          280 ---qqqqqql----qarppqqhqqqqpqgirpqftaptqvpvppgwnqlpsgalqpppaq 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                203 QQIQQQQQQQQQQQQQQQQQQQQQQQQQQQQALEAQPPI----QQPPMQQPQPPPSQ 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             259 A-----LPQQLQQM------HHTQHHQPPPQPQQPPVAQNQPSQLPP 294
                       Similarity
                                                                                      369 AA;
       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                         96IT-MI02663.
                                                                                                                                                                                                                                                                                                                                                                                                                                          97FR-0016059.
 10.3%; Score 311.5; DB 19; Length 369; 32.1%; Pred. No. 8.1e-12; stive 32; Mismatches 149; Indels 75;
Gaps
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344 cnwnvplyrtttrvpfg 360
                                                    441 GPLNTPVNPSSVMSPAG 457
                                                                                                     289 qqlgqcvsqpqqqqqlgqqqqlahgtflqphqiaqlevmtsialrt-----lptm 343
                                                                                                                                                      390 PQPGQPSSQP--NSNVSSGPAPSPSSFLPSPSPQPSQ-----SPVTARTPQNFSVPSP 440
                                                                                                                                                                                                     229 arsqmlqqsschvmqqqccqqlpqipqqsryeairaivysiilqeqqqvqgsiqtqqqqp 288
                                                                                                                                                                                                                                                            354 APGVQVSQSSLPMLSSPSPGQQVQTPQ------SMPPPPQPS 389
                                                                                                                                                                                                                                                                                                             179 pq---qppfsqqq----qpvllqqqipfvhpsilqqlnpckvflqqqcspwampqs---1 228
                                                                                                                                                                                                                                                                                                                                                                     294 PQSQTQPLVSQAQALPGQMLYTQPPLKFVRAPMVVQQPPVQPQVQQQQTAVQTAQAAQMV 353
                                                                                                                                                                                                                                                                                                                                                                                                                      126 pfsqqqpvlpqqppfsqqqpppfsqqlppfsqq-----qqpvlpqqppfsqqqqpip 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                        237 ALEAQPFI--QQPPMQQPQPPP-SQALPQQLQQMHTQHHQPPPQPQQPPVAQNQPSQLP 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             189 ----QQQQHLIKLHHQ-NQQQI----QQQQQQLQRIAQLQLQQQQQQQQQQQQQ---QQQQQ 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   134 LQQQQQQQFQAQQQAALQQQQQ---QQQQQQFQAQQSAMQQQFQAVVQQQQQ----LQQQQ 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            66 ppfsqqqpvlpqqpsfsqqqlppfsqqqppfsqqqpvlpqqpsfsqqqlppfsqqlp 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6 lerpsqqqplppqqtlshhhqqqplqqqphqfpqqqpcsqqqqpplsqqqppfsqqqq 65
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Search completed: February 28, 2002, 19:38:03 Job time: 665 sec

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OM protein - protein search, using sw model
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Maximum DB seq length: 2000000000
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Perfect score:
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Maximum Match 100%
Listing first 45 summaries
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      Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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/cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
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US-08-855-323A-2
US-08-9625-188-20
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QY 60 QSLTGGPAAGAAGIGMPPRGPGQSLGGMGSFGAMGQPMSLSGQPPPFGTSGMAPHSM	Query Match 12.7%; Score 382.5; DB 4; Length 1 Best Local Similarity 28.1%; Pred. No. 1.6e-19; Matches 151; Conservative 67; Mismatches 218; Indels	Pattion IBM	TITLE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION: NUMBER OF SEQUENCES: CORRESPONDENCE ADDRE ADDRESSES: CHIRON STREET: 4560 HORE CITY: EMERYVILLE CITY: EMERYVILLE STATE: CA COUNTRY: USA ZIP: 94608 COMPUTER READABLE FO MEDIUM TYPE: F10	ALIGNMENTS  ESULT 1 5-08-916-352-2 Sequence 2, Application US/08916352 Patent No. 6166191 GENERAL INFORMATION: GAPPLICANT: CHIRON CORPORATION	28 205.5 6.8 542 1 US-08-328-809-8 Seq 29 205.5 6.8 542 5 PCT-US92-11107-13 Seq 30 203 6.7 713 1 US-08-190-802A-63 Seq 31 202.5 6.7 1187 1 US-08-320-559-28 Seq 32 202.5 6.7 1187 3 US-08-545-86D-28 Seq 34 202.5 6.7 1187 5 PCT-US94-04496-28 Seq 36 202.5 6.7 1210 1 US-08-324-569-26 Seq 37 202.5 6.7 1210 1 US-08-345-86D-26 Seq 38 201.5 6.7 1210 3 US-08-345-8692-26 Seq 39 201.5 6.7 855 2 US-08-816-93A-2 Seq 40 201.5 6.7 855 2 US-08-816-672-2 Seq 41 201.5 6.7 855 4 US-09-466-672-2 Seq 42 197.5 6.6 846 3 US-09-107-847-2 Seq 43 197.5 6.6 846 4 US-09-496-672-55 Seq 44 197.5 6.6 846 4 US-09-496-672-55 Seq 45 196.5 6.5 1876 2 US-08-609-049A-28 Seq
PMSLSGQPPPGTSGMAPHSM 115 	Length 1004; Indels 101; Gaps 2		AS		Sequence 8, Appli Sequence 13, Appl Sequence 63, Appl Sequence 28, Appl Sequence 28, Appl Sequence 28, Appl Sequence 28, Appl Sequence 26, Appl Sequence 26, Appl Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 5, Appli Sequence 5, Appli Sequence 5, Appli Sequence 5, Appli Sequence 55, Appli Sequence 55, Appli

22;

MOLECULE TYPE:

TOPOLOGY:

SS: single linear

protein

TYPE: amino STRANDEDNESS:

SEQUENCE CHARACTERISTICS

amino acids

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US-08-991-300-2
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INFORMATION FOR SEQ ID NO: 2:
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APPLICANT:
APPLICANT:
                                                                                                                               FILING DALL.

CLASSIFICATION: 800
PRIOR APPLICATION DAFA:
APPLICATION NUMBER: IT MI 96/A 002663
APPLICATION NUMBER: 19-D3C-1996
APPLICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: ISOLATION AND CHARACTERIZATION OF A GENE TITLE OF INVENTION: ENCODING A LOW MOLECULAR WEIGHT GLUTENIN NUMBER OF SEQUENCES: 6
                 REFERENCE/DOCKET NIMBER: 22
TELECOMMUNICATION IN COMMITION:
TELEPHONE: 703-41:3000
TELEPAX: 703-413-2220
                                                                                                                                                                                                                                                             CURRENT APPLICATION JATA:

APPLICATION UMBER: US/08/901 300

FILING DATE:
                                                                                                    FILING DATE: 19-D3C-1996
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,6
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                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC
OPERATING SYSTEM:
SOFTWARE: Patent1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                402 NVSSGPAPSPSSFLISPSPQPSQ------SPVTARTPQNFSVPSPGPLNTPVN 448
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE:
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STREET: 155 S. JEFFERSON DAVIS HIGHWAY
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PORCEDDU, ENRICO
MERCHITELLI, CINZIA
CARDELLI, LUISA ERCOLI
CARDELLI, LUISA ERCOLI
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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V: 830
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Best Local :
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                                     OPERATING SYSTEM: DOS

SOFMARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:

PRIOR APPLICATION NUMBER: US/08/918,914

FILING DATE: Filed Herewith
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                       APPLICANT: Magna, Holly
APPLICANT: Yocum, Sue
APPLICANT: MUTTY, LYNN E.
TITLE OF INVENTION: HUMAN NUCLEOTIDE PYROPHOSPHORYLASE
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Dr.
                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     189 ----QQQQHLIKLHHQ-NQQQI----QQQQQQLQRIAQLQLQQQQQQQQQQQQQQ---QQQQQ 236
FILING DATE:
                     APPLICATION NUMBER:
                                                                                                                                                                                    COMPUTER:
                                                                                                                                                                                                                                                                                                            STREET: 31/4 FOR CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   294 PQSQTQPLVSQAQALPGQMLYTQPPLKFVRAPMVVQQPPVQPQVQQQQTAVQTAQAAQMV 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          237 ALEAQPPI--QQPPMQQPQPPP-SQALPQQLQQMHHTQHHQPPPQPQQPPVAQNQPSQLP 293
                                                                                                                                                                                                                                                                                                    STATE:
                                                                                                                                                                                                                                                                          COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          66 PPFSQQQQPVLPQQPSFSQQQLPPFSQQQQPPFSQQQQPVLPQQPSFSQQQLPPFSQQLP 125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6 LERPSQQQPLPPQQTLSHHHQQQPIQQQPHQFPQQQPCSQQQQQPPLSQQQQPPFSQQQQ 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION:
                                                                                                                                                                                                                                                    94304
                                                                                                                                                                                                                                                                                               CA
                                                                                                                                                                                                                                                                          USA
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Lawton, Michael
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mitchell, Peter
                                                                                                                                                                          IBM Compatible
                                                                                                                                                                                                          Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----SMPPPPQPS 389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          75; Gaps
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US-08-853-310-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2, Application US/08853310 Patent No. 5948640
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Randazzo, Filippo
TITLE OF INVENTION: Mammalian Additional Sex Combs (Asx) Acts as a Tumor Suppress
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IMMEDIATE SOURCE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                              COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                  ATTORNEY/AGENT INFORMATION:
NAME: Guth, Joseph H.
REGISTRATION NUMBER: 31,
                                                                                                                                    CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LIBRARY: GELL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            334 QPQVQQQQTAVQTAQAAQMVAPGVQVSQSSLPMLSSPSPGQQVQTPQSMPPPP 386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             103 PPPGTSGMAPHSMAVVSTATPQTQLQLQQVALQQQQQQQQFQQQQQAALQQQQQQQQQQQ 162
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TOPOLOGY: 111
                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
                                                                                                                                                                                                                                                                                                              STREET: 4560 Hort
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER:
                                                                                                FILING DATE:
                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                STATE:
REFERENCE/DOCKET NUMBER:
                                                                           CLASSIFICATION: 514
                                                                                                                APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QQQQQQQQQQQQALEAQPPIQQPPMQQPQPPPSQALPQQLQQMHHTQHHQPPPQPQQP 282
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QQRQQNPQQPQQTTQFGQSQIQ---LQSGPVPPQQ-----HPQQQQPQQQPELE 355
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PAPPAQQYAPR----APEYPSAQQQQQQ---REQQQREQQHREHQARLQQHQQQQQQQQ 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RSPLDQHAQLYQQRMSQYRENFNQRHPARPKADPCPGGFCAPVP-----QAPQ--QERPT 408
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RESULT 5
US-08-728-323A-2
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                                                                                                                                                                                                            sequence 2, Application US/08728323A Patent No. 5948676
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Best Local
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                                                                                                                                                                  GENERAL INFORMATION:
APPRITCANT: Chang, Yuan
              APPLICANT: Chang, Yua
APPLICANT: Bohenzky,
APPLICANT: Russo, Jan
APPLICANT: Edelman, I
APPLICANT: Moore, Pat
TITLE OF INVENTION: I
TITLE OF INVENTION: I
TITLE OF INVENTION: E
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION: TELEPHONE: (510) 923-3888
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LENGTH: 903 amino acid
CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              490
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           324 ALQQAQLHQRQLLAQAANNNLLQQQQQQQQQNVALPTTQAKFIAKPLNIISMTRPANASPT
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                                                                                                                                                                                                                                                                                                                                                                   448 NPS 450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    546 SNITTATGSMAAAVAAAPPQNVLKQEELLVSGAVGAGALPAGLPPNVMGVGRPGVYKVIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    358
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9.7%;
Local Similarity 25.2%;
tes 137; Conservation
                                                                                                                                                                                                                                                                                                                             666 QPA 668
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TOPOLOGY: lin
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                                                                                                                                Bohenzky, Roy A.
Russo, James J.
                                                                                            Edelman, Isidore S. Moore, Patrick S.
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                                        Encoding Same And Uses
                                                        Immediate Early Protein From Kaposi's Sarcoma-Associated Herpesvirus, DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        --GVPTTIAQQRLQPKM---PTGKGRKATSNRLPPGAVNLERTY 489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 292.5; DB 2;
Pred. No. 3.7e-13;
6; Mismatches 151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -QHHQPP-PQPQQPPVAQNQPSQLPPQSQTQPLVSQ 304
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----PAPSPSSFL-----
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; ORGANISM: Ashbya goss//pii
US-09-625-188-20
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                                                                                                                                                                                                                                                                                                                                                                                       RESULT
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                                                                                                                                  SOFTWARE: Pat
SEQ ID NO 20
LENGTH: 729
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-278-0400
TELEPAX: 212-391-0525
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1162 amino acids
TYPE: amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                           Sequence 20, Application US/09625188 Patent No. 6307037
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                       FILE REFERENCE: PB/5-31285P
CURRENT APPLICATION NUMBER:
CURRENT FILING DATE: 2000-0
NUMBER OF SEQ ID NOS: 44
                                                                                                                                                                                                                                         TITLE OF INVENTION: Fingal Target Genes and Methods FILE REFERENCE: PB/S-31285P1
                                                                                                                  LENGTH: 72
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 10036
COMPUTER READABLE FCRM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         301 LVSQAQALPGQMLYT)PPLKFVRAPMVVQQPPVQPQVQQQQTAVQTAQAAQ 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  436 LSIQSSQQQQEPQQQEPQQQEPQQQEPLQEPQQQEPQQQEPLQEPQQQEPQQQEPQQQEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     244 IQQPPMQQPQP-PPS_ALPQQLQ-QMHHTQHHQPPP-QPQQPPVAQNQPSQLPPQSQTQP 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             496 LQEPQQQE------PQQQEPQQQEPQ-----QQEPQQQEPQQQEPQQQEPQQQEPQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: U
ZIP: 10036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/728,323A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               l Similarity 35.9
83; Conservative
                                                                                                                                                                         PatentIn Ven. 2.1
                                                                                                                                                                                                                                                                                     No. 6307037artis AG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cooper & Dunham LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         435
                                                                                                                                                                                                             2000-07-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9.6%; Score 288; DB 2; Length 1162; 35.9%; Pred. No. 1.1e-12; ative 28; Mismatches 90; Indels 30
9.5%; Score 286; DB 4; 28.0%; Pred. No. 8.4e-13;
                                                                                                                                                                                                                              US/09/625,188
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                 Length 729;
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US-08-194-468-2
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                                                                                                                     TELECOMMUNICATION INFORMATION:
TELEPHONE: (6.19)-546-4737
TELEFAX: (6.19)-546-9392
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Montmi
                            MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                    CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Reiter, Stephen E.
REGISTRATION NUMBER: 31,1
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     567 NGPKNAAAALQNTNGISQVDLSLLAKVPPPANPADQ 602
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    524 -----QHPPQQPQQQNSQQAI-VGQSQQQVTSGQQKGSSR----NSISKTLQV 566
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     317 PPLKFVRAPMVVQQPPVQPQVQQQQTAVQTAQAAQMVAPGVQVSQSSLPMLSSPSPGQQV 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   497 SQAHSQQHQQQHQQQQQQQQQQQQQQPQ------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    257 SQALPQQLQQMHHTQHHQPPPQPQQPPVAQNQPSQLPPQSQTQPLVSQAQALPGQMLYTQ 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    459 LHHQ-QQQLQQQQHHL------QQQQHQQQQQQSLSQQP-----QQQQQSQQ 496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     197 LHHQNQQQIQQQQQCQRTAQLQLQQQQQQQQQQQQQQQQALEAQPPIQQPPMQQPQPPP 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      399 ATGLQQPLPQPQRQSLSYNLVTPLSSDMNLPPQSSQGGILPHQAPAQTQPQSQALQHHQH 458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          144 QQQQQAALQQQQQQQQQQQ----FQAQQSAMQQQFQAVV---QQQQQLQQQQQQQQQHLIK 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        344 -GIPSSISGLTTSQPPTPHLEWGTTGRRQSSTFYPS----QSNTEIPPMHLTGQVQSSQL 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      287 QRSRFSFTDPFSSEQTNMGSQQPDLITTPLKGHQDTGKSFLLMESDEINDSIWGNGT--- 343
                                                   TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: FILING DATE: 10-FE
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STATE: California
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                                                                                                 LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9007
                                                                       amino acid
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                                                                                                 2441 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                   US/08/194,468
                                                                                                                                                                                                                                                                        31, 192
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NAME/KEY: VARIANT
LOCATION: (1)...(2441)
OTHER INFORMATION: Xaa
US-08-961-739-2
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US-08-961-739-2
; Sequence 2, Application US/08961739A
; Patent No. 6063583
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                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                             SEQ ID NO 2
                                                                                                  Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Montminy, Marc R.

TITLE OF INVENTION: Methods for Treating Diabetes Mellitus
FILE REFERENCE: SALK1650-1
CURRENT APPLICATION NUMBER: US/08/961,739A
CURRENT FILING DATE: 1997-10-31
CURRENT APPLICATION NUMBER: US 194,468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                     EARLIER FILING DATE: 1994-02-10
                                                                                                                                                                                                                                                                 FEATURE:
                                                                                                                                                                                                                                                                                 ORGANISM: Mus
                                                                                                                                                                                                                                                                                                        TYPE: PRT
                                                                                                                                                                                                                                                                                                                       ENGTH: 2441
1981 GMPP-----GRDGMGTPGSQMTPVGLNVPRPNQVSG-----PVMSSMPPG---QWQQAP 2026
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                                     74 GMPPRGPGQSLGGMGSFGAMGQPMSLSGQPPPGTSGMAPHSMAVVSTATPQTQLQLQQVA 133
                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     74 GMPPRGPGQSLGGMGSFGAMGQPMSLSGQPPPGTSGMAPHSMAVVSTATPQTQLQLQQVA 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ------LPIQGSSMGQMAAPMGQLGQM--GQPGLGADSTPN-IQQALQQRILQQQQMKQ 2302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GPLNTPVNP--SSVMSPAGSSQAEEQQYLDKLKQLSKYIEPL 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PSPRIQP-QPSPHHVSPQTGTPHPGLAVTMASSMDQGHLGNPEQS---AMLPQ-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QTAQAAQ-----MVA------PGVQVSQSSLPMLSSPSPGQQVQTPQSMPPPPQ 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AQNQPSQLPPQSQTQPLVSQAQALPGQMLYTQPPLKFVRAPMVVQQPPVQPQVQQQQTAV 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QQQQQQQQQQQNSASLAGGMAGHSQFQQPQGPGGYAPAMQQQRM----QQH------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QAGVPRPGVPPPQPAMGGLNPQGQALNIMNPGHNPNMTNMNPQYREMVRRQLLQHQQQQQ 2206
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                                                                                  141;
                                                                                  Conservative
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                                                                                                  9.4%;
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                                                                              40; Mismatches 165;
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                                                                                                Score 283; DB 3; Pred. No. 5.8e-12;
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Pred. No. 5.8e-12;
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                                                                                                                   Length 2441;
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                                                                                Indels 176;
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                                                                              Gaps
                                                                                22;
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APPLICANT: Eckner, Ric
APPLICANT: Ewen, Mark
                                                                              TELEPHONE: (617) 542-2290
TELEFAX: (617) 451-0313
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Williams Ph.D., Kathle
REGISTRATION NUMBER: 34,380
REFERENCE/DOCKET NUMBER: DFC
                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Livingston, David
TITLE OF INVENTION: NUCLEIC ACID, ENCODING TRANSCRIPTION
TITLE OF INVENTION: FACTOR P300 AND USES OF P300
                                                    SEQUENCE CHARACTERISTICS:
                                                                                                                                         TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                             APPLICATION NUMBER: FILING DATE: 14-APF CLASSIFICATION: 436
                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE:
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                                                                                                                                                                                                                                                                                                                                                                                          Floppy disk
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PCT-US95-04682-2
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: NUCLEAR THE OF INVENTION: FAMINAMER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Florpy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPATIBLE PC-DOS OPERATING SYSTEM: PC-DOS MS-DOS
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                       CLASSIFICATION:
ATTORNBY/AGENT INFOFMATION:
NAME: Holliday C. Heine, Ph.D.
REGISTRATION NUMBER: 34,346
                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04682
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2376 LASNPGMANLHGASATDLGLSTDNSDLNSNLSQSTL 2411
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                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/227,536
FILING DATE: 14-April-1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            191 QQHL-IKLHHQNQQQIQQQQ-----QQLQRIAQLQLQQQQQQQQQQQQQQQQQQQQALEAQ--- 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            131 QVALQQQQQQQFQQDQQAALQQQQQQQQQQQFQAQQSAMQQQFQAVVQQQQQLQQQQQQ 190
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           300 PLVSQAQALPGQMLYTQPPLKFVRAPMVVQQPPVQPQVQQQQTAVQTAQAAQMVAPGVQV 359
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  REFERENCE/DOCKET NUMBER: DFCI-308Xq999
                                                                                                                                                                                                            CLASSIFICATION:
                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
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Ten Post Office Square
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                                                                                                                                14-April-1994
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TITLE OF INVENTION: NEW USE
FILE REFERENCE: P32261
CURRENT APPLICATION UMBER: US/09/393,569
CURRENT FILING DATE: 1999-09-10
EARLIER APPLICATION NUMBER: GB 9907261.3
EARLIER FILING DATE: 1999-03-29
EARLIER APPLICATION NUMBER: GB 9819779.1
EARLIER FILING DATE: 1998-09-10
NUMBER OF SEQ ID NOS: 5
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: BINGHAM,
APPLICANT: CASE, PI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: 1
MOLECULE TYPE:
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US-09-393-569-2; Sequence 2, Application US/09393569; Patent No. 6277979
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APPLICANT: LAWSON, SALLY NEALE
APPLICANT: NEWTON, RICHARD ANTHONY
APPLICANT: PIERCY, VALERIE
APPLICANT: RAUSCH, OLIVER LARS
APPLICANT: RAUSCH, PRAVIN
APPLICANT: REITH, ALASTAIR DAVID
APPLICANT: SANGER, GARETH JOHN
APPLICANT: SANGER, GARETH JOHN
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TELEPHONE: (617) 542-2290
TELEPAX: (617) 451-0313
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2083 AFIKQRAAKYANSNPQPIPGQPGMPQGQPGLQPPTMPGQQGVHSNPAMQNMNPM-QAGVQ 2141
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2196 GAGPGIGPGMANHNQFQQPQGVGYPPQPQQRMQHHMQQMQQGNMGQIGQLPQALGAEAGA 2255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2142 RAGLPQQQPQQQLQPPMGG-----MSPQAQQMNMNHNTMPSQFRDILRRQQMMQQQQQQ 2195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 131 QVALQQQQQQQFQQQQQAALQQQQQQQQQQQQFQAQQSAMQQQFQAVVQQQQQQLQQQQQQQ 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              418 PSPQPSQSPVTARTPQNFSVPSP-GPLNTPVNPSSV 452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   191 QQHL-IKLHHQNQQQIQQOQ-----QQLQRIAQLQLQQQQQQQQQQQQQQQQQQQQQALEAQ--- 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                360 SQSSLPMLSSPSPGQQVQTPQSMPPPPQPSPQPGQPSSQPNSNVSSG--PAPSPSSFLPS 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   300 PLVSQAQALPGQMLYTQPPLKFVRAPMVVQQPPVQPQVQQQQTAVQTAQAAQMVAPGVQV 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 242 --PPIQQPPMQQPQPPPSQALPQQLQQMHHTQHHQPPPQPQQPPVAQNQPSQLPPQSQTQ 299
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2414 amino acids
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SEQ ID NO 2

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 12
US-08-267-803B-9
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                                                                                                                                                                                                                                                    TITLE OF INVENTION: Gene Sequence for Spinocerebellar Patent NO. 5834183
TITLE OF INVENTION: Type 1 and Method for Diagnosis NUMBER OF SEQUENCES: 85
                                                                                                                                                                                                                                                                                                                                                                                                                                         sequence 9, Application US/08267803B
Patent'No. 5834183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 115;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION: APPLICANT: Orr, H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                     APPLICANT:
APPLICANT:
                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   335 SGEPSSILNLPGESTLRRDFLRLQLANKERSEALRRQQLEQQQRENEEHKRQLLAERQKR 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100 SGQPP-----PGTSGMAPHSMAVV-----STATPQTQLQLQ------QVA 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                395 IEEQKEQRRRLEEQQRREKELRKQQEREQRRHYEEQMRREEERRRAEHEQEYIKRQLEEE 454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       134 LQQQQQQQ----QFQQQQQAALQQQQQQQQQQQQQQSAMQQQFQAVVQQQ----QQLQQQ 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      792 --- RPASYKKAIDEDLTALAKELRELRIEETNRPMKKVTDYSSSSEESESSSEEEEED 845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               451 SVMSPAGSSQAEEQQYLDKLKQLSKY-IEPLRRMINKI-----DKNEDRKKD 496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                392 PG-QPSSQPNSNVSSGPAPSPSSFLPSPSPQPSQSPVTARTPQNFSVPSPGPLNTPVNPS 450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   353 VAPG-----VQVSQSSL----PMLSSP----SPGQQVQTPQSMPPPPQPSPQ 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             628 VTSHRVEMPRQNSDPTSENPPLPTRIEKFDRSSWLRQEEDIPPKVPQRTTSISPA-LARK 686
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     285 AQN-----QPSQLPP-----QSQTQPLV---SQAQAL-PGQMLYTQ---------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              508 QEQRPVEKKPLYHYKEGMSPSEKPAWAKEVEERSRLNRQSSPAMPHKVANRISDPNLPPR 567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   243 PIQQPPMQQP------PPV 284
                                                                                                        COUNTRY: USA
ZIP: 55458-1415
                                                                                                                                                                     CITY: Minneapolis
                                                                                                                                                                                     STREET:
                                                                                                                                                                                                             ADDRESSEE:
  SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GGSQPGSQAGSSERTRVRANSKS---EGSPVLPHEPAKVKPEESRDITRPS-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NSPGNGSALGPRIGSQPIRASNPDLRRTEPILESPLQRTSSG---SSSSSSTPSSQPSSQ 743
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SESFSISGVQPARTPPMLRPVDPQIPHLVAVKSQGPALTASQSVHEQPTKGLSGFQEALN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----PPL----KFVRAPMVVQQPPVQPQVQQQQTAVQTAQAAQM 352
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                                                                                                                                                                                       E: Mueting, Raasch, Gebhardt & Schwappach, P.O. Box 581415
                                                                                                                                                                                                                                                                                                                                   Ranum, Laura P.W. Chung, Ming-yi Zoghbi, Huda Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
  PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                Harry T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8.0%; Score 241; DB 4; 21.4%; Pred. No. 2.9e-09;
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Version
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      #1.25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-267-803B-9
                                                                                                                                                                                                                                                      US-09-041-886-17; Sequence 17, Application US/09041886; Patent No. 6235872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          밁
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                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 816 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
                                               CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Dri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
                                                                                                                                           TITLE OF INVENTION: Proapoptotic TITLE OF INVENTION: Polypeptides
                                                                                                                                                                                      APPLICANT: Bredesen, Dale E. APPLICANT: Rabizadeh, Sharroz
                                                                                                                            NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         212
                                                                                                                                                                                                                                                                                                                                                                                    408 PSTLNDKSGLHLGKPGHRSYALSPHTVIQTTHSA 441
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 201 NQQQIQQQQQQIQRIAQIQIQQQQQQQQQQQQQQQQALEAQPPIQQPPMQQPQPPPSQAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          159 VASAAGATTPSQRSQLEAYSTLLANMGSLSQTPGHKAEQQQQQQQQQQQQQQQQHQH------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                149 -AALQQQQQQQQQQQFQAQQ------SAMQQQFQAVVQQQQQLQQQQQQQQQHLIKLHHQ 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      118 VST-----ATPQTQLQLQQVALQQQQQQQQQQQQQQQ------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: MCCOrmack, Myra H. REGISTRATION NUMBER: 36, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 46 LPGNPGGRGHGGGRHGPAGTSVELGLQQGIGLHKALSTGLDYS---PPS----APRSVPV 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          62 LTGGPAAGAAGIGM-PPRGPGQSLG---GMGSFGAMGQPMSLSGQPPPGTSGMAPHSMAV 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH:
               STATE:
                                        CITY:
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                             PVTARTPQNFSVPSPGPLNTPVNPSSVMSPAGSS 459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AGGKSVPHPYESRHVVVHPSPSDYSSRDPSGVRASVMVLPNSNTPAADLEVQQATHREAS 407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QTPQSMPPPPQP-----SPQPGQPSSQPNSNVSSGPAPSPSSFLPSPSPQPSQ------S 425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SGSHFV-----PREATKKAESSRLQQAIQAKEVLNGEMEKSRRYGAPSSADLGLGK 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PPLKFYRAPMYVQQPPVQPQVQQQQTAVQTAQAAQMYAPGVQVSQSSLPMLSSPSPGQQV 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PQQLQQMHHTQHHQPPPQPQQPPVAQNQPSQLPPQSQTQPLVSQAQAL--PGQ--MLYTQ 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTLPAAYATPQPGTPVSPVQYAHLPHTFQFIGSSQYSGTYASFIPSQLIPPTANPVTSA 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -QQNQYVHISSSPQNTGRTASPPAI----PVHLHPH----QTMIPHTLTLGPPSQVVMQYAD 296
                                        San Diego
               California
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States
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                                                            Drive,
                                                                                                                                                Peptides, De and Methods
                                                               Suite 700
                                                                                                                                                  Dependence
ds of Use
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US-09-041-886-23

Sequence 23, Application US/09041886

Patent No. 6235872

GENERAL INFORMATION:
                                                                                                                                                                                                                                     RESULT 14
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NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 91,815
REFERENCE/DOCKET NUMBER: P-LJ 2626
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9901
TELEPHONE: (619) 535-9901
TELEPHONE: (619) 535-8949
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 816 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-041-886-17
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Best Local Similarity 25.6
Matches 116; Conservitive
APPLICANT: Bredesen, Dale E.
APPLICANT: Rabizadeh, Sharroz
TITLE OF INVENTION: Proapoptotic Peptides, Dependence
TITLE OF INVENTION: Polypeptides and Methods of Use
NUMBER OF SEQUENCES: 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Flo.ppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                        408 PSTLNDKSGLHLGKFGHRSYALSPHTVIQTTHSA 441
                                                                                                                                                                                                                                                                                                                                                         426 PVTARTPQNFSVPSEGPLNTPVNPSSVMSPAGSS 459
                                                                                                                                                                                                                                                                                                                                                                                                                                                      377 QTPQSMPPPPQP-----SPQPGQPSSQPNSNVSSGPAPSPSSFLPSPSPQPSQ-----S 425
                                                                                                                                                                                                                                                                                                                                                                                                          348 AGGKSVPHPYESRHVVVHPSPSDYSSRDPSGVRASVMVLPNSNTPAADLEVQQATHREAS 407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             297 SGSHFV-----PREATKKAESSRLQQAIQAKEVLNGEMEKSRRYGAPSSADLGLGK 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         317 PPLKFYRAPMYVQQ1PVQPQVQQQQTAVQTAQAAQMVAPGVQVSQSSLPMLSSPSPGQQV 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          244 -QQNQYVHISSSPQNTGRTASPPAI---PVHLHPH---QTMIPHTLTLGPPSQVVMQYAD 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        261 PQQLQQMHHTQHHQLPPQPQQPPVAQNQPSQLPPQSQTQPLVSQAQAL--PGQ--MLYTQ 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             212 -----GSPPPA--- 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              201 NOQQIQQQQQQQQQQQQQQQQQQQQQQQQQQALEAQPPIQQPPMQQPQPPPSQAL 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               159 VASAAGATTPSQRS(LEAYSTLLANMGSLSQTPGHKAEQQQQQQQQQQQQQQQQHQH----- 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              149 -AALQQQQQQQQQQQQCFQAQQ-----SAMQQQFQAVVQQQQQQQQQQQQQQQQHLIKLHHQ 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              118 VST----ATPQTQIQLQQVALQQQQQQQQQQQQQ------148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99 ATTLPAAYATPQPG"PVSPVQYAHLPHTFQFIGSSQYSGTYASFIPSQLIPPTANPVTSA 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               46 LPGNPGGRGHGGGRHGPAGTSVELGLQQGIGLHKALSTGLDYS---PPS----APRSVPV 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62 LTGGPAAGAAGIGM PPRGPGQSLG---GMGSFGAMGQPMSLSGQPPPGTSGMAPHSMAV 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TVPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               92122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7.7%; Score 232; DB 4; Length 816; 25.6%; Pred. No. 6.8e-09; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US/09/041,886
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 7.7%; Score 231.5; DB 4; Length 1185; Best Local Similarity 21.6%; Pred. No. 1.1e-08; Matches 136; Conservative 62; Mismatches 213; Indels 219; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (619) 535-89 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Rel
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ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 1185 amino aci
TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
470 -----LKQLSKYIEPLRRMIN---KIDKNEDRKKDLSKMKSLLDILTDPSKRCP 515
                                             717 SATQIKQEPAEEYETPESPVPPARSPSPPPKVVDVPSHASQSARFNKHLDRGFNSCARSD 776
                                                                                                                                            659 SFRTGTPPGYRGTSPPAGPGTFKPGSPTVGPGPLPPAGPSGLPS--LPPPPPAAPASGPPL 716
                                                                                                                                                                                       600 -PTVTTSSATLSTVIATVASSPAGYKTASPPGPPPYGKRAPSPGAYKTATPPGYKPGSPP 658
                                                                                              429 ART-----PQNFSVP-SP-GPLNTPVNPSSVMS-PAGSSQ-AEEQQYLDK------ 469
                                                                                                                                                                                                                                                                                  334 QPQVQQQQTAVQTAQAAQMVAP-GVQVSQSSLPM----LSSPSPG-QQVQTPQSMPPPPQP 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         354 PSPHSLPPASSSAPAPPMRF------PYSSSSSSAAASSSSSSSSSSASPFPASQAL 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       555 QAGPNGPPVSSSSNSSSSTSQGSYPCSHPSPSQGPQG-----APYPF------PPV 599
                                                                                                                                                                                                                                                                                                                                                                           279 ---PQQPPVAQNQPSQLPPQSQTQPL--VSQAQALPGQMLYTQPPLKFVRAPMVVQQPPV 333
                                                                                                                                                                                                                                                                                                                                                                                                                              501 -----NSGPPPPGAFPHPLEGGSSHHAHPYAMSPSLGSLRPYPPGPAHLPPPHSQVSYS 554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          245 QQPPMQQPQPPPSQALPQQLQ--QMHHTQ-------278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     466 TGAQSTAHPPVSTHHHHH----- 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  406 PSYPHSFPPPTSLSVSNQPPKYTQPSLPSQAVWSQGPPPPPPYGRLLANSNAHPGPFPPS 465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 168 -----SAMQQQFQAVVQQQQQLQQQ-----187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  303 PPPALRPLNNA-SASPPGLGAQPL-PGH----LPSPYAMGQGM---GGLPPGPEKGPTLA 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             55 PMNALQSLTGGPAAGAAGIGMPPRGPGQSLGGMGSFGAMGQPMSLSGQPPPG-----TSG 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 4370 La
CITY: San Diego
STATE: Californi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REGISTRATION NUMBER: 31
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/09/041,886 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: U
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)GY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1185 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                535-8949
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cathryn A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Release #1.0, Version #1.25
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US-08-906-865-4
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US $08-906-865-4
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                                                                                                                                                                                                                                     Query Match 7.7%; Score 231; DB 3; Length 696; Best Local Similarity 28.9%; Pred. No. 6.6e-09; Matches 89; Conservative 31; Mismatches 112; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Patent No. 6040168
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 4, Application US/08906865
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 201-343-1684
INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                 HYPOTHETICAL: N
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein DESCRIPTION: /desc =
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 696 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDLIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: DNA ENCODING THE HUMAN SYNAPSIN III GENE
TITLE OF INVENTION: AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: *...
STREET: Floor
                                 282 ----PPVAQNQPSQLP-PQSQTQPLVSQAQALP--GQMLYTQPPLKFVRAPMVVQQPPVQ 334
                                                                           441 ALPLGRQTSQQPAGPPAQQEPPPQGGPPQPGPQRQGPPLQQ-----RPPPQGQQHL 493
                                                                                                                                                        381 RDHIIEVVGSSMPLIGDHQDEDKQLIVELVVNKMAQALPRQRQRDASPGRGSHGQTPSPG 440
                                                                                                                                                                                             191 QQHLIKLHHQNQQQI-QQQQQQQQQQQQQQQQQQQQQQQQQQQ------ 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   827 ERELERSVKLAQEGRAPVECPSLGPVPHRP 856
494 SGLGPPAGSPLPQRLPSPTSAPQQPASQA-APPTQGQGRQSRPVAGGPGAPPAA-RPPAS 551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             516 LKTLOKCEIALEKLKNDMRC----PLPHRP 541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     777 LYFVPLEGSKLAKKRADLVEKVRREAEQRAREEKEREREREREKER----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: ZUL ... TELEPHONE: ZUL ... TO NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Hackensack
STATE: New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: (ZIP: 07601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE:
                                                                                                              -----QQQQALEAQPPIQQPPMQQPQPPPSQALPQQ-----LQQMHHTQHHQPPPQPQQ--- 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E: David A. Jackson, Esq.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 USA
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linear
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Porton, Barbara
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kao, Hung-Teh
                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        201-487-5800
                                                                                                                                                                                                                                                                                                                                                                                                                       /desc = "Synapsin Ia"
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                                                                                                                                                                                                                                     Gaps
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Search completed: February 28, 2002, 19:38:35 Job time: 387 sec

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Wang

J, TY

Liu C,
Wang Z,
Zhou P,

Asundi V, ( Wehrman T, : Goodrich R,

Chen R, Drmanac

Ma Xue

Qian XB, Yang Y,

Ren F, Zhang v

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a Y, e AJ, RT;

(HYSE-)

HYSEQ INC

Zhao Tang

Novel nucleic acids and such as central nervous

polypeptides, useful for system injuries -

treating disorders

Claim 1; SEQ ID NO 1658; 10078pp; English.

WPI; 2001-442253/47. P-PSDB; AAM40299.

The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, Activinjoinhibin activity, chemotactic/chemokinetic activity, hamostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and

Sequence 2556 BP;

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specification

disorders.
The sequence data for this patent did

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19-JUL-2000;
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19-OCT-2000;
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KW Lpukaemia; ss.
XX Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                           The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system diseases, such as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
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                                                                                                                                                                            Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, Activin/Inhibin activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel nucleic acids and polypeptides, useful for treating disorders such as central nervous system injuries \cdot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-442253/47.
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                                                                                                               The sequence data for this patent did not form part of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQ ID NO 5230; 10078pp; English.
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2000US-0552317.
2000US-0598042.
2000US-0620312.
2000US-0653450.
2000US-0662191.
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2000US-0727344.
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Wehrman T, Xo
, Goodrich R,
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, Xu C, Xue AJ,
R, Drmanac RT;
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Yang Y,
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771 A; 1143

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592 T;

0 other;

MetGlnGlnProGlnProProProSerGlnAlaLeuProGlnGlnLeuGl 265

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alignment_scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             688 CGTGTCTACGGCAACTCCACAGACCCAGCTGCAGCTCCAGCAGGTGGCCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               638 GGGCAGCCGCCTCCTGGGACCTCGGGGATGGCCCCTCACAGCATGGCTGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MetArgLysAlaGlyValAlaHisSerLysSerSerLysAspMetGluSe 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GlyGlnProProProGlyThrSerGlyMetAlaProHisSerMetAlaVa 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            euGlyGlyMetGlySerPheGlyAlaMetGlyGlnProMetSerLeuSer 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         aAlaGlyAlaAlaGlyIleGlyMetProProArgGlyProGlyGlnSerL 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SerValSerAspProMetAsnAlaLeuGlnSerLeuThrGlyGlyProAl 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CCAGGCTCATTATCCATTTTCGAGACATTCATAACAAGAAATCTCAAGCT
                 lnGlnGlnGlnAlaLeuGluAlaGlnProProIleGlnGlnProPro 248
                                                                                                                                                                                     HisGlnAsnGlnGlnGlnIleGlnGlnGlnGlnGlnGlnLeuGlnArgIl 215
                                                                                                                                                                                                                                                                       nglnLeu.GlnglnGlnGlnGlnGlnGlnHisLeuIleLysLeuHis 198
                                                                                                                                                                                                                                                                                                                                                                      nGlnSerAlaMetGlnGln.GlnPheGlnAla.ValValGlnGlnGlnGl 182
                                                                                                                                                                                                                                                                                                                                                                                                                         laLeuGlnGlnGlnGlnGlnGlnGlnGln.GlnPheGlnAlaGl 166
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                                                                               AGCACAGCTGCAGCTCCAACAACAGCAACAGCAGCAGCAGCAGCAGCAGC
                                                                                                     CATCAAAATCAGCAACAGATACAGCAGCAGCAACAGCAGCTGCAGCGAAT
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AGCAGCAGCAGCAGGCTTTGCAGGCCCAGCCAATTCAGCAGCCACCG 1087
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1738 AGTACCTGGACAAGCTGAAGCAGCTGTCGAAGTACATCGAGCCCCTGCGC 1787
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                                                                                                                                                                                                                1888 CCCTGAAGACCTTGCAAAAGTGTGAGATCGCCCTGGAGAAACTCAAGAAT 1937
                                                                                                                                                                                                                                                                                                                                  1838 TAAGATGAAGAGCCTTCTGGACATTCTGACAGACCCCTCGAAGCGGTGTC 1887
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          315 rGlnProProLeuLy;;PheValArgAlaProMetValValGlnGlnProP 332
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                                                                                                                                       AspMet.ArgCysProLeuProHisArgProArgCysHisArgProAsnS 548
                                                                                                                                                                                                                                                         roLeuLysThrLeuGlaLysCysGluIleAlaLeuGluLysLeuLysAsn 531
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1988 GCAGTACCTATGCCAGCCGCTCCTGGATGCCGTCCTGGCCAACATCCGCT 2037
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seq\_name: /SIDS2/gcgdata/geneseq/geneseqn/NA2000.DAT:AAC59039

seq\_documentation\_block: AAC59039 standard; cDNA; 1388 BP

AAC59039;

02-FEB-2001 (first entry)

Human secreted protein coding sequence SEQ ID NO: 60.

antiallergic; hepatotropic; antidiabetic; antiinflammatory; antiulcer; vulnerary; anticonvulsant; antibacterial; antifungal; antiparasitic; cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder; neurological disease; infection; human; secreted protein; ss. Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral; antiallergic; hepatotropic; antidiabetic; antiinflammatory; antiulcer;

Homo sapiens.

WO200055175-A1.

21-SEP-2000.

09-MAR-2000; 2000WO-US06049.

11-JUN-1999; 03-DEC-1999; 12-MAR-1999; 99US-0124144. 99US-0138574. 99US-0168667.

(HUMA-) HUMAN GENOME SCI INC

Ruben SM, Komatsoulis G;

P-PSDB; AAB27609 WPI; 2000-638175/61.

Isolated nucleic acid molecule encoding a human secreted protein used in preventing, treating or ameliorating a medical condition ı S

Claim 1; Page 372; 428pp; English.

The invention relates to the isolation of genes AAA58990-A59039 encoding CC 50 human secreted proteins AAB27560-B27609. The genes can be used to CC generate fusion proteins by linking to the gene for the human CC immunoglobulin G FC portion (SEQIDI) for increasing the stability of CC conditions, e.g. by protein or gene that human protein only: The genes and CC conditions, e.g. by protein or gene therapy. The genes are isolated CC conditions, e.g. by protein or gene therapy. The genes are isolated CC conditions, e.g. by protein or gene therapy. The genes are isolated CC control of the diagnosis, treatment and prevention of: (a) cancer, e.g. breast CC control of the diagnosis, treatment and prevention of: (a) cancer, e.g. breast CC control of the diagnosis, treatment and prevention of: (a) cancer, e.g. breast CC control of the diagnosis, treatment and prevention of: (a) cancer, e.g. bone CC control of the diagnosis, treatment and prevention of: (a) cancer, e.g. bone CC control of the diagnosis, treatment and prevention of: (a) cancer, e.g. bone CC control of the diagnosis, treatment and tract, liver, lung, or urogenital; CC control of the diagnosis, autoimmune thyroiditis, diabetes mellitus, Crohn's CC disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c) cardiovascular disorders such as myocardial ischaemias; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and CC epilepsy, and (f) infectious diseases e.g. cerebral anoxia and CC and parasitic infectious diseases such as viral, bacterial, fungal

Sequence 1388 BP; 364 A; 378 C; 343 G; 297 T; 6 other;

alignment\_scores:

Quality: 1597.00 Ratio: 5.006

Length: Gaps:

Percent Similarity: 100.000

Percent Identity: 98.746

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alignment_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17 rHisValPheLeuLysAlaLysThrArgAspGluTyrLeuSerLeuValA 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99 ATGAGGAAAGCTGGTGGCACA.AGTAAATCCAGCAAGGATATGGAGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MetargLysalaGlyValalaHisSerLysSerSerLysAspMetGluSe 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CCAGGCTCATTATCCATTTTCGAGACATTCATAACAAGAAATCTCAAGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 laArqLeuIleIleHisPheArqAspIleHisAsnLysLysSerGlnAla
                                                                                                                                                                                                                                                                         aAlaGlyAlaAlaGlyIleGlyMetProProArgGlyProGlyGlnSerL 84
                                                                                                                                                                                                                                                                                                                                                                        euGlnGlnGlnGlnGlnGlnGlnHisLeuIleLysLeuHisHisGln
                                                                                                                                                                                                                                                                                                                                                                                                                                                    nSerAlaMetGlnGlnGlnPheGlnAlaValValGlnGlnGlnGlnGlnL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LeuGlnGlnGlnGlnGlnGlnGlnGlnGlnPheGlnAlaGlnGl 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CGTGTCTACGGCAACTCCACAGACCCAGCTGCAGCTCCAGCAGGTGGCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       lValSerThrAlaThrProGlnThrGlnLeuGlnLeuGlnGlnValAlaL 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GlyGlnProProGlyThrSerGlyMetAlaProHisSerMetAlaVa 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TCCGTCAGTGATCCTATGAATGCACTCCAGAGCCTGACTGGCGGACCTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SerValSerAspProMetAsnAlaLeuGlnSerLeuThrGlyGlyProAl 67
                                                                                                                                                                                                   TCCAGCAGCAGCAGCAGCAGCATCTAATTAAATTGCATCAA
                                                                                                                                                                                                                                                                                                                                                                                                                            GAGTGCCATGCAGCAGCAGTTCCAAGCAGTAGTGCAGCAGCAGCAGCAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CTACAGCAGCAGCAGCAGCAGCAACAGCAGCAGTTCCAGGCTCAGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              euGlnGlnGlnGlnGlnGlnGlnPheGlnGlnGlnGlnGlnAlaAla 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TGCGGGAGCCGCTGGAATTGGCATGCCTCCTCGGGGCCCGGGACAGTCTC
                                                                                                                                                                                                                                        tHisHisThrGlnHisHisGlnProProProGlnProGlnGlnProProV
                                                      CAGCCACAGCCTCCGCCCTCCCAGGCTCTGCCCCAGCAGCTGCAGCAGAT
                                                                                                                                               lnGlnGlnAlaLeuGluAlaGlnProProIleGlnGlnProProMetGln
                                                                                         GlnProGlnProProProSerGlnAlaLeuProGlnGlnLeuGlnGlnMe
                                                                                                                              AGCAGCAGGCTTTGCAGGCCCAGCCAATTCAGCAGCCACCGATGCAG
to: AAC59039
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  247
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 184
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                                                                                                                               847
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                                                                                                                                                                                                                                        234
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seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA2001.DAT:AAF65986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    seq_documentation_block:
                         The present sequence is one of 3351 sequences in a library of human CC polynucleotides. The library is used to detect differentially expressed CC genes correlated with a cancerous state of a mammalian call and can cC detect colon, prostate, breast and lung cancer. The library can be used to produce probes for detection of mRNA and to produce additional copies CC of the polynucleotides. The probes can be used for chromosome mapping of CC the polynucleotide and for detection of transcription levels. Ribozymes CC or antisense oligonucleotides can be generated. The polynucleotides and CC their gene products are used as genetic or biochemical markers (e.g. in CC blood or tissues) that will detect the earliest changes along the CC carcinogenesis pathway and/or monitor the efficacy of therapies and CC preventive interventions. The polynucleotides, polypeptides and CC preventive interventions. The polynucleotides, polypeptides and CC creat the cancers and proliferative disorders such as neoplasia, CC dysplasia and hyperplasia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1048
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           868
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       02-JUL-1999;
02-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel human polynucleotide, SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAF65986 standard; cDNA; 386
                                                                                                                                                                                                                                                                                                                    Claim 9; Page 793; 1046pp; English.
                                                                                                                                                                                                                                                                                                                                                   Library of polynucleotides for diagnosing a cancerous state of mammalian cell and detecting cancer, particularly of the colon prostate, comprises 3351 human polynucleotide sequences -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      breast cancer; lung cancer; cancer detection; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               09-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAF65986;
                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-091805/10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Crkenjakov R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Reinhard C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Williams LT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (CHIR ) CHIRON CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TTGGTGTCACAGGCGCAAGCTCTCCCTGGACAAATGTTGTATACCCAACC 1047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TTGCTCAGAACCAACCATCACAACTCCCGCCACAGTCGCAGACCCAGCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        \verb|alAlaGlnAsnGlnProSerGlnLeuProProGlnSerGlnThrGlnPro|
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         oProLeu 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LeuValSerGlnAlaGlnAlaLeuProGlyGlnMetLeuTyrThrGlnPr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACCAATT 1054
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cytostatic; gene therapy; colon cancer; prostate
                                                                                                                                                                                                                                                                                                                                                                                                                                                         C, Randazzo F, ov R, Drmanac S, Garcia V, Jones
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2000WO-US18374.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Escobedo J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99US-0142310.
99US-0142311.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Innis MA,
Kennedy GC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Innis MA, Garcia PD, Kinger J,
Kennedy GC, Pot D, Lamson G, Drn
Dickson M, Labat I, Leshkowitiz
LW, Strache-Crain B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ВP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Drmanac
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or
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Sequence 386

BP; 50 A;

88 C;

138 G;

110 T;

0 other;

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seq_documentation_block:
ID AAI10775 standard; ENA; 436 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA2001.DAT:AAI10775
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Align seg 1/1 to reverse of: AAF65986 from: 1 to: 386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-668-119-3 x AAF65986/rev
           04-FEB-2000; 2000US-)180312.
26-MAY-2000; 2000US-)207446.
30-JUN-2000; 2000US-)08408.
03-AUG-2000; 2000US-)632366.
21-SEP-2000; 2000US-)234667.
27-SEP-2000; 2000US-)234593.
04-OCT-2000; 2000GB-)024263.
                                                                                                                                                                                                                                                                                                                             Probe; human; microarray; gene expression; cervical epithelial cell; cervical cancer; ss.
                                                                                                                                                                                                                   09-AUG-2001
                                                                                                                                                                                                                                                      WO200157278-A2
                                                                                                                                                                        30-JAN-2001; 2001WO-JS00670.
                                                                                                                                                                                                                                                                                                                                                                                 Probe #708 for gene expression analysis in human cervical cell sample.
                                                                                                                                                                                                                                                                                                                                                                                                                         12-OCT-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                186 nGlnGlnGlnGlnGlrGlnHisLeuIleLysLeuHisHisGlnAsnGlnG 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             170 MetGlnGlnGlnPheClnAlaValValGlnGlnGlnGlnGlnLeuGlnGl 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       286 nAsnGlnProSerGlnLeuProProGlnSer 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              270 ThrGlnHisHisGlnFroProProGlnProGlnGlnProProValAlaGl 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        253 lnProProProSerGlnAlaLeuProGlnGlnLeuGlnGlnMetHisHis 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                169 GGCTTTGCAGGCCCACCCACCAATTCAGCAGCCTCCGATGCAGCAGCCAC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   236 nAlaLeuGluAlaGlrProProIleGlnGlnProProMetGlnGlnProG 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         220 LeuGlnGlnGlnGlnClnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGl 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              319 GCAGCAGCAGCAGCATTTAATTAAATTGCATCAACAATCAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       369 ATGCAGCAGCAGTTCCTAGCAGTAGTGCAGCAGCAGCACTAGCTCAGCTA 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     269 ACCAGATACAGCAGCAGCTAGCAGCTGCAGCGAATAGCACAGCTGCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        203 lnGlnIleGlnGlnGlnGlnGlnLeuGlnArgIleAlaGlnLeuGln 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19 GAAC.....CTCGTGCCGAATTCG 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACACAGCACCACCAGCCACCACCAGCCAGCAGCCTCCAGTTGCTCA 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AGCCTCCGCCCTCCCAGGCTCTGCCCCAGCAGCTGCAGCAGATGCATCAC 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Quality:
Ratio:
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4.788
92.913
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Percent Identity: 88.189
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              270
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seq_documentation_block:
ID AAI32033 standard; DNA; 436 BP
                                                                                                                                                                    seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA2001.DAT:AAI32033
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 alignment_scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-668-119-3 x AAI10775
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Percent Similarity:
                                                                                                                                                                                                                                                                                                                17-OCT-2001 (first entry)
                                                                                                                                                                                                                     396 ATTAAATTGCATCATCAAAATCAGCAACAGGTA 428
                                                                                                                                                                                                                                                 195 IleLysLeuHisHisGlnAsnGlnGlnGlnIle 205
                                                                                                                                                                                                                                                                                                                                                                                                                                   161 nGlnPheGlnAlaGlnGlnSerAlaMetGlnGlnGlnPheGlnAlaValV 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   145 GlnGlnGlnAlaAlaLeuGlnGlnGlnGlnGlnGlnGlnGlnGlnGl 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     196 AGCTCCAGCAGGTGGCGCTGCAGCAGCAGCAGCAGCAGCAGCAGCTTCCAG 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                128 lnLeuGlnGlnValAlaLeuGlnGlnGlnGlnGlnGlnGlnGlnDheGln 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention relates to human single exon nucleic acid probes (SENP). The present sequence is one such probe. The SENPs are derived from human Hela cells. The SENPs can be used to produce a single exon microarray, which can be used for measuring human gene expression in a sample derived from human cervical epithelial cells. By measuring gene expression, the probes are therefore useful in grading and/or staging of diseases of the cervix, notably cervical cancer. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                             296 GCAGTTCCAGGCTCAGCAGAGTGCCATGCAGCAGCAGTTCCAAGCAGTAG 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          246 CAGCAGCAGCAGCGCGCGCTACAGCAGCAGCAGCAGCAGCAACAGCA 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  168 .....GACTCTGGTCTTTTCTCAGCCCAGCTGC 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                111 aProHisSerMetAlaValValSerThrAlaThrProGlnThrGlnLeuG 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 436 BP; 105 A; 127 C; 117 G; 87 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 25; SEQ ID No 708; 487pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human cervical epithelial cells -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-488901/53.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     95 GlnProMetSerLeuSerGlyGlnProProFroGlyThrSerGlyMetAl 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             413.50
4.307
86.486
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Percent Identity: 78.378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length:
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Probe #719 used to measure gene expression in human placenta sample

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S \overset{\times}{\times} C \overset{\circ}{\times} C \overset{\circ}{\times} C \overset{\circ}{\times} C \overset{\circ}{\times} \overset{
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        alignment_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Align seg 1/1 to: AAI32033
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26-MAY-2000;
30-JUN-2000;
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genetic disorder; ss.
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2000US-0608408.
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alignment\_block: US-09-668-119-3 x AAI00701

Percent Similarity:

Quality:

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Identity: 78.378

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                                                                                                                                                                                                                                                       The present invention relates to novel single exon nucleic acid probes. The present sequence is one such probe. The probes are useful for measuring human gene expression in a human breast sample, where the probe hybridises at high stringency to a nucleic acid expressed in the human breast. The probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human breast, particularly those diseases with polygenic aetiology. The diseases include: breast cancer, disorders of development, inflammatory diseases of the human treatment of the human treatme
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                                                                                                                                                                                                               of the breast, fibrocystic changes, proliferative breast disease and non-carcinoma tumours.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 25; SEQ ID No 692; 322pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel
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                                                                           Sequence 436 BP; 105 A; 127
                                                                                                                                    at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                          Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
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26-MAY-2000; 2000US-0207456.
30-JUN-2000; 2000US-0688408.
03-AUG-2000; 2000US-0632366.
21-SEP-2000; 2000US-0234687.
27-SEP-2000; 2000US-0234687.
04-OCT-2000; 2000GB-0024263.
The present invention relates to human single exon nucleic acid probes (SENP). The present sequence is one such probe. The SENPs are derived from human HeLa cells. The SENPs can be used to produce a single exon microarray, which can be used for measuring human gene expression in a
                                                                                                                                                                  Claim 25; SEQ ID No 9950; 487pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Probe; human; microarray; gene expression; cervical epithelial cell;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Probe #9950 for gene expression analysis in human cervical cell sample
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAI20017;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     396 ATTAAATTGCATCAACAATCAGCAACAGGTA 428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          195 IleLysLeuHisHisGlnAsnGlnGlnGlnIle 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              178 alGlnGlnGlnGlnLeuGlnGlnGlnGlnGlnGlnGlnHisLeu 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     161 nGlnPheGlnAlaGlnGlnSerAlaMetGlnGlnGlnPheGlnAlaValV 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             128 lnLeuGlnGlnValA..aLeuGlnGlnGlnGlnGlnGlnGlnGlnGlnPheGln 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12-OCT-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAI20017 standard; ENA; 316 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             296 GCAGTTCCAGGCTCACCAGAGTGCCATGCAGCAGCAGTTCCAAGCAGTAG 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              246 CAGCAGCAGCAGCGCICGCTACAGCAGCAGCAGCAGCAGCAGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               145 GlnGlnGlnAlailaLeuGlnGlnGlnGlnGlnGlnGlnGlnGlnGl 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               196 AGCTCCAGCAGGTGGCGCTGCAGCAGCAGCAGCAGCAGCAGTTCCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             111 aProHisSerMetAlaValValSerThrAlaThrProGlnThrGlnLeuG 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       95 GlnProMetSerLeuserGlyGlnProProProGlyThrSerGlyMetAl 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ························GACTCTGGTCTTTTCTCAGCCCAGCTGC
                                                                                                                                                                                                                         genome-derived single exon nucleic acid probes useful zing gene expression in human cervical epithelial cells
                                                                                                                                                                                                                                                                                                                                                                                                Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                            Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                Rank DR;
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seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA2001.DAT:AAI45215
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                                                                                                         04-FEB-2000;
26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
Penn SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              203 GCATCTAATTAAATTGCATCAACAAATCAGCAACAGGTA 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      126 GlnLeuGlnLeuGlnGlnValAlaLeuGlnGlnGlnGlnGlnGlnGlnGl 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sample derived from human cervical epithelial cells. By measuring gene expression, the probes are therefore useful in grading and/or staging of diseases of the cervix, notably cervical cancer. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                  (MOLE-) MOLECULAR DYNAMICS INC.
                                                                       04-OCT-2000;
                                                                                                                                                                                                                                                         09-AUG-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                        Probe #13901 used to measure gene expression in human placenta sample.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               17-OCT-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          153 GCAGTAGTGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            176 AlaValValGlnGlnGlnGlnGlnLeuGlnGlnGlnGlnGlnGlnGl 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            142 nPheGlnGlnGlnGlnAlaAlaLeuGlnGlnGlnGlnGlnGlnGlnG 159
                                                                                                                                                                                                                       30-JAN-2001; 2001WO-US00663
                                                                                                                                                                                                                                                                                                WO200157272-A2
                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                         genetic disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                        Probe; microarray; human; placenta; antenatal diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAI45215;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAI45215 standard; DNA; 316 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       192 nHisLeuIleLysLeuHisHisGlnAsnGlnGlnGlnIle 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   103 AACAGCAGCAGTTCCAGGCTCAGCAGTGCCATGCAGCAGCAGTTCCAA 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     159 lnGlnGlnPheGlnAlaGlnGlnSerAlaMetGlnGlnPheGln 175
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 CAGCTGCAGCTCCAGCAGGTGGCGCTGCAGCAGCAGCAGCAGCAGCAGCA 52
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Hanzel DK,
                                                                  ; 2000US-0180312.
2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-0236359.
2000US-0236359.
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4.912
Chen W,
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Rank DR;
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seq_name:
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  04-FEB-2000; 2000US-0180312.
26-MAY-2000; 2000US-0207456.
30-JUN-2000; 2000US-068408.
03-AUG-2000; 2000US-0632366.
                                                                                                                                                                                                                                                                                                                                                                                                                                     176 AlaValValGlnGlnGlnGlnGlnLeuGlnGlnGlnGlnGlnGlnGlnGlnGl 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention relates to single exon nucleic acid probes (SENP). The present sequence is one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of human genetic disorders.
                                                                                                                                                                            Probe; human; breast disease; breast cancer; development disorder; inflammatory disease; proliferative breast disease; non-carcinoma t
                                                                                                                                                                                                                    Probe #5716 used to measure gene expression
                                                                                                                                                                                                                                                                                                                                                                  153
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           159 lnGlnGlnGlnPheGlnAlaGlnSerAlaMetGlnGlnGlnPheGln 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 25; SEQ ID No 13901; 654pp; English.
                                                                   29-JAN-2001; 2001WO-US00661
                                                                                                                                                                                                                                                                                                    AAI05725 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            analyzing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 316 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 CAGCTGCAGCTCCAGCAGGTGGCGCTGCAGCAGCAGCAGCAGCAGCAGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AACAGCAGCAGTTCCAGGCTCAGCAGTGCCATGCAGCAGCAGTTCCAA
                                                                                                                                                                                                                                                                                                                                                                                                                       GCAGTAGTGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2001-488897/53
                                                                                                                                                                                                                                                                                                                                        /SIDS2/gcgdata/geneseq/geneseqn/NA2001.DAT:AAI05725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        genome-derived single exon nucleic acid probes useful for zing gene expression in human placenta -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Quality:
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                                                                                                                                                                                                                                              (first entry)
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4.912
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Gaps:
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0
98.750
                                                                                                                                                                                                                  in human breast sample
                                                                                                                                                                            non-carcinoma tumour
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 102
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seq_documentation_block:
ID          AAV29009 standard:
XEXTX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       alignment_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Align seg 1/1 to: AAI05725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-668-119-3 x AAI05725
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27-SEP-2000;
04-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention relates to novel single exon nucleic acid probes. The present sequence is one such probe. The probes are useful for measuring human gene expression in a human breast sample, where the prob hybridises at high stringency to a nucleic acid expressed in the human breast. The probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human breast, particularly those diseases with polygenic actiology. The diseases include: breast cancer, disorders of development, inflammatory diseases of the breast, fibrocystic changes, proliferative breast disease and
                                                                                                                                                                                                                                                  153
                                                                                                                                                                                                                                                                                   176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         non-carcinoma tumours.

Note: The sequence data for this patent did not form specification, but was obtained in electronic format
                                                                                                                                                                                      203
                                                                                                                                                                                                                     192
                                                                                                                                                                                                                                                                                                                 103
                                                                                                                                                                                                                                                                                                                                              159
                                                                                                                                                                                                                                                                                                                                                                                                         142 nPheGlnGlnGlnGlnAlaAlaLeuGlnGlnGlnGlnGlnGlnGlnG
                                                                                                                                                                                                                                                                                                                                                                                                                                                           126 GlnLeuGlnLeuGlnGlnValAlaLeuGlnGlnGlnGlnGlnGlnGlnGlnGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 25; SEQ ID No 5716; 322pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel single exon nucleic acid in a human breast -
                                          28-AUG-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (MOLE-)
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                                                                                                                                                                                                                                                                                                                                                                                                                                          3 CAGCTGCAGCTCCAGCAGGTGGCGCTGCAGCAGCAGCAGCAGCAGCA
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                                                                                                                                                                                      GCATCTAATTAAATTGCATCAAAAATCAGCAACAGGTA
                                                                                                                                                                                                                   nHisLeuIleLysLeuHisHisGlnAsnGlnGlnGlnIle 205
                                                                                                                                                                                                                                                                                                                                GCAGTAGTGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCA
                                                                                                                                                                                                                                                                                  AlaValValGlnGlnGlnGlnGlnLeuGlnGlnGlnGlnGlnGlnGlnGlnGl
                                                                                                                                                                                                                                                                                                                 AACAGCAGCAGTTCCAGGCTCAGCAGAGTGCCATGCAGCAGCAGTTCCAA
                                                                                                                                                                                                                                                                                                                                                                              GTTCCAGCAGCAGCAGCAGCGGCGCGCTACAGCAGCAGCAGCAGCAGCAGC
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2000US-0236359.
2000GB-0024263.
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4.912
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                                                                                                         cDNA; 3879
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C; 87
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                44 T; 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               to measuring
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   80
0
98.750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                other;
                                                                                                                                                                                      242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ot form part of the printed format directly from WIPO
                                                                                                                                                                                                                                                                                  192
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                                                                                                                                                                                                                                                                                                                                                                                                           159
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Human polyhomeotic 1 (hph1) oncogene

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Criticology of this polynucleotide comprises a novel human oncogene termed complynomeotic 1 (hphl) that is implicated in neoplastic disorders. Criticology for a 1004-amino acid polypeptide (see ANM37856). The gene critical polypeptide consisting of at least 22 contiguous amino acids; (2) an hphl fusion protein; (3) antibodies which specifically bind to a composition of hphl protein; (3) antibodies which specifically bind to a composition of hphl protein; (5) a homologously recombinant cell having care and (c) a splice donor site, where the TUI is located cupstream to a coding sequence of an hphl gene, where the exogenous cregulatory sequence; (b) an exogenous cregulatory sequence; (b) an exogenous cregulatory sequence; (b) an exogenous cregulatory sequence of an hphl gene, where the exogenous cregulatory sequence of an hphl gene, where the exogenous cregulatory sequence of an hphl gene, where the exogenous cregulatory sequence of an hphl gene with the coding sequence of the hphl gene, where the exogenous creaming neoplastic; (7) a method of identifying neoplastic tissue of a being neoplastic; (7) a method to aid in the diagnosis or mRNA, creaming the expression of the hphl gene indicates neoplasia creaming the products can also be used to inhibit hphl expression to choose the expression to hopping the expression to the products can also be used to inhibit hphl expression to conspirate the expression can have retodermal dysplasia, congenital alveolar dysplasia, epithelial dysplasia of the cervix, fibrous dysplasia of bone, or mammary dysplasia or consumers. Similarly, in tumours where hphl expression is not these disorders, decreasing hphl expression can help to suppress considering hphl down-regulation can suppress metastases. Can hisense polynuclectides can also be used to induce differentiation of conferentiation and test compounds which affect this process.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 7; Page 25-27; 39pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Isolated human poly:omeotic 1 oncogene - used to develop products for diagnosis and therapy of proliferative and developmental disorders, e.g. neoplasia, dysplasia or hyperplasia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO9807860-A1
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Sequence 3879 BP; 967 A; 1108 C; 954 G; 850 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      06-FEB-1997;
23-AUG-1996;
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alignment_scores:
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Ratio: 1.367
Percent Similarity: 53.422
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-668-119-3 x AAV29009
                                                                                                                                                                  1423 ...CCCATGCTTCAGTCTTCACCCTTGTCTTCCACCTGATGCAGCCCCT 1470
                                                                                                                                                                                                                                                                                                                                         1395 GCAGCAAGCCCAAACCCTGGTCGTTCAG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1316 AGCCGCAAGCCACCACCTCACTGCCCCTCAGCCACCACAGGTCCCACCT 1365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1172 AACAGGTGGTGATCCAGCAGCAGCATTGCCATCCACCAC.....CAGCAG 1215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1122 CCAGCCCCATTCACTGATTCAGCAACAGCAACAGATCCACCTCCAGCAGA 1171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1072 ACACCTGCGCCCAGCCAGACACTTATTAGCTCAGCCACCTACACACAGAT 1121
1471 AAGCCACCAATTCCC.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1216 CAGTTCCAGCACCGGCAGTCCCAGCTCCTTCACACAGCTACACCCTCCA 1265
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   172 nGlnPheGlnAlaValValGlnGlnGlnGlnGlnLeuGlnGlnGlnGlnG 189
                                                                            299 GlnProLeuValSerGlnAlaGlnAlaLeuProGlyGlnMetLeuTyrTh 315
                                                                                                                                                                                                                                              282 roProValAlaGlnAsnGlnProSerGlnLeuProProGlnSerGlnThr 298
                                                                                                                                                                                                                                                                                                                                                                                                                265 nGlnMetHisHisThrGlnHisHisGlnProProProGlnProGlnGlnP 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             249 MetGlnGlnProGlnProProSerGlnAlaLeuProGlnGlnLeuGl 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                236 ln...........AlaLeuGluAlaGlnProProIleGlnGlnProPro 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      204 GlnIleGlnGlnGlnGlnGlnLeuGlnArgIleAla...GlnLeuGl 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            189 lnGlnGln.....GlnHisLeuIleLysLeuHisHisGlnAsnGlnGln 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            156 GlnGlnGlnGlnGlnGlnPheGlnAlaGlnGlnSerAlaMetGlnGl 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              139 lnGlnGlnFheGlnGlnGlnGlnAlaAlaLeuGlnGlnGlnGln 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    972 CCAGGGCAGCCAGACAGAGGCAGAAAGTGCAGCAGCAGAAGGCAGAAG 1021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           122 rProGlnThrGlnLeuGlnLeuGlnGlnValAlaLeuGlnGlnGlnGlnG 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 922 GGTACAGGAGTGGTGCAGCCCTTGCCTGCAGCCCAAACAGTGACTGTGAG 971
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         106 GlyThrSerGlyMetAlaProHisSerMetAlaValValSerThrAlaTh 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               878 AGTTGCCTTCCTCAGGA.....ATGGGTGGTGGGAGCTGTCCCAGGAAG 921
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     828 AGGGTCCATGGGTCCAGGTGGAGGTGGGCAGGCACATGGTGGTTTGGGTC 877
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   778 CAGTCCCTCAACCTTAGTCAAGCTGGTGGAGGCAGTGGGAATAGCATCCC 827
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                89 erPheGlyAlaMetGlyGlnProMetSerLeuSerGlyGlnProProPro 105
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             76 o.....ProArgGlyProGlyGlnSerLeuGlyGlyMetGlyS 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Percent Identity: 28.707
Length:
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seq_documentation_block:
ID AAV21060 standard;
                                                                                                                                                                                                                                seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA1998.DAT:AAV21060
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   09-JUL-1998
                                                                 AAV21060;
                                                                                                                                                                                                                                                                                                                                                                                                                               CCTACACTAGCCATGGTGT.....CTAGACAAATGGGTGACTCAAA 2168
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AlaArgThrProGlnAsnPheSerValProSerProGlyProLeuAsnTh 445
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                                                                                                                                                                                                                                                                                                                                                                etArgCysProLeuProHisArgPro 541
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                                                                                                                                                                                                                                                                                                  .....CCCCACAGGCCA 2182
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(first entry)
                                                                                                                                   cDNA; 3879 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1637
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SXCCCCCCCCCCCCXXXXXIII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  06-FEB-1997;
23-AUG-1996;
04-DEC-1996;
                           gene identifies the subject as having neoplastic tissue. The hph1 oncogene functions to suppress neoplasia and dysplastic or hyperplastic cell growth as well as to induce cellular differentiation. The cDNA, protein and vectors can be used as diagnostic and therapeutic tools for proliferative and developmental disorders and to identify a pl3 region of a human chromosome 12. They can be used for the detection, diagnosis or prognosis of neoplasia or for detecting a genetic predisposition to neoplasia. They can also be used to treat tumours.
                                                                                                                                                                        The present sequence encodes a novel human tumour suppressor gene termed polyhomeotic 1 (hphl). The hphl gene maps to human chromosome 12pl3, a region which is frequently lost in non-small cell lung cancer and breast cancer. A method of identifying neoplastic tissue of a human comprises comparing the expression of a hphl gene in a tissue of being neoplastic with the expression of a hphl gene in a tissue of the human which is normal. Under-expression of the hphl
                                                                                                                                                                                                                                                                                                                                                 Isolated human poly:homeotic 1 oncogene - used to develop products for diagnosis and therapy of proliferative and developmental disorders, e.g. neoplasia, dysplasia or hyperplasia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tumour suppressor gene; identification; neoplast
                                                                                                                                                                                                                                                                                                                    Claim 5; Pages 25-27; 40pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            W09807858-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    neoplasia; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cDNA encoding the a tumour suppressor gene called polyhomeotic
Sequence 3879 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                             P-PSDB; AAW52830.
                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1998-169162/15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (CHIR ) CHIRON CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26-FEB-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  96US-0024349
96US-0031569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     97US-0036939
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        97WO-US14866
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     or gene; polyhomeotic 1; hph1; human chromosome 12p13; neoplastic tissue; cellular differentiation; diagnosi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /*tag=
965 A; 1108 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ۵ı
954 G; 850 T; 2 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        diagnosis;
                                                                                                                                                                                                gene
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alignment_block:
                                                                                                                                                                                                                                                                                                      alignment_scores:
                                                                                                                                                  Align seg 1/1 to: AAV21060
                                                                                                                                                                                       US-09-668-119-3 x AAV21060
                                                                                                                                                                                                                                               Percent Similarity:
                                                                         778 CAGTCCCTCAACCTTAGTCAAGCTGGTGGAGGCAGTGGGAATAGCATCCC
828 AGGGTCCATGGGTCCAGGTGGAGGTGGCAGGCACATGGTGGTTTGGGTC
                                 76 o.....ProArgGlyProGlyGlnSerLeuGlyGlyMetGlyS
                                                                                                            60 GlnSerLeuThrGlyGlyProAlaAlaGlyAlaAlaGlyIleGlyMetPr 76
                                                                                                                                                                                                                                                                                  Quality:
                                                                                                                                                                                                                                                                  Ratio:
                                                                                                                                                                                                                                               384.00
1.367
53.422
                                                                                                                                                    from:
                                                                                                                                                                                                                                                   Percent Identity:
                                                                                                                                                    to: 3879
                                                                                                                                                                                                                                               526
23
28.707
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89 87

391	$In {\tt ValGlnThrProGlnSerMetProProProProGlnProSerProGln}: \\$	375
1659	ACAGCTGGCAGCTGTACCT	538
375	erSerLeuP	358
358 1637	ThrAlaValGlnThrAlaGlnAlaAlaGlnMetValAlaProGlyValGl	342 588
341 1587	TGTCAGCTGCCCAGC#ACCACCACCCCATATCCCTGTGCAAGTT	328 544
327 1543	rGlnProProLeuLysPheValArgAlaProMetVal	315 494
315 1493	GlnProLeuValSerc.lnAlaGlnAlaLeuProGlyGlnMetLeuTyrTh:::   ::: :: :: :: :: :: :: :: :: :: ::	299 471
298 1470	H D	
282 1422	nGlnMetHisHisThrGlnHisHisGlnProProProGlnProGlnGlnP     :: :::    GCAGCAAGCCCAAACCCTGGTCGTTCAG	265 395
265 1394	MetGlnGlnProGlnFroProProSerGlnAlaLeuProGlnGlnLeuGl 	249 366
248 1365	lnAlaLeuGluAlaGlnProProIleGlnGlnProPro	236 316
236 1315	nLeuGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnG	219 266
219 1265	GlnIleGlnGlnGlnGlnGlnLeuGlnArgIleAlaGlnLeuGl 	20 <b>4</b> 216
203 1215	GnHisLeuIle    :::      ATCC/.GCAGCAGATT	189 172
189 1171	nGInPheGlnAlaVa:ValGlnGlnGlnGlnGlnGlnLeuglnGlnGlnGlnGllGllGlll :::::::	172 122
172 1121	GlnGlnGlnGlnGlnGlnFheGlnAlaGlnGlnSerAlaMetGlnGl :::	156 072
155 107]	InGlnglnGlnPheG:.nGlnGlnGlnGlnAlaAlaLeuGlnGlnGlnGln :::	139 022
139 102	rProGlnThrGlnLeuGlnLeuGlnGlnValAlaLeuGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnG	122 972
122 971	GlyThrSerGlyMetAlaProHisSerMetAlaValValSerThrAlaTh	106 922
105 921	erPheGlyAlaMetG.LyGlnProMetSerLeuSerGlyGlnProProPro ::::::::::::::::::::::::::::::	878

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DR	XX	PR	X P F	× B	×Z	× S	XX	X E	X D	X A	seq_	seq_																	
WPI;	(MIK	15-Ј	28-M	31-M	JP10	Pinc	Pinc	New	28-Л	AAV2	docume AAV22	name:	533 2169	2128	517	507 2081	495 2031	1981	479	462 1931	445 1890	1849	429	1799	425	408 1749	1699	392	1660
1998-2544	I-) MIKIMOTO	JUL-1996;	MAY-1997;	MAR-1998.	0080285-A.	tada fucat	tada fucat	DNA sequence	JUL-1998 (f	2682;	ntation 682 sta	/SIDS2/gc	etArgCysPr AC	CCTACACTAG	LysThrLeuGlnLys.	CAAGCAGTGA	sAspLeu ::::    CAGTCTTGGA	GCCAAAGCATCTCCAGTAGCAGAAAGCCCCAAAAGTC	ProLeuArgA	luGluGlnGl ::::::::: ACTCTGAGGA	rProValAsnProS     :::   :  CCCGGGTAAACCCC	GCCCAGGTCCCTGCTGCCTTCTATATGC	AlaArgThrF	GGACAGCACA		aProSerPro	GCCCATTTGG	ProGlyGlnF	AC
10/23.	TO SEIYAKU	96JP-0184	97JP-0138			ù.	.a; proteir	isolat	irst ent		_block: indard; DNA;	gdata/gene	gCysProLeuProHis        CCCCAC	AGCCATGGTGT.	inLys.CysG	ACTAGTAGC	Ser GAA	CTCCAGTAG	rgMetIleA:	.nTyrLeuAsj :     :GGAGAGAGA	rose	CTGCTGCCT	roGlnAsnP	TGTGGTAAA		SerProSerSerPheLeuProSe	SCCTCCTCGC	yGlnProSerSerG	TTCCCGGGG
	J KK.	1459.	3461.				n; cosmetic	ed from Pi	ry)		2214 BP.	seq/genes	ArgPro 54        AGGCCA 21		GluIleAlaLeuGluLy	As	LysMetLysSerLeuLeuAs     :::   :::  AAAGCTGAATCAGTGGCTAA	::: CAGAAAGCCC	${\tt roLeuArgArgMetIleAsnLysIleAs}$	luGluGlnGlnTyrLeuAspLysLeuLys :::::::    crcrgaggaggagagagagatgatgtctcc	MetSer	TCTATATGCA	heSerValPr	н.		LeuProSerProSer    ::: GCCCCTGGGATGACC	CACCTTCATC	lnProAsnSe	
							c; ds.	inctada fuc				eqn/NA1998	1 82	AGACA	euGluLysLe	pProSerLysAr	pile :::: TGTGAA	 AAAAGTCATG	рLysAsnGluAspArgLy	GlnLeuSerLy    :::::     ACATTGGGTTC	ProAlaGlySer	AGTCT	roSerProGly	ACCACCTCCT	a	Pr	CCATTTGGCCTCGTCGCCACCTTCATCCCAGGCTCCTGGTGC	erGlnProAsnSerAsnValSerSerGly	  ACAGTGCAG
								ucata.				.DAT:AAV226		AATGGGTGACTCAAA	sLeuLysAsnAspM	LysArgCysProLeu     CCTTCAGTACCGCCT	TGCTAATACTC	:::   ::: ATGGACGAGAAGAG	- to	luGluGlnGlnTyrLeuAspLysLeuLysGlnLeuSerLysTyrIleGlu ::::::::	AlaGlySerSerGlnAlaG     ::: ::   :     :::	GTGCACTT	oGlyProLeuAsnTh	CTCCTCACCTGTTGTA	erprovalmhr	OGInProSerGin.	GGTGCACTGCA	SerGlyProAl	
												82		2168	533	516 2127	2080	2030	495	1980	1930	1889	445	18	428	424 1791	174	408	169

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179 .GlnGlnGlnGlnGlnLeuGlnGlnGlnGlnGlnGlnGlnGln.	1138 TAATGTCTCCTAATGCGTCCCTTAT	178	1188 TGCTTTAGCAGAGGC	178	167 .GlnSeralaMetGlnGlnClnPheGlnAlaValVal ::: :::::      ::: ::: 1238 AAGACATCCTTCAAATCGTCAATTTGAGATTTTGTGC	133 GINGINGINGINGINGINGINGINGINGINGINGINGING	8 8 ACCI	137 nGlnGlnGlnGlnGlnPheGlnGlnGl ::::       :::::    :: 1388 AGAGCAGCTAGAGCTCCAGCTCCA	121 laThrPro.GlnThrGlnLeuGlnLeuGlnGlnValAlaLeuGlnGlnGl          :: ::      :::   1438 CTCCGCCTCCGCCTCCAAGTCCACCTCCGGCTCCTGCAGCAGCG	104 oProGlyThrSerGlyMetAlaProF 	88 GlySerPheGlyAlaMetGlyGlnProMetS :::   1   1   1502AGTCCTCCA	71 laGlyIleGlyMetProProArgGlyProG	60 nSerLeuThrGlyGlyPro	50 AlaSerValSerAspPro	Align seg 1/1 to reverse of: AAV22	us-09-668-119-3 x AAV22682/rev .	alignment_scores: Quality: 381.50 Ratio: 1.408 Percent Similarity: 45.394 Perc	SQ Sequence 2214 BP; 393 A; 451 C	The present sequence represer fucata. The polypeptide be us	Claim 1	XX PT New cDNA and e.g. vector, host of produce polypeptide in high yie.
GlnGlnGlnGlnGlnGln    :::   :::   :::  CAGCGGCAGCACCAGCGCCTCCGCC	ACCACTCATTTGTCTAGAAGCTGAA		TCCATTACTCCTGE		TTGCTACTGCTGA	ACCTGCAAGATCCTTT	aAlaLeuGlnGlnGln    :::   :::  GAAGCTGATGCAGATG	ngln :::: :ccgccgccrccrccrccgracc		AlaproHisSerMetAlaValValSerThrA         CACCAGCAGCAGCTAGTGCAGCGGCTAAAG	SerLeuSerGlyGlnProPr     	lyGlnSerLeuGlyGlyMet	AlaAlaGlyAlaA      :::     AGCAGCGGCAGCGGCTGCAGCAG	rj L	22682 from: 1 to: 2214	•	Length: 597 Gaps: 25 ent Identity: 25.628	; 891 G; 479 T; 0 other;	its a new DNA sequence isola ed as an ingredient in cosm	e.	cell and polypeptide .
192 1039	1089	178	1139	178	178 1189	1239	i io o	147 1339	137 1389	121 1439	104 1474	87 1503	71 1532	60 1582					ated from Pinctad		used to cosmetics

	GTCGTCATCATAGTCATATTCCCAAT	321
470	diskidastro-ladiacijus in Sulastro-lastro-da da d	л
454 322	ProSerProGlyProLeuAsnThrProValAsnProSerSerValMetSe    :::	438 371
372	InProSerGinSerProValThrAlaArgThrProGinAsnPheSerVal    ::: ::   :::     :::    CTCCTGCGCCTGCTCCAGCACCAGCACCAGCACCACCTCCGGCACCACCA	421 421
N	cccaarccaagrccgagrcaagcaccrgcrccr	- 51
421	roAlaProSerProSerSerPheLeuProSerProSerPr	404
404 456	ProSerProGlnProGlyGlnProSerSerGlnProAsnSerAsnValSe	388 479
480	ATAAATCGTCTCCACCGCCAAGTCCGCCAAGACCTCCAAGTCCG	529
387	yGlnGlnValGlnThrProGlnSerMetProProProProGln	372
530	Ď	576
372	GlyValGlnValSerGlnSerSerLeuProMetLeuSerSerProSerP	355
7	INGLIFICAÇÃO AND	620
ω 55	lncincinmhralaValcinmhralacinalaalacinMetValalaPr	u
338 621	alArgAlaProMetValValGlnGlnProProValGlnProGlnValGln:::     :::      :::         :::     :::	322 667
899	GCAGCAGCAGCTCCTCCAAGTCTACCTGCGCCTCCTCCTGCAGCGGCAG	717
322	euProGlyGlnMetLeuTyrThrGlnProProLeuLysPheV	305
718		746
305	ProGlnSerGlnThrGlnProLeuValSerGlnAl	289
747	AGTCCGCCACCGAGTCCTCCAAGTCCACCTGCG	779
288	nProProProGlnProGlnGlnProProValAlaGlnAsnGln	272
780	CCTCCA	792
272	ProSerGlnAlaLeuProGlnGlnLeuGlnGlnMetHisHisThrGlnH	255
793	::	ω
255	${\tt luAlaGlnProProIleGlnGlnProProMetGlnGlnProGlnProPr}$	239
839	:::::            :::	888
238	lnGlnGlnGlnGlnGlnGlnGlnGlnGlnAlaLeu	225
889	: : :	938
224	ArgIleAlaGlnLeuGlnLeuGlnGlnGln	213
ū		80
213	lnTleGlnGlnGlnGlnGlnLeuGl	_
203 989	TCCTCCTCCACCTCCACCACCACCACCACCACCACCACCA	193 1038
)		•

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PR 15-JUL-1996; 96JP-0184459.

XX PA (MIKI-) MIKIMOTO SEIYAKU KK.

XX P-SCDB; AAW56163.

XX PT New cDNA and e.g. vector, host cell and polypeptide - used produce polypeptide in high yields, which is used in cosmet yellow the produce polypeptide in high yields, which is used in cosmet XX PS Claim 2; Pages 7-9; 15pp; Japanese.

XX PS Claim 2; Pages 7-9; 15pp; Japanese.

XX PS Claim 2; Pages 7-9; 15pp; Japanese.

XX Sequence 3331 BP; 762 A; 701 C; 1022 G; 846 T; 0 other;
                                                                                                              alignment_scores:
Quality: 381.50
Ratio: 1.408
Percent'similarity: 45.394
                                               alignment_block:
U$-09-668-119-3 x AAV22683/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         seq_documentation_block:
D AAVZ2683 standard; cDNA to mRNA; 3331 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             seq_name://SIDS2/gcgdata/geneseq/geneseqn/NA1998.DAT:AAV22683
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              271 CACCGC...... 251
ign seg 1/1 to reverse of: AAV22683 from: 1 to: 3331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  487 eAspLysAsnGluAspArgLysLysAspLeuSerLysMetLysSerLeuL 504
                                                                                                                                                                                                                                                                                                       The present sequence represents a new DNA sequence isolated from Pinctada fucata. The encoded polypeptide be used as an ingredient in cosmetics.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 173 GCCGAAACGCAACCACATGCCCATGGATCATAAACCA 137
                                                                                                                                                                                                                                                                                                                                                                                                                         New cDNA and e.g. vector, host cell and polypeptide - used to produce polypeptide in high yields, which is used in cosmetics {\sf polypeptide} in high yields, which is used in cosmetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31-MAR-1998.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          JP10080285-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pinctada fucata.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pinctada fucata; protein; cosmetic; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New DNA sequence is lated from Pinctada fucata.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  537 uPro......HisArgProArgCysHisArgPro 546
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              521 ysCysGluIleAlal.euGluLysLeuLysAsnAspMetArgCysProLe 537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28-MAY-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28-Jul-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAV22683;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     240 PCCAGCACCGCCAGCCCCAGGCGCCCCCCCCCCCGACAC..... 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               504 euAspIleLeuThrAspProSerLysArgCysProLeuLysThrLeuGln 520
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          97JP-0138461.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers 50..2266
                                                                                                              Gaps: 25
Percent Identity: 25.628
                                                                                                                                                                     Length:
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272	5 oProSerGlnAlaLeuProGlnGlnLeuGlnGlnMetHisHisThrGlnH	255
	:::	88 8
л	Glualadin BroproTiedindin BroproMetdindin Brogin Brobr	
238 888	GlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnG	225 937
938	CCGCGTCTACCTCCTCGTCCACCGTAGAAACCAACACCACCGAGTCCTCC	987
ن د	nArgIleAlaglnIenglnIenglnglnglngln	213
213	GlnIleGlnGlnGlnGlnGlnGlnLeuGl	20 <b>4</b> 1037
1038	TCCTCCTCCACCACCTCCACCTCCTCCGCCACCACCAGCGGCTGCGGCGG	1087
203	hisLeuIleLysLeuHisHisGlnAsnGlnGln	193
192	.Gingingingingingingingingingingingingingi	179 1137
	TAATGTCTCCTAATGCGTCCCTTATACCACTCATTTGTCTAGAAGCTGAA	1187
178	78	178
1188	7 TGCTTTAGCAGAGGCTTTTGCAGAGGCTCCATTACTCCTGAGAAGGTCTT	123
178	8	17
1238	AAGACATCCTTCAAATCGTCAATTTGAGATTTTGTGCT	1287
178	7 .GlnSerAlaMetGlnGlnGlnPheGln	16
166 1288	55 GlnGlnGlnGlnGlnGlnGlnPheGlnAlaGln	133
1338	7 ACCTCCGTTACCACCACCGCCTCCACCTC	138
154		148
147 138	77 nglnglnglnglnglnpheglnglnglngln	137 1437
137 1431	laThrPro.Gl	121 1487
148	J4 OFFIGELYTHISETGLYMECHLIAPTOHISSETMECHIAVALVALVALSETTNIA      ::: ::::::::	1522
o on	AG	155
104	8 GlySerPheGlyAlaMetGlyGlnProMetSerLeuSerGlyGlnProP	8
155	1 IaGLYILeGLYMetProProArgGLYProGlyGLnSerLeuGlyGLyMet	158
158	   AAGTGCTCTTCCTCCACCACCTGATGCAGCAGCC	163
	nSerLeuThrGlvGlvProAlaAlaGlv	
163	50 AlaSerValSerAspPro	168

name:\frac{1}{SIDS2/gcgdata/geneseq/geneseqn/NA1999.DAT:AAZ32021	<b>'</b> 5
ProHisArgProArgCysHisArgPr	
#45	
ysCysGluIleAlaLeuGluLysLeuLysAsnAspMetArgCysPro	
89 TCCAGCACCGCCAGCTCCCCAGGCGCCTCCGCCCCCTCCG	
04 euAspIleLeuThrAspProSerLysArgCysProLeuLy	
99	
87 eAspLysAsnGluAspArgLysLysAspLeuSerLysMetLysSerLeu	
20 CACCGC	
luProLeuArgArgMetIleAs	
454 PPOALAGLYSERSER.GLIAALAGLIGGLIGGLIGYTLEMASPLYSLEU 4/0 454 PPOALAGLYSERSER.GLIAALAGLIGGLIGGLIGYTLEMASPLYSLEU 4/0 454 PPOALAGLYSERSER.GLIAALAGLIGGLIGGLIGGLIGGLIGGLIGGLIGGLIGG	
O CCAGCACCACCTCCGGCGCCAGCTCCCATTCCACCGTCATCCATC	
rProGlyProLeuAsnThrProValAsnProSerSerValMetSe 4	_
TGCGCCTGCTCCAGCACCAGCACCAGCA	_
roSerGlnSerProValThrAlaArgThrPr	
CCCAATCCAAGTCCGAGTCCAGCACCTGCTCCTG	
OA TO TO THE TERMINATURE TO THE TERMINATURE TO THE TOTAL PROPERTY OF A PROPERTY OF THE TERMINATURE TO THE TH	
ProGInProG1yGinProSerSerGinProAsnSer 	
78 AATCAAATAAATCGTCTCCACCGCCAAGTCCGCCAAGACCTCCAAGTCCG 5	
lyGlnGlnValGlnThrProGlnSerMetProProProProGln 38	1.5
CACCAAGATCATCGAAATC	•
yValGlnValSerGlnSerSerLeuProMetLeuSerSe	1.3
669GCAGCAGCGGCAGCTGCAGCAGCAGCAGCACCTCCAGCTCC 626	~
hrAlaValGlnThrAlaGlnAlaAlaGlnMetValAlaP	1.1
716 CAGCGGCTGCGGCTGCGGCAGCTCCACCCACCCCCCGGCG 670	~1
largalaproMetValValGlnGlnProProValGlnPro	(4)
CIGCGCCTCCTCC	~1
lnAlaLeuProGlyGlnMetLeuTyrThrGlnPr	(4)
95	7
.89 ProSerGlnLeuProProGlnSerGlnThrGlnProLeuV	N
828AGTCCGCCACCGAGTCCTCCAAGTCCACCTGCG	œ
72 isHisGlnProProProGlnProGlnGlnProProVa	N
841 ACCGAGTCCTCCA 829	8

seq\_

alignment\_block: US-09-668-119-3 x AAZ32021/rev

Percent Similarity:

Percent Identity:

Align seg 1/1

to reverse of: AAZ32021

from: 1

to: 3331

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seq_documentation_block:
ID AAZ32021 standard; DNA; 3331 BP.
                                                       alignment_scores:
                                                                                                                                                             A ARZ32000 and ARZ32001 encode, and ARY49501 and ARY49502 represent, human metalloprotease thrombospondin (METH) proteins METH1 and METH2 CC respectively. METH1 and METH2 have been found to be potent inhibitors of crespectively. METH1 and METH2 have been found to be potent inhibitors of concer and other disorders related to angiogenesis including abnormal cc wound healing, inflammation, rheumatoid arthritis, psoriasis, condimetrial bleeding disorders, diabetic retinopathy, some forms of condimetrial bleeding disorders, diabetic retinopathy, some forms of conditions degeneration, haemangiomas, and arterial-venous malformations. They may be useful in treating deficiencies or disorders of the immune cc system, by activating or inhibiting the proliferation, differentiation, or or mobilisation (chemotaxis) of immune cells. The etiology of these cimmune deficiencies or disorders may be genetic, somatic, such as concer or some autoimmune disorders, acquired (e.g. by chemotherapy or toxins), or infectious. They can also be used to treat inflammatory conditions, both chronic and acute conditions. The products can also be used for detection and diagnosis. AAZ32002 to AAZ32080, and AAY49503 to incention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; METH1; METH2; anti-anglogenic; metalloprotease thrombospondin; cancer; diagnosis; hyperproliferative disorder; autoimmune disease; anglogenesis inhibitor; abnormal wound healing; inflammation; rheumatoid arthritis; psoriasis; endometrial bleeding disorder; diabetic retinopathy; macula degeneration; haemangioma; detection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human METH1 related EST D86074.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1999-590684/50.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Iruela-Arispe L, Hastings GA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (IRUE/) IRUELA-ARISPE L.
(HAST/) HASTINGS G A.
(RUBE/) RUBEN S M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23-JAN-1998;
28-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22-JAN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29-JUL-1999.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO9937660-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              arterial-venous malformation; immune deficiency; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 322-324; 457pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New isolated metalloprotease thrombospondin polypeptides, useful for treating hyperproliferative disorders, cancers or autoimmune disorders
                                                                                                               Sequence 3331 BP; 762 A; 701 C; 1022 G; 846 T; 0 other;
                                                                                                                                                       invention.
                                     Quality:
                   Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98US-0072298.
98US-0098539.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99WO-US01313.
381.50
1.408
45.394
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                   Length:
Gaps:
   597
25
25.628
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1680	AlaSerValSerAsp?rometAsnalaIeuGl     ::::::::       	60
6 <b>6</b>	Ala      GCA	71 1581
71 1580	laGlyIleGlyMetP::oProArgGlyProGlyGlnSerLeuGlyGlyMet   ::: 	87 1552
88 1551	GlySerPheGlyAlaMetGlyGlnProMetSerLeuSerGlyGlnProPr	104 1523
104 1522	oProGlyThrSerGl^MetAlaProHisSerMetAlaValValSerThrA	121 1488
121 1487	laThrPro.GlnThrGlnLeuGlnLeuGlnGlnValAlaLeuGlnGlnGl	137 1438
137 1437	nglnglnglnglnglheheglnglnglngln	147 1388
148 1387	ACCTCCGTTACCACCICCGCCTCCACCTCCAGCTGAAGCTGATGCAGATG	15 <b>4</b> 1338
155 1337	GlnGlnGlnGlnGlnGlnGlnPheGlnAlaGln	166 1288
167 1287	.GlnSerAlaMetGlrGlnGlnPheglnAlaValVal	178 1238
178		178
	TGCTTTAGCAGAGGC1TTTGCAGAGGCTCCATTACTCCTGAGAAGGTCTT	1188
178 i 1187	TAATGTCTCCTAATGCGTCCCTTATACCACTCATTTGTCTAGAAGCTGAA	178 1138
179 1137	GLnGlnGlnGlnGlnLeuGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnG	192 1088
193 1087	HisLeuIleLysLeuHisHisGlnAsnGlnGln        :::::    ::::::::::::::::::::::	203 1038
20 <b>4</b> 1037	GlnIleGlnGlnGlnGlnGlnGlnLeuGl     :::      ::             CAGCTGCAGCAGCAGCAGCAGCACGTCTGCGGGCCTCCTCCTCGA	213 988
213 987	nArgIleAlaGlnLeu3lnLeuGlnGlnGlnGln	22 <b>4</b> 938
225 937	GlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnAlaLeu 	238 888
239	GluAlaGlnProProIleGlnGlnProProMetGlnGlnProGlnProPr	· Ui
255	lnGlnLeuGlnGlnMetHisHisThrGlnH	272

CCTCCGCCCCTCCGACAC CCTCCGCCCCTCCGACAC euLysasnAspMetArgCy :::::   ::::  CGTAAAGACCTGCACTG CysHisargPro 546    :::    garCaTAAACCA 186	20 CACCGC	OSETSETVE         GTCATCATC GTCATCATC TYTLEUASF :::::: CATATTCCC	04 rSerGlyProAlaProSerProSerSerPheLeuProSerPro	372 roGlyGlnGlnValGlnThrProGlnSerMetProProPro ::::::::::::::	339 GlnGlnGlnThrAlaValGlnThrAlaGlnAlaGlnAlaGlnMetVe :::   :::   669	InProc	Incescactions Tocach Carefic Carcing Control Carefic C	41 ACCGAGTCCTCCA
AC 2 CysProLe 5     :: TGCTCCAT 2	TCCGC  LysserLeuL :::	TServalMetse 4	erProSerProG 4 ::   :::   ::ACCTGCTCCTG 4 AsnPheSerVal 4 CCGGCACCACCA 4	Prop      CCTC	nMetValAlaPr       ACCTCCAGCTCC erSerProSerP           CATCGAAATCTA	ysPheV: CGGCAG ValGln:::	uValSerGlnAl :::::       .GCGGCTGCGGC	AlaGlnAsnGln
46 37 23		54 71 70 70 21	.21 .71 .37	387 529 505	355 626 372 579	322 717 338 670	796 305 767	00 N

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1.4e-05

1.7e-05

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OM bf: US-09-668-119-3 to: Issued_Patents_NA:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence Strd Orig ZScore EScore Len /cgn2_6/ptodata/2/ina/6B_COMB.seq:US-08-916-352-1 + /cgn2_6/ptodata/2/ina/6A_COMB.seq:US-08-864-038A-1 -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Search information block:
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_6/ptodata/2/ina/5B_COMB.seq:US-08-224-482-3
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   1.4e-05
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                                   9.1e-06
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TOPOLOGY: 1:
; MOLECULE TYPE:
US-08-916-352-1
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US-09-668-119-3 x US-08-916-352-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Align seg 1/1 to: US-08-916-352-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1, Application US/08916352
Patent No. 6166191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: 510-923-2707
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
                                                                      878 AGTTGCCTTCCTCAGGA.....ATGGGTGGTGGGAGCTGTCCCAGGAAG 921
                                                                                                                                                                                                                              828 AGGGTCCATGGGTCCAGGTGGAGGTGGGCAGGCACATGGTGGTTTGGGTC 877
                                                                                                                                                                                                                                                                                                                                                                               778 CAGTCCCTCAACCTTAGTCAAGCTGGTGGAGGCAGTGGGAATAGCATCCC
106 GlyThrSerGlyMetAlaProHisSerMetAlaValValSerThrAlaTh 122
                                                                                                                                                89 erPheGlyAlaMetGlyGlnProMetSerLeuSerGlyGlnProProPro 105
                                                                                                                                                                                                                                                                                             76 o.....ProArgGlyProGlyGlnSerLeuGlyGlyMetGlyS 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                 60 GlnSerLeuThrGlyGlyProAlaAlaGlyAlaAlaGlyIleGlyMetPr 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: 510-655-3542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: POTTER, JANE REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/916,352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        94608
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4560 HORTON STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3879 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CHIRON CORPORATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               384.00
1.367
53.422
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HUMAN POLYHOMEOTIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       μength: 526
Gaps: 23
Percent Identity: 28.707
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   from: 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               to: 3879
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     236.00
+ 235.50
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1.7e-05
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408 1748	ProGlyGlnProSerSerGlnProAsnSerAsnValSerSerGlyProAl.	392 699
391 1698	InValGlnThrProGlnSerMetProProProProGlnProSerProGln	375 660
375 1659	nValSerGlnSerSerLeuProMetLeuSerSerProSerProGlyGlnG ::::::::    ACAGCTGGCAGCTGCTGTACCT	638
358 1637	AG :: A	
341 1587	ValGlnGlnProProValGlnProGlnValGlnGlnGlnGln :::               TGTCAGCTGCCCAGCAACCACCCCATATCCCTGTGCAAGTT	328
327 1543	largalaPrometVal. ::::    ::::: Caagccgccrcagttag	315 494
315 1493	lnAlaGlnAlaLeuProGlyGln	299 471
298 1470	LeuP	282
282 1422	HisTh:GlnHisHisGlnProProProGlnProG:::  ,      CAAACCCTGGTCGTTCAG	395
265 1394	MetGlnGlnP     ACTCAG	366
248 1365	lnA.aLeuGluAlaGlnProPro 	236
236 1315	nLeuGlnGln            GTTGGCGCAG	219 1266
219 1265	GlnIleGlnGlnGlnGlnGlnGlnLeuGlnArgIleAlaGlnLeuGl     :::   ::::   :::      :::   CAGTTCCAGCACCGG:AGTCCCAGCTTCCTTCACACAGCTACACACCTCCA	204
203 1215	InGlnGlnGlnHisLeuIleLysLeuHisHisGl::    :::      :::	189 L172
189 1171	nGlnPheGl	172 1122
172 1121	5 GlnGlnGlnGln3lnGlnPheGlnAlaGlnGlnSerAlaMetGlnGl 	156 1072
155 1071	Inglnglnphe@lnglnglnglnal :::        ::: CAGATGGGAGTGGCC\GCAGAATGTGGGCAT	139 1022
139 1021	2 rProGlnThrGlnLe.JGlnLeuGlnGlnValAlaLeuGlnGlnGlnGlnGl : :::    ::: ::::::    ::: 2 CCAGGGCAGCCAGACAGAGGCAGAAGTGCAGCAGCAAGAAGGCAGAAAG	12: 97:
971	2 GGTACAGGAGTGGTG TAGCCCTTGCCTGCAGCCCAAACAGTGACTGTGAG	92:

seq_documentation_block:     Sequence 1, Application US/08864038A     Patent No. 6001592     GENERAL INFORMATION:	
<pre>seq_name: /cgn2_6/ptodata/2/ina/6A_COMB.seq:US-08-864-038A-1</pre>	
533 etArgCysProLeuProHisArgPro 541	
517 LysThrLeuGlnLys.CysGluIleAlaLeuGluLysLeuLysAsnAspM 533	
507LeuThraspProSerLysArgCysProLeu 516            :::     2081 CAAGCAGTGAACTAGTAGCCTTGACCCCCGCCCCTTCAGTACCGCCT 2127	
495 sAspLeuSerLysMetLysSerLeuLeuAspIle 506 ::::    :::   :::   :::   :::     ::	
479 ProLeuArgArgMetIleAsnLysIleAspLysAsnGluAspArgLysLy 495 :::	
462 luGluGlnGlnTyrLeuAspLysLeuLysGlnLeuSerLysTyrIleGlu 478 ::::::::::::::::::::::::::::::::::::	
445 rProValAsnProSerSerValMetSerProAlaGlySerSerGlnAlaG 462     :::   :::::::     :::    :::	
429 AlaArgThrProGlnAsnPheSerValProSerProGlyProLeuAsnTh 445    ::::::       :::        ::::::: 1849 GCCCAGGTCCCTGCTGCCTTCTATATGCAGTCTGTGCACTT 1889	
425SerProValThr 428	
408 aProSerProSerSerPheLeuProSerProSerProGlnProSerGln. 424	

178	167 .GlnSerAlaMetGlnGlnGlnPheGlnAlaValVal	### ##################################	IlySerPheGlyAlaMetGlyGlnProMetSerLeuSerGlyGlnProPr   104	71 laGlyIleGlyMetProProArgGlyProGlyGlnSerLeuGlyGlyMet 87   :::         1531 CTGCGGCAGATCCCCCACCAAGACCGCCT	CACCTCCACGCATTTGTCTTCTCAAAGCCCTTCT 158  Pro	ign seg 1/1 to reverse of: US-08-864-038A-1 from: 1 to: 2	#lignment_scores:	TELECOMUNICATION INFORMATION: TELEPHONE: (212)986-2340 TELEPAX: (212)953-7733 INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 2214 TYPE: nucleic acid STRANDEDNESS: double TOPOLOGY: linear ORIGINAL SOURCE: ORGANISM: Pinctada fucata CELL TYPE: mantle epithelial cell DS-08-864-038A-1
178	₽ • ▶ •			t 8	15 71 15	to: 1 60		

45	8 ProSerProGlyProLeuAsnThrProValAsnProSerSerValMetSe	438
37:	CTCCTGCGCCTGCTCCAGCACCAGCACCAGCAC	421
43	lnProSerGlnSerProValThrAlaArgTh	421
4 2	4 rSerGlyProAlaProSerProSerProFerProGerProGerProGerProGerProGerProGerProGerProGerProGerProGerProGerGerGerProGerProGerGerGerGerGerGerGerGerGerGerGerGerGerG	404 455
45	ProSerProGlnProGlyGlnProSerSerGlnProAsnSerAsnVal	388 479
486	roglyGlnGlnValGlnThrProglnSerMetProProProProG ::::::::::::::::::::::::::::::::::::	372 529
37; 53(	oglyValGlnValSerGlnSerSerLeuProMet	355 576
355 577	GlnGlnGlnThrAlaValGlnThrAlaGlnAlaAlaGlnMetValAlaPr 	339 620
338 621	2 alargalaProMetValValGlnGlnProProValGlnProGlnValGln ::	322 667
<b>σ</b> Ν	aGlnAlaLeuProGlyGlnMetLeuTyrThrGlnPro	305 717
305 718	ProSerGlnLeuProProGlnSerGlnThrGlnProLeuValSerGlnAl	289 746
288 747	<pre>! isHisGlnProProProGlnProGlnGlnProProValAlaGlnAsnGln :::        :::    :::     :::  AGTCCGCCACCGAGTCCTCCAAGTCCACCTGCG</pre>	272 779
780	oProSerGlnAlaLeuProGlnGlnLeuGlnGlnMetHisHisThrGlnH        ACCGAGTCCTCCA	255 792
255 793	GlualaGlnProProIleGlnGlnProProMetGlnGlnProPr:::	239 838
238 839	accrccgcagcagcagcagcagcagcagcagcagcagcagcagarccrc	225 888
22 <b>4</b> 889	nArgIleAlaGlnLeuGlnLeuGlnGlnGlnGlnGln	213 938
213 939	LeuGl    ::  TCTGCGGCCTCCTCCTCGA	20 <b>4</b> 988
203 989	HisLeuIleLysLeuHisHisGlnAsnGlnGln:        :::::    :::::: TCCTCCTCCACCACCTCCACCTCCGCCACCACCAGCGGCTGCGGGGG	193 1038
192 103	.GlnGlnGlnGlnGlnLeuGlnGlnGlnGlnGlnGlnGlnGlnGlnGln	179 1088
0	TAATGTCTCCTAATGCGTCCCTTATACCACTCATTTGTCTAGAAGCTGAA	1138

to: 3331

1087 TOCTCCTCCACCACCTCCACCTCCTCCGCCACCACCACCACGGGGTGCGGCGG	; MOLECULE TYPE: CDNA to mRNA ; ORIGINAL SOURCE: ; ORGANISM: Pinctad; fucata
	DNESS: double Y: linear
179 .GlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnG	; LENGTH: 3331 ; TYPE: nucleic acid
	TELEPAX: (212)953-7733; ; INFORMATION FOR SEQ ID NO: 2:
178	; TELECOMMUNICATION INFORMATION: ; TELEPHONE: (212)986-2340
1237 TGCTTTAGCAGAGGCTTTTGCAGAGGCTCCATTACTCCTGAGAAGGTCTT	; REGISTRATION NUMBER: 22,389 ; REFERENCE/DOCKET NUMBER: F-5610
178	; ATTORNEY/AGENT INFORMATION: ; NAME: C. Bruce Hamburg
167.GLnSerAlaMetGlnGlnGlnPheGlnAlValValVal	PRIOR APPLICATION DATA:  APPLICATION UNMER: JF 8-184459  FILING DATE: 15-701V-1996
	ct 6.1 A: US/08/864,038A
	ER READABLE FO UM TYPE: Disk UTER: IBM Con ATING SYSTEM:
137 nGlnGlnGlnGlnGlnPheGlnGlnGlnGlnGln	CITY: Tsurcity  CITY: Mie-prefecture  COUNTRY: JAPAN  1 17 P. 514-01
121 laThrPro.GlnThrGlnLeuGlnLeuGlnGlnValAlaLeuGlnGlnGl	R OF SEQUENCES: SPONDENCE ADDRESSESSEE: 812-5 P
OPr ACC	TITLE OF INVENTION: NOTALINING SAID CDNA, VECTOR TITLE OF INVENTION: CONTAINING SAID CDNA, HOST CELLS TRANSFORMED WITH SAID TITLE OF INVENTION: VECTOR, POLYPEPTIDE PRODUCED THEREBY, METHOD OF PRODUCING TITLE OF INVENTION: SAID POLYPEPTIDE, DNA ENCODING SAID POLYPEPTIDE AND ANTIBODY TITLE OF INVENTION: TO SAID POLYPETIDE. DNA ENCODING SAID POLYPEPTIDE AND ANTIBODY
88 GlySerPheGlyAlaMetGlyGlnProMetSerLeuSerglyGlnProPr	). Application ). 6001592 INFORMATION: NAME: Kunio NAK
71 laGlyIleGlyMetProProArgGlyProGlyGlnSerLeuGlyGlyMet   :::                    1580 CTGCGGCAGATCCCCACCAAGACCGCCT	
60 nSerLeuThrGlyGlyProAlaAlaGlyAlaA	537 uProHi::ArgProArgCysHisArgPro 546 :
50 AlaSerValSerAspProMetAsnAlaLeuG1	521 LysCysGluIleAlai.euGluLysLeuLysAsnAspMetArgCysProLe 537 ::::::   ::::   :: 196
alignment_block: US-09-668-119-3 x US-08-864-038A-2/rev	250
alignment_scores: Quality: 381.50 Ratio: 1.408 Percent Similarity: 45.394 Percent Identity: 25.628	471 LysGlnLeuSerLysTyrIleGluProLeuArgArgMetIleAsnLysI1 487 ::::: 271 CACCGC
; CELL TYPE: mantle epithelial cell; FEATURE: mRNA; LOCATION: from 1 to 3331; LIDENTIFICATION METHOD: E (by experiment) US-08-864-038A-2	371 CCAGCACCACCTCCG 3CGCCAGCTCCCATTCCACCGTCATCATCCCAGTC 322 454 rProAlaGlySerSer.GlnAlaGluGluGlnGlnTyrLeuAspLysLeu 470   :::::         ::::::::::::::::::::::

alignment\_scores:

Quality: Ratio:

381.50 1.408

Length: Gaps:

Percent	Similarity: 45.394 Percent Identity: 25.628
lignmen US-09-6	t_block: 68-119-3 x US-08·864-038A-4/rev
Align s	of: US-08-864-03
50 1680	GCATTT
60 1630	1/Pro
71 1580	rgGlyProGlyGlnSe:
88 1551	heGlyAlaMetGlyGlnProMetSerLeuSerGlyGlnProP 
104 1522	ProGlyThrSerGl
121 1487	nThrGlnLeuGlnLeuGlnGlnVa: :::      :::::: CCTC(:ACCTCCAAGTCCACCTCCC
137	ngIngIngIngIngIngIngIngIngIngIngIngIngIn
148 1387	GlnAlaAlaLeuGlnGlnGln 154
155 1337	GlnGlnGlnGlnGlnGlnGlnPheGlnAlaGln
167 1287	.GlnSerAlametGlnGlnGlnPheGlnAlaValVal
178 1237	TGCTTTTAGCAGAGGCTTTTTGCAGAGGCTCCATTACTAGGAGAGGCTCTTT 1100
178	
1187	ATGTCTCCTAATG( GTCCCTTATACCACTCATTTGTCTAGAAGCTGA
179 1137	.GlnGlnGlnGlnGlrLeuGlnGlnGlnGlnGlnGlnGlnGlnGln 192     :::      :::    :::   :::   :::   :::   :::   :::   :::   :::
193 1087	CCTCCTCCACCACCTCCACCTCCTCCGCCACCACCACCAGCGGCTGCGGCGG 1038
204 1037	IleGlnGlnGlnGlnGlnGln
213 987	nargIlealaGlnLeuGlnLeuGlnGlnGlnGln
225	GlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnAlaLeu 238

537 223	LysCysGiuileAlaLeuGiuLysLeuLysAsnAspMetArgCysProLe	245
4	TCCAGCACCGCCAGCTCCCCAGGCGCCTCCGACCCCTCCGACAC	α
N	euAspIleLeuThrAspProSerLysArgCysProLeuLysThrLeuGln  :::	0
9		299
504	eAspLysAsnGluAspArgLysLysAspLeuSerLysMetLysSerLeuL	487
487 300	LysGlnLeuSerLysTyrIleGluProLeuArgArgMetIleAsnLysIl	471 320
321	CCATTCATCATCGTCATCGCTGTCGTCATCATAGTCATATTCCCAATCTC	7
470	rProAlaGlySerSer.GlnAlaGluGluGlnGlnTyrLeuAspLysLeu	454
454 371	ProSerProGlyProLeuAsnThrProValAsnProSerSerValMetSe     :::               :::   :::	438 420
421	THE TRANSPORT OF THE TR	470
437	lnProSerGlnSerProValThrAlaArgThrProGlnAsnPheSerVal	421
471		504
421	rSerGlyProAlaProSerProSerSerPheLeuProSerProSerProG	404
	CCAAGTCCACCTCCGAGACCTCCG	528
404	ProSerProGlnProGlyGlnProSerSerGlnProAsnSerAsnValSe	388
387 529	coglyGlnGlnValGlnThrProGlnSerMetProProProProGln::::::::::::::::::::::::::::::::::::	372 578
579	Oc. y va. G. II va. I G. II SET SET LEUP FOMET LEUSETSET FOSEFF   G. ::	625
J		Л
355 626	GlnGlnGlnThrAlaValGlnThrAlaGlnAlaAlaGlnMetValAlaPr :::   :::	339 669
338 670	alArgAlaProMetValValGlnGlnProProValGlnProGlnValGln ::	322 716
سو		766
322	${\tt aGlnAlaLeuProGlyGlnMetLeuTyrThrGlnProProLeuLysPh}$	305
305 767	ProSerGinLeubroProGinSerGinThrGinProLeuValSerGinAl	289 795
9	AGTCCGCCACCGAGTCCTCCAAGTCCACCTGCG	2
Φ	isHisGlnProProProGlnProGlnGlnProProValAlaGlnAsnGl	7
272 829	OPTOSETGINALALEUPTOGINGINLEUGINGINMETHISHISTNTGINH	255 841
842	7 CATATCCTCCGAGGCCACCAAGACCTCCGAGGCCTCCAAGTCCGCC	88
- α	TCCGGCAGCAGCGGCGGCAGCAGCAGCAGCAGCAGCAGCAG	ν ω
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seq_documentation_block:
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                                                                                                                                                                                                                                       alignment_scores:
                                                                                                                                                                                                                                                                                                      US-08-998-416-915
                                                                                                                  lignment_block:
US-09-668-119-3
                                                                                                                                                                               Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 915, Appl Patent No. 6239264
                                                                           Align seg 1/1 to:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO: 915:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: CH 0016/97
FILING DATE: 31-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Melgs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: PF/5-30306/A/CGC1976
TELECOMMUTICATION INFORMATION:
TELEPHONE: 919-541-8587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             537 uPro......HisArgProArgCysHisArgPro 546
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: GENOMIC DNA SEQUITITLE OF INVENTION: AND USES THEREOF NUMBER OF SEQUENCES: 1152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/998,416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      222 GCCGAAACGCAACCACATGCCCATGGATCATAAACCA 186
                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                      20 ThrAlaThrProGlnThrGlnLeuGlnLeuGlnGlnValAlaLeuGlnGl 136
                                                                                                                    -668-119-3 x US-08-998-416-915
                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE:
                                                                                                                                                                                                                                                                                                                           ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH:
ACCGCTCTCTCAATCTCATCCTCAGCAACAACAAGGTTCACAAGCTCA 164
                                                                                                                                                                                                                    Quality:
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T: 3054 Cornwallis Road
Research Triangle Park
: No. 6239264th Carolina
                                                                                                                                                                                                                                                                                                                                                                                                                    nucleic acid
                                                                                                                                                                                                    Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                         688 base pairs
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/ENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSYPII
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Knechtle, Philipp
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Steiner, Sabine
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                                                                             US-08-998-416-915
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2.816
60.309
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seq_name: /cgn2_6/ptodata/2/ina/5B_COMB.seq:US-08-728-323A-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1, Application US/08728323A Patent No. 5948676
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   184
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                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                          COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               650 AGCAG.....TCTCAGCAGCAGAAGCTT 672
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                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            298 hrGlnProLeuValSerGlnAlaGlnAlaLeu 308
                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
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CITY: N
                                                                                                                                                       ZIP:
                                                                                                                                                                        COUNTRY:
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APPLICATION NUMBER: US/08/728,323A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   uGlnGlnGlnGlnGlnGlnHisLeuIleLysLeuHisHisGlnA 201
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GCAGCAGCTACTTCAACAACAACAAGGTTCACAAGCTCAGCAGCAGCTAC 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      nProProValAlaGlnAsnGlnProSerGlnLeuProProGlnSerGlnT 298
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                                                                                                                                                       10036
                                                                                                                                                                                                                         New York
                                                                                                                                                                            New York
Y: U.S.A.
                                                                                                                                                                                                                                               1185 Avenue of the Americas
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Moore, Patrick S.
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                                                                                                                                                                                                                                                                      Cooper & Dunham LLP
                                                                                                                                                                                                                                                                                                            Immediate Early Protein From Kaposi's Sarcoma-Associated Herpesvirus, DNA Encoding Same And Uses Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                Isidore S.
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alignment_block:
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; LOCATION:
US-08-728-323A-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ratio: 1.602 Gaps: 9
Percent Similarity: 57.143 Percent Identity: 30.904
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AMME: White, John P.

REGISTRATION NUMBER: 28,678

REFERENCE/DOCKET NUMBER: 0579

TELECOMMUNICATION INFORMATION:

TELEPHONE: 212-278-0400

TELEPAX: 212-391-0525

INFORMATION FOR SEQ II) NO: 1:
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                                                1892 AGCAGGATGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 1941
                                                                                                                                               1842 GCAGCAGCAGGATGAGCAGCAGCAGGATGAGCAGCAGGATGAGCAGC 1891
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  173 GlnPheGlnAlaValValGlnGlnGlnGlnGlnLeuGlnGlnGlnGlnGl 189
                                                                                   156 lnGlnGlnGlnGlnGlnGlnPheGlnAlaGlnGlnSerAlaMetGlnGln 172
                                                                                                                                                                               139 nGlnGlnGlnPheGln3lnGlnGlnGlnAlaAlaLeuGlnGlnGlnGlnG 156
                                                                                                                                                                                                                                                                                                  123 ProGlnThrGlnLeuGlnLeuGlnGlnValAlaLeuGlnGlnGlnGlnGl 139
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  73 leGlyMetProProArgGlyProGlyGlnSerLeuGlyGlyMetGlySer 89
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TENGTH: 3485 L...
TYPE: nucleic ac.d
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linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:

APPLICANT: Chang, Yuan
APPLICANT: Bohenzky, Roy A.
APPLICANT: Bohenzky, James J.
APPLICANT: Russo, James J.
APPLICANT: Edelman, Isidore S.
APPLICANT: Moore, Patrick S.
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                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/08/770,379
FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: POLYPEPTIDES FROM KAPOSI'S SARCOMA-ASSOCIATED TITLE OF INVENTION: HERPESVIRUS, DNA ENCODING SAME AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    337 lGlnGlnGlnThrAlaValGln 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               321 PheValArgAlaProMetValValGlnGlnProProValGlnProGlnVa 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       304 lnAlaGlnAlaLeuProGlyGlnMetLeuTyrThrGlnProProLeuLys 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     271 GlnHisHisGlnProProProGlnProGlnGlnProProValAlaGlnAs 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            256 roSerGlnAlaLeuProGlnGlnLeuGln.....GlnMetHisHisThr 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         287 nGlnProSerGlnLeuProProGlnSerGlnThrGlnProLeuValSerG 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            239 uAlaGlnProProIleGlnGlnProProMetGlnGlnProGlnProProP 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      206 lnGlnGlnGlnGlnLeuGlnArgIleAlaGlnLeuGlnLeuGlnGln 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         189 nGlnGlnGlnHisLeuIleLysLeuHisHisGlnAsnGlnGlnGlnIleG 206
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                                                                                                                                                                                                                                                                                                                                                                              STREET: 1185 A
CLASSIFICATION:
                                                                                                                                                                                                                                                                                            COUNTRY: UZIP: 10036
                                                                                                                                                                                                                                                                                                                                                               STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                       New York
                                                                                                                                                                                                                                                                                                                                                                                                                   E: Cooper & Dunham LLP
1185 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                          U.S.A.
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REFERENCE/DOCKET NUMBER: 52
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400

ATTORNEY/AGENT INFORMATION: NAME: White, John P.

REGISTRATION NUMBER:

28,678

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alignment_scores:
Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 alignment_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-770-379-20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Align seg 1/1 to reverse of: US-08-770-379-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20439 CAGCAGCAGGAGC.
                                                                               20055 GATGAGCAGCAGGATGAGCAGCAGCAGCAGCAGCAGCAGGATGA 20006
                                                                                                                                                                                                                                                                                                                                                                                          20205 GATGAGCAGCAGCAGGATGAGCAGCAGCAGCAGCAGCAGGATGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20328
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INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENCTH: 32207 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          106 yThrSerGlyMetAlaProHisSerMetAlaValValSerThrAlaThr, 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE:
189 nGlnGlnHisLeuIleLysLeuHisHisGlnAsnGlnGlnIleG 206 :|||||||||
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    73 leGlyMetProProArgGlyProGlyGlnSerLeuGlyGlyMetGlySer 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23 aLysThrArgAspGluTyrLeuSerLeuValAlaArgLeuIleIleHisP 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7 AlaHisSerLysSerSerLysAspMetGluSerHisValPheLeuLysAl 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: li
                                                                                                                                                                                                                                                                                                                                                                                                                                       ProGlnThrGlnLeuGlnLeuGlnGlnValAlaLeuGlnGlnGlnGlnGl 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PheGlyAlaMetGlyGlnProMetSerLeuSerGlyGlnProProProGl 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CGGGAGCCCCA.....GCAGCGGGAGCCACAGCAGCAGCGGGAGCCACAGCA 20285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AGGAGCC.....ACAGCAGCAGGAGCCACAGCAGCGGGAGCCACAGCAG 20329
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          heArgAspIleHisAsnLysLysSerGlnAlaSerValSer.AspProMe
                                                                                                                                                                                                                                                                                                                                     nGlnGlnPheGlnGlnGlnGlnAlaAlaLeuGlnGlnGlnGlnG
                                                                                                                               GlnPheGlnAlaValValGlnGlnGlnGlnGlnLeuGlnGlnGlnGlnGl 189
                                                                                                                                                                                  AGCAGGATGAGCAGCAGGATGAGCAGCAGGATGAGCAGCAGCAG
                                                                                                                                                                                                                               lnGlnGlnGlnGlnGlnPheGlnAlaGlnGlnSerAlaMetGlnGln 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ratio:
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1.602
57.143
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seq_documentation_block:
; Sequence 20, Application
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sequence 20, Application US/08757669A
Patent No. 6183751
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19811
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                    ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 45185-F
                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              337 lGlnGlnGlnGlnThrAlaValGln 345
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: UNIQUE ASSOCIATED KAPOSI'S SARCOMA VIRUS TITLE OF INVENTION: SEQUENCES AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: New York COUNTRY: U.S.A.
                                                                                                                                      FILING DATE:
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET:
                                                                                                                                                                                               APPLICATION NUMBER: US/08/757,669A
                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 10036
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    roSerGlnAlaLeuProGlnGlnLeuGln.....GlnMetHisHisThr 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGAGCAGCAGGATGAGCAGCAGCAGGATGAGCAGCAGCAGGATGAGC 19812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GAGCAGGAGCAGGAGTTAGAGGAGCAGGAGCAGGAGTTAGAGGAGCAGGA 19574
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         uAlaGlnProProIleGlnGlnProProMetGlnGlnProGlnProProP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E: Cooper & Dunham LLP
1185 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bohenzky, Roy A. Russo, James J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chang, Yuan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Edelman, Isidore S. Moore, Patrick S.
                                                                                                                                                                                                                                                     Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19624
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TELEPHONE: (212) 278-0400
TELEPAX: (212) 391-0525
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 32207 base pairs
TYPE: nucleic acid
STEANNEAUERIC ACID

20:

STRANDEDNESS:

linear

DNA (genomic) double

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alignment_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Align seg 1/1 to reverse of: US-08-757-669A-20 from: 1 to: 32207
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206 Inglnglnglnglng.nLeuglnArgIleAlagInLeuglnLeuglngln 222 ::||||||||:::: |||::: ||| || :::||| 1961 AGCAGCAGCAGGATGAGCAGCAGCAGGATGAGCAG 19912
                                                                                                                                 20005 GCAGCAGCAGGAT.. ...GAGCAGCAGCAGGATGAGCAGCAGCAGGATG 19962
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20105 AGCAGGATGAGCAGCAGCAGGATGAGCAGCAGCAGCAGCAGCAG 20056
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                                                                                                                                                                                                189 nGlnGlnHisLeuIleLysLeuHisHisGlnAsnGlnGlnGlnIleG 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                        156 lnGlnGlnGlnGlnGlnPheGlnAlaGlnGlnSerAlaMetGlnGln 172
                                                                                                                                                                                                                                                                                                                              173 GlnPheGlnAlaValValGlnGlnGlnGlnGlnLeuGlnGlnGlnGlnGl 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   123 ProGlnThrGlnLeu3lnLeuGlnGlnValAlaLeuGlnGlnGlnGlnGl 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             106 yThrSerGlyMetAlaProHisSerMetAlaValValSerThrAlaThr. 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       90 PheGlyAlaMetGly3lnProMetSerLeuSerGlyGlnProProProGl 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             56 tAsnAlaLeuGlnSerLeuThrGlyGlyProAlaAlaGlyAlaAlaGlyI 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         73 leGlyMetProProArgGlyProGlyGlnSerLeuGlyGlyMetGlySer 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             40 heArgAspIleHisAsnLysLysSerGlnAlaSerValSer.AspProMe 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23 aLysThrArgAspGlıTyrLeuSerLeuValAlaArgLeuIleIleHisP 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7 AlaHisSerLysSerSerLysAspMetGluSerHisValPheLeuLysAl 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ratio:
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1.602
57.143
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seq_name: /cgn2_6/ptodata/2/ina/5B_COMB.seq:US-08-991-300-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1, Application US/08991300 Patent No. 5973225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: D'OYLLL,
APPLICANT: PORCEDDU, ENRICO
APPLICANT: PORCEDDU, ENRICO
APPLICANT: MERCHITELLI, CIIOZIA
APPLICANT: CARDELLI, LUISA ERCOLI
TITLE OF INVENTION: ISOLATION AND CHARACTERIZATION OF A GENE
TITLE OF INVENTION: ENCODING A LOW MOLECULAR WEIGHT GLUTENIN
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ANDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ANDRESSEE: OBLON, SPIVAK MAVIS HIGHWAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19573 GCAGGAGTTAGAGGAGCAGGAGCAG 19549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19623 GAGCAGGAGCAGGAGTTAGAGGAGCAGGAGCAGGAGCAGGA 19574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19811 AGCAGCAGGATGAGCAGCAGCAGCAGGATGAGCAGCAGCAGGAT 19762
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19861 GGAGCAGCAGGATGAGCAGCAGCAGCAGCAGCAGCAGGATGAGC 19812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19911 CAGCAGGATGAGCAGGAGCAGGAGGAGCAGGAGCAGGATGAGCA 19862
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19711 GGAGGAGCAGGAGCAGGAGTTAGAGGAGCAGGAGCAGGAGTTAGAGGATC 19662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19761 GAGCAGCAGCAGGATGAACAGGAGCAGCAGGAGCAGCAGCAGCA 19712
                        ATTORNEY/AGENT INFORMATION:
NAME: OBLOW, NORMAN F.
REGISTRATION UNMBER: 24,618
REFERENCE/DOCKET NUMBER: 22:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: IT MI 96/A 002663
FILING DATE: 19-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compartible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                337 lGlnGlnGlnGlnThrAlaValGln 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         321 PhevalArgAlaProMetValValGlnProProValGlnProGlnVa 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 304 lnAlaGlnAlaLeuProGlyGlnMetLeuTyrThrGlnProProLeuLys 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   287 nGlnProSerGlnLeuProProGlnSerGlnThrGlnProLeuValSerG 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           271 GlnHisHisGlnProProProGlnProGlnGlnProProValAlaGlnAs 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             256 roSerGlnAlaLeuProGlnGlnLeuGln.....GlnMetHisHisThr 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         239 uAlaGlnProProIleGlnGlnProProMetGlnGlnProGlnProProP 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     223 GlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnAlaLeuGl 239
                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/991,300 FILING DATE: 16-DEC-1997
TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22202
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703-413-2220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           USA
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                                                                                            2264 - 0201 - 0X
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; MOLECULE TYPE: DNA (genomic) US-08-991-300-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-668-119-3 x US-08-991-300-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Align seg 1/1 to: US-08-991-300-1 from: 1 to: 1107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 1107 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            191 nGlnHisLeuIleLysLeuHisHisGln...AsnGlnGlnGlnIle.... 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          134 LeuGlnGlnGlnGlnGlnGlnGlnPheGlnGlnGlnGlnGlnAlaAl 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    182 GlnGln......GlnGlnGlnGlnGln......GlnGlnGl 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   116 AACAGCAACCATGTTCACAGCAACAACAACCACCACTTATCGCAACAA 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       165 laGlnGlnSerAlaMetGlnGlnGlnPheGlnAlaValValGlnGlnGln 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              150 aLeuGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnBheGlnA 165
                                                   574 CTACTGCAACAACAATACCATTTGTTCATCCATCTATCTTGCAGCAACT 623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        233 nGlnGlnAlaLeuGluAlaGlnProProIle.....GlnGlnProP 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        316 CTACCGCAACAACCATCATTTTCGCAGCAACAACTACCACCATTTTCACA 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  416 CATTTTCGCAGCAACAACCACCACCATTTTCACAGCAACTACCACCATTT 465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         248 roMetGlnGlnProGlnProProPro...SerGlnAlaLeuProGlnGln 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      220 LeuGlnGlnGlnGlnGlnGlnGlnGlnGlnGln......GlnGl 233
330 nProProValGlnProGlnValGlnGlnGlnGlnThrAlaValGlnThrA 347
                                                                                                                                                                                                                                                                                                                                                                                                                                           264 LeuGlnGlnMetHisHisThrGlnHisHisGlnProProProGlnProGl 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          366 GCAACTACCACCATTTTCGCAGCAACAACCAGTACTACCGCAACAACCAC 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16 TTGGAGAGACCATCGCAGCAACAACATTACCACCACAACAACATTATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              66 GCACCACCAACAACAACCATCCAACAACAACCACCACCAATTTCCAC 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACAACCAGTTCTACCGCAACAACCATCATTTTCGCAGCAACAACTACCAC 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CAACAACCACCATTTTCGCAGCAACAACCACCATTTTCACAGCAACA 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ........GlnGlnGlnGlnGlnLeuGlnArgIleAlaGlnLeuGln 219
                                                                                                                                                                                                                                                                                                                                                                              TCGCAGCAA......CAACAACCAGTACTACCGCA 494
                                                                                                       TyrThrGlnProProLeuLysPheValArgAlaProMetValValGlnGl 330
                                                                                                                                                           lnThrGlnProLeuValSerGlnAlaGlnAlaLeuProGlyGlnMetLeu 313
                                                                                                                                                                                                                                                                            ACAACCACCATTTTCGCAACAACAACAACAACCAATTCCACCGCAA.... 540
                                                                                                                                                                                                                                                                                                                             nGlnProProValAlaGlnAsnGlnProSerGlnLeuProProGlnSerG 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
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1.724
55.864
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: 17
: 35.802
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seq_documentation_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TYPE: DNA; ORGANISM: Cryptosporidium parvum US-08-700-651-1
                                                                                                                                                                                                                                                                                                                                             alignment_block:
US-09-668-119-3 x US-08-700-651-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  alignment_scores:
                                                                                                                                                                                                                                                                                    Align seg 1/1 to: US-08-700-651-1 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                 Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: PETERSEN, CAROLYN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1, Application US/08700651B Patent No. 6015882
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: NELSON, RICHARD, C.
APPLICANT: GUT, JIRI
APPLICANT: GUT, JIRI
TITLE OF INVENTION: VACCINES, ANTIBODIES, PROTEINS, GLYCOPROTEINS, DNAS AND RNAS
TITLE OF INVENTION: FOR PROPHYLAXIS AND TREATMENT OF CRYPTOSPORIDUM
TITLE OF INVENTION: INFECTIONS
FILE REFERENCE: 480.19-4(HV)
CURRENT APPLICATION NUMBER: US/08/700,651B
CURRENT APPLICATION NUMBER: US/08/751
EARLIER FILING DATE: 1997-08-14
EARLIER APPLICATION NUMBER: 08/415,751
EARLIER FILING DATE: 1995-04-03
NUMBER: OF SEQ. ID NOS: 15
COMMENCE: DESCRIPTION OF SEQ. ID NOS: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: LEECH, JAMES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Ver.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          844 CAAACTCAGCAGCAGCAACCCCAACAGTTGGGCCAATGCGTTTCCCCAACC 893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           744 GCAGTTGCCGCAAATACCCCAGCAATCCCGCTATGAGGCAATCCGTGCTA 793
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                364 LeuProMetLeuSerSerProSerProGlyGlnGlnValGlnThrProGl 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   347 laGlnAlaAlaGlnMetValAlaProGlyValGlnValSerGlnSerSer 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 426 ProValThrAlaArgThr 431
                                                      596 ACTACTACTACTACGACAACAACAACAACGACAACAACAACAAC 645
                                                                                                                                                                                                                           113 HisSerMetAlaValValSerThrAlaThrProGlnThrGlnLeuGlnLe 129
                                                                                       129 uGlnGlnValAlaLeuGlnGlnGlnGlnGlnGlnGlnGlnBheGlnGlnG 146
                                                                                                                                                                     546 CATACACTAAATGTGTTGGAGTGAAACACAACAACAACAACAACAACAACT 595
146 lnGlnGln......AlaAlaLeuGlnGlnGlnGlnGlnGlnGlnGln 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TGCCATGTGATG......CAACAACGATGTTGCCA 743
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           nSerMetProPro...ProProGln.ProSerProGlnProGlyGlnPro 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CCAACAACAGTCGCAACA 911
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TCGTCTACTCCATCATCCTGCAAGAACAACAACAGGTTCAGGGTTCCATC 843
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SerSerGlnProAsnSer......Asn.ValSerSerGlyProAlaP 409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   roSerProSerSerPheLeuProSerProSerProGlnProSerGlnSer 425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                              309.50
2.437
54.741
                                                                                                                                                                                                                                                                                                                                                                                                                                 Percent Identity: 43.966
                                                                                                                                                                                                                                                                                          to: 5163
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	COUNTRY: USA ZIP: 94306-1840 ZIP: 94306-1840 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible COMPUTER: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION UNMBER: US/08/928,361B
	PETERS, Sherma Alto
INS, , ANALOGS AND ERAGN SIS OF CRYPTOSPORIL	Carolyn PEPTIDES, POLYPEPTIDES, GLYCOPROTE FIHEIR FUNCTIONAL MUTANTS, VARIANTS FOR TREATMENT AND DETECTION/DIAGNO SPECIES INFECTIONS STORM TO THE PROPERTY OF
	documentation_b quence 4, Appli tent No. 607151
	_name: /cgn2_6/ptodata/2/ina/6A_COMB.seq:US-08-928-361B-4
	293 OPrOGInSerGInThrGlnProLeuValSerGlnAlaGlnAlaLeu 308
293	281 GlnProProValAlaGlnAsnGlnProSerGlnLeuPr 2
280 1124	OProProGlnProGln      ACAACAACAACAA
264 1074	-
258 1024	7 4
243 977	2b7 lnGlnGlnGlnGlnGlnGlnGlnGlnAlaLeuGluAlaGlnProPro :
227 927	8 uGlnLeuGlnGlnGlnGln
218 877	nGlnGlnGlnLeuGlnArgIleAlaGlnLe            ACAACCACAACTACAACCACAACAACT
201 830	185 lnGlnGlnGlnGlnGlnGlnHisLeuTleLysLeuHisHisGlnAsn:
185 795	174
173 745	160 GlnGlnGlnPheGlnAlaClnGlnSerAlaMetGlnGlnGlnGln
695	> —

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alignment_block:
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; MOLECULE TYPE:
US-08-928-361B-4
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Ratio: 2.437
Percent Similarity: 54.741
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PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 60/026,062
FILING DATE: 13-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: Verny, Hana
REGISTRATION NUMBER: 30,518
REFERENCE/DOCKET NUMBER: 480.76-1(HV
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 5163 base pairs
                                                                                                                               977 ...CAACAACAACAACAACAACTACAACTACCAAGAAACCAACAACT 1023
                                                                                                                                                                                                                           877 ACAACCACAACCACAACCACAACCACAACTACCAAGAAACCAACAAC 926
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                                                                                      244 IleGlnGlnProProMetGlnGlnProGlnProProProSerGln.... 258
                                                                                                                                                                                                                                                                                                                 830 CAACAACCACCACAACTACAACCACCACTACAACCA...CAACAACT 876
                                                                                                                                                                                                                                                                                                                                                        202 GlnGlnGlnGlnGlnGlnGlnGlnLeuGlnArgIleAlaGlnLe 218
                                                                                                                                                                                                                                                                                                                                                                                                       160 GlnGlnGlnPheGlnAlaGlnGlnSerAlaMetGlnGlnGln...... 173
                                                                                                                                                                                                                                                                  185 lnGlnGlnGlnGlnGlnHisLeuIleLysLeuHisHisGlnAsn 201
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
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Gaps: 9
Percent Identity: 43.966
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EARLIER FILING DATE: 1995-04-03

NUMBER OF SEQ ID NOS: 15

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 2

LENGTH: 5318

TYPE: DNA

ORGANISM: Cryptosporidium parvum
US-08-700-651-2
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Quality:
Ratio:
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Patent No. 6015882
GENERAL INFORMATION:
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APPLICANT: LEECH, JAMES
APPLICANT: LEECH, JAMES
APPLICANT: LEECH, JAMES
APPLICANT: NELSON, RICHARD, C.
APPLICANT: GUT, JIRI
TITLE OF INVENTION: VACCINES, ANTIBODIES, PROTEINS, GLYCOPROTEINS, DNAS AND RNAS
TITLE OF INVENTION: FOR PROPHYLAXIS AND TREATMENT OF CTYPTOSPORIDIUM PARVUM
TITLE OF INVENTION: INFECTIONS
TITLE REPERENCE: 480.19-4(HV)
CURRENT APPLICATION NUMBER: US/08/700,651B
CURRENT APPLICATION NUMBER: 08/415,751
ERRLIER APPLICATION NUMBER: 08/415,751
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     546 CATACACTAAATGTGTTGGAGTGAAACACCAACAACAACAACAACAACT 595
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                                                                                                                                                                                                                                                                     646 TACTACAACTACTACCACTACTACTACGACAACAACAACAACAACAACAA 695
                                                     185 lnGlnGlnGlnGlnGlnGlnHisLeuIleLysLeuHisHisGlnAsn 201
                                                                                                     .....PheGlnAlaValValGlnGlnGlnGlnGlnLeuG 185
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2.437
54.741
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alignment_block:
US-09-668-119-3 x US-08.928-361B-3
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Ratio: 2.437 Gaps: 39
Percent Similarity: 54.741 Percent Identity: 43.966
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                                                      1124 CAACTACCACGAAACCAACAACAACAACAACTACTACTACTACA 1173
                                                                                                                                                                    293 oProGlnSerGlnThr3lnProLeuValSerGlnAlaGlnAlaLeu 308
                                                                                                       281 GlnProProValAlaGlnAsnGlnProSerGln.....LeuPr 293
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                227 lnGlnGlnGlnGlnGlnGlnGlnAlaLeuGluAlaGlnProPro 243
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                645 TACTACAACTACTACCACTACTACGACAACAACAACAACAACAACAA 694
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LENGTH: 5318 base pair
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alignment_block:
US-09-668-119-3 x US-08-928-361B-2
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Ratio: 2.335
Percent Similarity: 51.626
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GENERAL INFORMATION:
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TELEFAX: 650-34.

INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
SEQUENCE FARACTERISTICS:
SEQUENCE FARACTERISTICS:
SEQUENCE FARACTERISTICS:
SEQUENCE FARACTERISTICS
SEQUENCE
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TITLE OF INVENTION: THEIR FUNCTIONAL MUTANT'S
TITLE OF INVENTION: FOR TREATMENT AND DETECT
TITLE OF INVENTION: SPECIES INFECTIONS
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSE: PETERS, VERNY, JONES & BIKSA
STREET: 385 Sherman Avenue, Suite 6
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1174 ACCAAGAAACCAACAACTACCACTGCCACAACAACTACTA 1219
                                                                                                                                                                                                                                                FILING LOCAL CHASSIFICATION:
CLASSIFICATION DATA:
PRIOR APPLICATION NUMBER: US 60/026,062
APPLICATION NUMBER: 13-SEP-196
13-SEP-196
996 TACTACAACTACTACCACTACTACGACAACAACAACTACTACGA 1045
                                                                                         146 ......GlnGlnGlnAlaAlaLeuGln 152
                                                                                                                                                                                        946 ACTACTACTACTACGACAACAACAACAACAACAACAACAACAACAAC 995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               113 HisserMetAlaValValSerThrAlaThrProGlnThrGlnLeuGlnLe 129
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TELEPHONE: 650-324-1677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: doub
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REGISTRATION NUMBER: 30,518
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ZIP: 94306-1840
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6071518
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THEIR EUNCTIONAL MUTANTS, VARIANTS, ANALOGS AND FRAGMENTS
FOR TREATMENT AND DETECTION/DIAGNOSIS OF CRYPTOSPORIDIUM
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Percent Identity: 41.057
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seq_documentation_block:
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Patent No. 6071518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
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ZIP: 94306-1840
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          234 GlnGlnAlaLeuGluAlaGlnProProIleGlnGlnProProMetGl 250
                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: PETERS, VERNY, JONES & BIKSA
STREET: 385 Sherman Avenue, Suite 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            laLeuProGlnGlnLeuGlnGlnMetHisHisThrGlnHisHis.....
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                                                                                                                                                                                            USA
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US-08-928-361B-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 650-324-1678
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                               2857
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2664 TACTACAACTACTACCACTACTACGACAACAACAACTACTACGA 2713
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2957 CAACAACAACTACTACTACAACCACGACAACAACAACCA.....CG
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MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 7334 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: 48
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-324-1677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                     182 lnGlnLeu.......GlnGlnGlnGlnGlnGlnGlnGlnHisLeuIle 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 113 HisSerMetAlaValValSerThrAlaThrProGlnThrGlnLeuGlnLe 129
                                  234 GlnGlnGlnAlaLeuGluAlaGlnProProIleGlnGlnProProMetGl 250
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Verny, Hana REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                  CACAACTACCAAGAAACCAACAACAACAACAACAACAACTACTA 2833
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                                                                                                                 lnGlnGlnGlnGln......GlnGlnGlnGlnGlnGlnGlnGln 233
                                                                                                                                                                                                      uGlnArgIleAlaGlnLeuGlnLeu...........GlnG
                                                                                                                                                                                                                                                                                      LysLeuHisHisGlnAsnGlnGlnGlnIleGlnGlnGlnGlnGlnLe
                                                                                                                                                                                                                                                                                                                                                                                                                                                              aGlnGlnSerAlaMetGlnGlnGlnPheGlnAlaValValGlnGlnGlnG 182
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                                                                                                                                                               ACGACAA.....CTACAACCACAAC 2783
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13-SEP-1996
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2.335
51.626
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		200	96	150	85	100	73	050	59

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 28, 2002, 19:34:08; Search time 20.75 Seconds (without alignments)
2125.545 Million cell updates/sec

Title: US-09-668-119-3
Perfect score: 3010
Sequence: 1 MRKAGVAHSKSSKDMESHVF.......WPTSAHLSSTIPCTAHSFQP 579

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5
Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0
Maximum Match 108
Maximum Match 108
Listing first 45 summaries

Database: PIR_68:*
1: pir1:*
2: pir2:*
4: pir4:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

and a second		<u> </u>			Result
298	21 22 22 23 23 23 23	14 15 16 17	110 110 112 113	1654801	11
323.5 323.5 323.5	333.5 330.5 330.5 327.5 327.5	345.5 345.5 342 337	383 378 377 377 377 372	447 439 439 399 384	Score
10.8 10.7 10.7 10.7	11.1 11.0 11.0 10.9			14.6 14.6 13.3 13.2	Query Match 1
357 359 981 684	374 613 357 1076 1008 2038	1390 1145 1457 947 1074	1018 1596 1307 1655 1234 1589	796 4957 5262 1893 2251 966	Length
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RGBYS5 S18235 T06982 T16060 A56154	T05923 S27770 S18236 T24887 T24887 S19033 A43742	T14004 T18235 T14577 T23107 T24877	A53185 A33106 T25563 T13998 T30160 T13606	T20393 T03455 T03454 T03454 A56158 T24490 S25365	ID
regulatory protein omega secalin prec glutenin low molec hypothetical prote Abl substrate ena	glutenin low molec hypothetical prote omega secalin prec hypothetical prote transcription acti female sterile hom		G-box-binding fact neurogenic locus m hypothetical prote gene mastermind pr hypothetical prote hypothetical prote	hypothetical prote ALR protein - huma ALR protein - huma eye development pr hypothetical prote CYC8 protein - yea RAF-28 - mouse	Description

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10.6 10.4 10.4 10.4 10.3 10.3 10.3 10.3 10.2 10.2 10.2	10.6
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T08588 S6925 A26892 JN0689 JN0689 J13828 A60637 T13828 A60637 T13692 A4194 66325 A4194 66326	в30843
stripe a/b protein stripe a/b protein Mopa box protein glutenin, high-mol glutenin high mole hypothetical prote cREB-binding prote merozoite antigen hypothetical prote glutenin low molec transcription fact talpha-fetoprotein hypothetical prote hypothetical prote glutenin, high mol	glutenin high mole

## ALIGNMENTS

OY 372 PGQQVQTPQSMPPPPQPSBQPSQQPSSQPNSNVSSGPAPSPSSFLPSPSPQPSQSPVTA 429	Db 511 APAPQAP APMQPQQPEKQYVTQPPTYKNNYQTAALGQVNTYSGQSKPQVYTYPGPSQV 568  Qy 323 RAPMVVQQPPVQPQVQQQTAVQTAQAAQMVAPGVQVSQSSLPMLSSPS 371    : : :   : :	163 407 223 456	OY 50 ASVSDPMNALQSLTGGPAAGAAGIGMPPRGPGQSLGGMCSFGAMGQPMSLSGQP 103	RESULT 1 T20393 T20393 Appothetical protein Dy3.5 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Accession: T20393 R;Eennard, N. submitted to the EMBL Data Library, June 1997 A;Reference number: Z19266 A;Accession: T20393 A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: DNA A;Residues: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: DNA A;Residues: 1-796 <will> A;Cross-references: EMBL:Z96047; PIDN:CAB09414.1; GSPDB:GN00019; CESP:DY3.5 A;Experimental source: clone DY3 C;Genetics: A;Genetics: A;Gene</will>	

Qy	30	VNP
04	482	PIPONKAVISKPAPATSSVVTPSPSQSLTQQIRKLPAVLYIDSKNESTKKTETLL 712 RMINIIDKNEDRKKDISKM 500
Db 5	13	DTYGLPLVTFYVDKTDKPAAIQRQLQQL 7
RESU TO34	JLT 2	
ALR C;Sp C;Da	protein becies: te: 24	ALR protein - human C.Species: Homo sapiens (man) C;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 21-Jul-2000 C.Accession: T03455
R; Pr Oncc A; Ti	R;Prasad, 1 Oncogene 1: A;Title: Si	d, R.; Zhadanov, A.B.; Sedkov, Y.; Bullrich, F.; Druck, T.; Rallapalli, R.; ye 15, 549-560, 1997 Structure and expression pattern of human ALR, a novel gene with strong hom
A; Ac A; St	A; Accession: A; Status: pr A; Molecule t	1703455 1: T03455 1: T03455 1: To3455 1: To345
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C; Ke	p positiperfami ywords	Map position: 12 Superfamily: human ALR protein Keywords: alternative splicing
Ma Ma	Query Mat Best Loca Matches	Match 14.6%; Score 439; DB 2; Length 4957; Local Similarity 27.7%; Pred. No. 4.7e-12; less 180; Conservative 38; Mismatches 163; Indels 268; Gaps 26;
6 V	76 P       3214 P	PPRGPGOSLGGMGSIGAMGQPMSLSGQPPPGTSGMAPHSMAVVSTATPQTQLQLQQ 131   :
ΔĀ	132 -	VALQQQQCQQFQQQQQAALQQQQQQ 157
ф	3267 I	LMGHRLVTAQQQQQCQQHQQQGSMAGLSHLQQSLMSHSGQPKLSAQPMGSLQQLQQQQQQL 3326
A 4	158 C 3327 C	QQQQQFQAQQSAMQCQFQAVVQ-QQQQLQQQQQQQALIKKLHHQNQQQIQQQQQLQRIA 216 
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g ~~₹.	251 - 3500 F	-QPQPPPSQ 268           PQPQPPSSLQLQPPLRLPGQQQQQVSLLHTAGGGSHGQLGSGSSSEASSVPHLLAQPSV 3559
¥	269 -	HTQHHQPPPQPPQQPPVAQNQPSQLPPQSQTQPLVSQAQALPGQMLYTQPPLK 320
6	0 0	LGDQPGSMTQNLLGPQQPMLERPMQNNTGPQPPKPGPVLQSGQGLPGVGIMPTVG 3615
8 8	321 F 3616 Q	FVRAPM - VVQQPP VQPQVQQQ QTAVQTAQAAQMV APGVQVS QS 362
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C; Superfamily: human ALR protein
C; Keywords: alternative splicing
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A;Cross-references: EMBL:AF010403; NID:g2358284; PIDN:AAC51734.1; PID:g2358285
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R;Prasad, R.; Zhadanov, A.B.; Sedkov, Y.; Bullrich, F.; Druck, T.; Rallapalli, R.; Ya Oncogene 15, 549-560, 1997
A;Title: Structure and expression pattern of human ALR, a novel gene with strong homo A;Reference number: Z14954; MUID:97388474
A;Accession: T03454
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C;Species: Homo sapiens (man)
C;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 21-Jul-2000
C;Accession: T03454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Gene: ALR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ouery Match 14.6%; Score 439; DB 2; Length 5262; Best Local Similarity 27.7%; Pred. No. 4.9e-12; Matches 180; Conservative 38; Mismatches 163; Indels 268; Gaps
4037 SSPQEPKRPSQLPSPSSQLPTEAQLPPTHPGTPK-PQGPTLEPPPPGRVSPAAAQLADTLF 4095
                                                                                                             3981 LLGCQPQLGGFPGPQTGPLQELGAGPRPQGPPRLPAPPGALSTGPVLGPVHPTP----PP 4036
                                                                                                                                                                                                                                     3921 QLRAQLQGVLAKNPQLRHLSPQQQQQLQALLMQRQLQQSQAVRQTPPYQEPGTQTSPLQG 3980
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                                                                                                                                                                                                                                                                                                                                                   3865 SLGDQPGSMTQNLLGPQQPMLERPMQNNTGPQPP--KPGPVLQSGQGLPG--VGIMPTVG 3920
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3805 PQPQPQPSSLQLQPPLRLPGQQQQQVSLLHTAGGGSHGQLGSGSSSEASSVPHLLAQPSV 3864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3745 LLTGKEQNTVDPAVSSEATEGPSTHQGGPLAIGTTPESMATEPGEVKPSLSGDSQLLLVQ 3804
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3519 PPQGPQGMLG-----PAQVAVLQQQHPGALGPQGPHRQVLMTQSRVLSSPQLAQQGQG 3571
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                                            397 SQPNSNVSSGPAPSPSSFLPSPSPSQSPVTARTPQNFSVPSP------ 440
                                                                                                                                                                    363 SL---PMLSS-PSP------GQQVQTPQSMPPPP------QPSPQPGQPS 396
                                                                                                                                                                                                                                                                                            321 FVRAPM--VVQQPP----VQPQVQQQ-----QTAVQTAQAAQMV----APGVQVS--QS 362
                                                                                                                                                                                                                                                                                                                                                                                                             269 -----HTQHHQPPPQPQQPPVAQNQPSQLPPQSQTQPLVSQAQALPGQMLYTQPPLK 320
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Superfamily: GLGF domain homology
848-924/Domain: GLGF domain homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;Miyamoto, H.; Nihonmatsu, I.; Kondo, S.; Ueda, R.; Togashi, S.; Hirata, K.; Ikegami, enes Dev. 9, 612-625, 1995
enes Dev. 9, 612-625, 1995
.Title: canoe encodes a novel protein containing a GLGF/DHR motif and functions with .Reference number: A56158; MUID:95212910
.Accession: A56158
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Species: Drosophila melanogaster;Date: 03-Oct-1995 #text_change 21-Jul-2000;Date: 03-Oct-1995 #sequence_revision 03-Oct-1995 #text_change 21-Jul-2000
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  TARTPQNFSVPSPGPLNTPVNPSSVMSPAGSSQAEEQQYLDKLKQLSKYIEPLRRMINKI 487
                                         ---YRQTEIKLAEMP-----DSNSLVDSVP-PQP----PAPTAQPLSSNTQQPK 1561
                                                                                  PGQQVQTPQSMPPPPQPSPQPGQPSSQPNSNVSSGPAPSPSSFLPSPSPQP----SQSPV 427
                                                                                                                                                                                                        SYVASNQGNNRPLHSGSNPWEREEREKDLEMRREHIRQWREQQISELSQIVSRSPMQEEQ 1465
                                                                                                                                                                                                                                                   --VAQNQPSQLPPQSQTQP----
                                                                                                                                                                                                                                                                                        VPPSTAPKPQQQQQRYLGQSLPAEDKPPLPPTATHPLFKATQQTAPGMNYVASTLDPPKG
                                                                                                                                                                                                                                                                                                                                   PPPSQA-LPQQLQQMHHTQ----HHQPPPQP-----
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                                                                                                                           LKTLILERDFERRAQELQEQ--EEQDQEQQYDKENVQELFRLAGGGQVSAIQTPITS---
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Pred. No. 1.1e-10;
8; Mismatches 196
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C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
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A;Introns: 188/3; 240/3; 420/1; 570/3; 596/1; 732/3; 778/3; 851/3; 1359/2; 1394/2; 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            submitted to the EMBL Data A; Reference number: Z19898 A; Accession: T24490
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A;Cross-references: EMBL:Z68108; PIDN:CAA92133.1; GSPDB:GN00028; CESP:T05A10.1
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                                                                                                                                                                                                                                                                                                                                                                                                                           331 PPVQPQVQQQQ-----TAVQTAQAAQMV--APGVQVSQSSLPMLSSPSPGQQVQT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       151 ARHQAEQQAQQQAQQQQQAQARQQEQQAQLAAIQQQVTPQQFAQILHMQQQLQQQQFQ-QQQ 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              σ
                                  --KTLQKCEIALEKLKNDMRCPLPHR--PRCHRPNSSTYASRSWMPSWPTSAHLSSTIP 571
KKKELEKAQIAQE--
                                                                                                                                                      SRIISENEVILQGDPVIRKKRPYHRQIGAQSSVDHDSNSGGSTRTSPGPKDSRMLQAASR 615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -- AQNNASQQRPSVASTPALSSTPQLNDLTQTMQAQ-LQQQLLLQQQQAQAQQAQQAQQ-AQQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PVAQNQPSQLPPQSQTQPLVS------QAQALPGQMLYTQPPLKFVRAPMVVQQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QQQQQQQQQQQQQQALEAQPPIQQPPMQQPQPPPSQALPQQLQQMHHTQHHQPPPQPQQP 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AMQQQFQAVVQQQQQQQQQQQQQQHLIKLHH--QNQQQIQQ----QQQQQQQRIAQLQLQQ 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SILKHNRYSEGGVGPSGAPSSPSKSQKSASFANERHLHTEHPISNLAKELNQL-TMLDKD 1620
                                                                                                                                                                                            NK-IDKNE--
                                                                                                                                                                                                                                   PPMKQNSNPSMNPSSTSTSASATSSHQILAPSLSKPLEQP---SSSKAASSGNESMSDHI
                                                                                                                                                                                                                                                                     RTPQNFSVPSPGPLNTPVNPSS-----VMSPAGSSQAEEQQYLDKLKQLSKYIEPLRRMI
                                                                                                                                                                                                                                                                                                              LQNQAREAQHRQLLISSTPAPRGGITMGTPIGIARREEQPVPSTVAVTTAPAAVRTPVAV
                                                                                                                                                                                                                                                                                                                                                    PQSMPPPPQ----
                                                                                                                                                                                                                                                                                                                                                                                       AQLAQQAQQQQQQQSQNRTVSQALQYIQSMQLQQRADGTPNAESQEERLAQMLNEQQQRM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QLQQQQQLQQQAQQLSQQQAQQQQQQLQQLQ---LQQFLQQQQQLH--QQRAAAQQAQ--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LQQQQLQQQQLQQQLQQQLQQQLQQVLQISQAQQQAQQAQHVQSRQMQPSQQSQVQA
                                                                           SQSLFELSGSKHFMGSLTSGQPLLRPIQAHNDPNYTPECIYCKLTFPNEAGLQAHEVVCG
                                                                                                                 ----DLSKMKSLLDILT----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                  ----PSPQPGQPSSQPNSNVSSGPAPSPSSFLPSPSPQPSQSPVTA 429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13.2%; 29.5%;
                                                                                                                                                                                            -DRKK-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Library,
---GNPHSALKRRHTHQDATLAMHS----PLAAHTPSNMP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   T05A10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  52; Mismatches 194;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 397; DB 2;
Pred. No. 1.6e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      November 1995
                                                                                                                 ----DPSKR-----CPL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 2251;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      176;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ::
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721
                                                                                                                 516
                                                                                                                                                                                                                                                                                                                                                                                                                             378
                                                                             675
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              269
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A; Residues: 1-546, 'K', 548-966 <TRU>
A; Cross-references: EMBL: M23440; NID:g171349; PIDN: AAA34545.1; PID:g171350 C; Genetics: A; Gene: SGD: CYC8; SSN6; CRT8 A; Cross-references: SGD: S0000316; MIPS: YBR112c A; Map Position: 2R C; Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOL. Cell. Biol. 7, 3637-3645, 1987
A;Title: Molecular analysis of SSN6, a gene functionally related to the SNF1 protein A;Accession: S25404; MUID:88065502
A;Accession: S25404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A:Cross-references: EMBL:X66247; NID:g3548; PIDN:CAA46973.1; PID:g3550 R;Mannhaupt, G.; Stucka, R.; Ehnle, S.; Vetter, I.; Feldmann, H. Yeast 10, 1363-1381, 1994
A;Title: Analysis of a 70 kb region on the right arm of yeast chromosome A;Reference number: S48255; MUID:95208357
A;Accession: S48277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Yeast 8, 397-408, 1992
A;Title: Molecular analysis of yeast chromosome II between CMD1 and LYS2: the excision A;Reference number: S25364; MUID:92327848
A;Accession: S25365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: DNA
A; Residues: 1-546, 'K', 548-966 <TRU>
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A; Accession: S25405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gene 73, 97-111, 1988
A;Title: Cloning and characterization of the CYC8 gene mediating glucose repression in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: EMBL:Z35981; NID:g536449; PIDN:CAA85069.1; PID:g536450; MIPS:YBR1120R;Schultz, J.; Carlson, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: DNA
A; Residues: 1-966 <FE2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: EMBL:X78993; NID:g476045; PIDN:CAA55615.1; PID:g4760 A;NOte: the nucleotide sequence was submitted to the EMBL Data Library, R;Feldmann, H.; Mannhautt, G.; Schwarzlose, C.; Vetter, I. submitted to the Protein Sequence Database, August 1994 A;Reference number: S45927
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: DNA
A; Residues: 1-966 <MAN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                #;.396-339/Domain: tetratricopeptide repeat homology <TT3>
#;.330-363/Domain: tetratricopeptide repeat homology <TT4>
#;.365-398/Domain: tetratricopeptide repeat homology <TT5>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Accession:
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A; Residues: 1-966 <MAW>
                                                                                                                                                                                                Query Match
rocal Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    )Description: required for complete derepression of ICL1; required for repression of SU Superfamily: unassigned tetratricopeptide repeat house for the superfamily: unassigned tetratricopeptide repeat house for the superfamily: unassigned tetratricopeptide repeat house, seywords: nucleus; transcription regulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;Alternate names: glucose repression mediator; protein YBR0908; protein YBR112c; SSN6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MoLecule type: DNA
Residues: 1-546, 'K', 548-966 <SCH>
Cross-references: EMBL:M17826; NID:g172725; PIDN:AAA35103.1; PID:g172726
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      224;257/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Trumbly
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                                                                  447 GNPLNTRISAQSANATASMVQQQHPAQQTPINSSATMYSNGASPQLQAQAQAQAQAQAQAQ 506
94 GQPMS--LSGQPPPGTSGMAPHSMAVVST------ATPQTQLQLQQVALQQQQQ 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                            295/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             97-111, 1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        S45980
                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                     tetratricopeptide repeat homology <TT1>
tetratricopeptide repeat homology <TT2>
                                                                                                                                                                                                                          12.8%;
                                                                                                                                                                                                60;
                                                                                                                                                                                         Score 384; DB 2; I
Pred. No. 2.8e-10;
0; Mismatches 195;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PIDN:CAA55615.1; PID:g476068
                                                                                                                                                                                                                                                        Length 966;
                                                                                                                                                                                                Indels 118; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               April 1994
                                 밁
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C;Species: Mus sp. (mouse)
C;Apecies: Mus sp. (mouse)
C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 01-Dec-2000
C;Accession: I53172; I66850; I66851
R;Nomura, M.; Takihara, Y.; Shimada, K.
Differentiation 57, 39-50, 1994
A;Title: Isolation and characterization of retinoic acid-inducible cDNA clones in Drosophila polyhomeotic protein.
Drosophila polyhomeotic protein.
                                                                                                                                                                                                                                                                C;Superfamily: SAM homology
F;373-476/Region: glutamine-rich
F;945-1011/Domain: SAM homology <SAM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Molecule type: mRNA
A;Residues: 1-1012 <RES>
A;Cross-references: GB:873882; NID:9688186; PIDN:AAB31766.1; PID:9688187
A;Accession: I66850
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A;Accession: I53172
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: mRNA
A; Residues: 1-75, 'V'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: mRNA
A; Residues: 1-75, 'V'
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                A;Gene: rae-28
                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: GB:S73884; NID:g688189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Accession:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: GB:S73883; NID:g688188
                                                                                                                       Matches
                                                                                                                                                                                  Query Match
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260 QSLNLSQAGGGSGNSLPGSMGPGGGGQAPGGLGQLPSSG----LTGGSCPRKGTGVVQPL 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   927 KEEAKMREEEQTSQEKSPQENTLPRENVVRQVEEDEN 963
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              471 KQLSKYIE-------PLRRMINKIDKNED 492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        867 PVEDEVRQHSKEENGTTEASAPSTEEAEPAASRDAEKQQDETAATTITVIKPTLETMETV 926
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            807 AEEATKAASVSPSTKPLNTEPESSSVQPTVSSESSTTKANDQSTAETIELSTATVPAEAS 866
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             747 NKLVNTATSIEENAKSEVSNQSPAVVESNTNNTSQEEKPVKANSIPSVIGAQEPPQEASP 806
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    350 AQMVAPGVQVSQSSLPMLSSPSPG------QQVQTP---QSMPP--PPQPSPQPGQP 395
                                                          60 QSLTGGPAAGAAGIGMP----PRGPGQSLGGMGSFGAMGQPMSLSGQ--PPPGTSGMAPH 113

    mouse

                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P-----GPLNTPVNPSSVMSPAGSSQAEEQQ---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QPLV-SQAQALPGQMLYTQPPLKFVRAP--MVVQQPP------VQPQVQQQQTAVQTAQA 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QPFSTQAMEHPQSSQLPPQQQQLQSVQHPQQLQGQPQAQAPQPLIQHNVEQNVLPQKRYM 686
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SSQPNSNVSSGPAPSPSSFLP-SPSPQPSQSPVTARTPQN-----FSVP---S 439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QQQQQQQQQQQQQQQQQQQQQQQQQQLQPLPRQQLQQKGVSVQMLNPQQGQPYITQPTVIQAHQL 626
                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                             <RE2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ARE3>
                                                                                                                                                   12.7%; score 383.5; DB 2; 26.7%; Pred. No. 3.1e-10;
                                                                                                                       68; Mismatches 206;
                                                                                                                                                                              Length 1012;
                                                                                                                       Indels 135;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ----YLDKL 470
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F9

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G-box-binding factor - slime mold (Dictyostelium discoideum)
C;Species: Dictyostelium discoideum
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 24-Sep-1999
C;Accession: A53185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  . . B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R;Schnitzler, G.R.; Fischer, W.H.; Firtel, R.A.
R;Schnitzler, G.R.; Fischer, W.H.; Firtel, R.A.
R;Schnitzler, G.R.; Fischer, W.H.; Firtel, R.A.
R;Firtle: Cloning and characterization of the G-box binding factor, an essential component A;Title: Cloning and characterization of the G-box binding factor, an essential component A; Reference number: A53185; MUID:94170994
A;Accession: A53185; MUID:94170994
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-708 <SCH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      γ
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                                                                                                                                                                                                                                                                      _말
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: GB:L29075; NID:g456561; PIDN:AAA21021.1; PID:g456562 C;Superfamily: G-box binding factor C;Keywords: DNA binding; transcription factor; zinc finger
                                                                                                                                                                                                                           Ş
     Qy
                                                                                                               20
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity Matches 170; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   376 PHSLIQQQQQIHLQQKQVVIQQQIAYHH---QQQFQHRQSQLLHTATHLQLAQQQQQQQQQQ 433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       397 SQPNSNVSSGPAPS-PSSFLPSPSPQPSQ------SPVTARTPQNF---SVPS 439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             483 MLQSSPLTLPPEPTSKPPIP------IQSKPPVAPIKPPQLGAAKMSATQQPP--PH 531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            284 VAQNQPSQLPPQSQTQPLVSQAQALPGQMLYTQPPLKFVRAPMV------VQQPPVQPQ 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       434 QQQQQQQQQQQQQQGTTLTAPQPP--QVPPTQ-----QVPPSQSQQQAQTLVVQP 482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           231 QOQQQQALEAQPPIQQPPMQQPQPPPSQALPQQLQQMHHTQHHQPPPQPQQ-----PP 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          174 FQAVVQQQQQLQQQQQQQ--QHLTKLHHQNQQQIQQQQQQQQQQQRAA-QLQLQQQQQQQQQQQQQQQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  316 PAAQTVTVSQGSQTEAESAAAKKAEADGSGQQSVGMNLTRTATPAPSQTLISSATYTQIQ 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         500 MKSLLDILTDPSKRCPLKTLQKCEIALEKLK-----NDM--RCPLPHRPRCHRP 546
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     579 SPPSSQAAPGALQECPPALAAGMTLAPVQGTAHVVKGGPTASSPVVAQVPAAFYMQSVHL 638
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 532 IPVQVVGTRQPGSAQAQALGLAQLAAAVP-----TPRGITGAVQPG-QAHLAS 578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      337 VQQQQTAVQTAQAAQMVAPGVQVSQSSLPMLSSPSPGQQVQTPQSMPPPPPQPSPQPGQPS 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            639 PGKAQT-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 440 PGPLNTPVNPSSVMSPAGSSQAEEQQYLDKLKQLSKYIEPLRRMINKIDKNEDRKKDLSK 499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       718 PTLALVSROMGDSKPPQA 735
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        547 NSSTYASRSWMPSWPTSA 564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                663 LASVLPTKASPAAESP-KVIEEKNSLGEKAEPVASLNANPPNSDLVALAPTPSAP----P 717
199 HONOQOIQ----QOOQQLQRIAQLQLQQQQQQQQQQQQQQQQALEAQPPIQQPPMQQPQPP 255
                                                       126 ОСИОРРООИО----ОООННООООООРОННООМООООННООМОООООННООМООООННООМО 182
                                                                                                            139 QQQQFQQQQAALQQQQQQQQQQQQAAQQSAMQQQFQAVVQQQQQLQQQQQQQQQHLIKLH 198
                                                                                                                                                                                                                                                                                                                                       44 HNKKSQASVSDPMNALQSLTGGPAAGAAGIGMPPRG-------PGQS-LGG 86
                                                                                                                                                                         66 SSNTPSFLLPPSSIMSSNVFPSHDGQYPDMPNMVDQYQIHPNQNPHYNYQYQLMFMQQQA 125
                                                                                                                                                                                                                              87 MGSFGAMGQPMS--LSGQPPPGTSGMAPHSMAVVS----TATPQTQLQLQQVALQQQQ 138
                                                                                                                                                                                                                                                                                     6
                                                                                                                                                                                                                                                                                  HHQGNSSSSSSSSSSQTIGGSDLSNISALPLPLPSIFTTAQNQMNPPILFPPTSSLLGG 65
                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                         12.7%; Score 383; DB 2; Length 708; 24.4%; Pred. No. 2.3e-10;
                                                                                                                                                                                                                                                                                                                                                                                                 57;
                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ----LAVKRKAESEEERDDLSA 662
                                                                                                                                                                                                                                                                                                                                                                                                    Indels 270;
                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                       23;
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Db		
Qy	256 PSQALPQQLQQMHHTQHHQPPPQPQQP	
Db	QIQMYPQQPQSLSNSGNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN	
Qy	283PVAQNQPS 290	
Db	::     296 LNNLTLSQNNTSGSNTPSPSTKGKRKHHETSNSEKKDSSGQTIPKCTRCNEAASWKHDKR 355	
Qy	291	
Ъ	356 RWWCKECKKAFTPGITKMQQVPQQAQLQPLQNHNQIIP-QLWDSQQNNSSQNTP 408	
Qу	332 PVQPQVQQQQTAVQTAQAAQMVAPGVQVSQ 361	
ДЪ	409 PTQPQNNMNQINHQLLQQQHQQAQLQAHLNLTASNQQVPPQLQQQINGGLPNNNNSLITQ 468	
Qy	362 SSLPMLSSPSPGQQVQTPQSMPPPP	
Db	469 NTLNSLSTSVSCPPCPLCRGISSWKHDKKRYFCKECKKPFTPVGAGLSPSS 519	_
Qy	91 QPGQPSSQPN	
Db		
Qy	20 PQP-SQSPVTARTPQNESVPS-PGPLNTPVNPSSV	
DЬ	INTUGGILLISGLOFFNOGGGDLMM VJ	
Qy	49	
DЪ	640 LNSFSNTGALLSSNGINLANLGNPLSQLNKKQKKRSD 676	
RESULT A33106 neurog N; Alte C; Spec C; Date	ULT 9 106 rogenic locus mam protein - fruit fly (Drosophila melanogaster) lternate names: mastermind protein pecies: Drosophila melanogaster pecies: Drosophila melanogaster ate: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 21-Jul-2000 cression: A36791. A37106: S13514	
R; Smc Genes A; Tit	moller, D.; Friedel, C.; Schmid, A.; Bettler, D.; Lam, L.; Yedvobnick, B. moller, D.; Lam, L.; Yedvobnick, B. es Dev. 4, 1688-1700, 1990 itle: The Drosophila neurogenic locus mastermind encodes a nuclear protein unusua eference number: A36391; MUID:91065516	ED.
A; Acc A; Sta A; Mol A; Res A; Crc A; Not C; Ger A; Ger A; Crc	A;Accession: A36391 A;Status: preliminary A;Molecule type: mRNA A;Residues: 1-1596 <smo> A;Cross-references: GB:X54251; NID:g8203; PIDN:CAA38152.1; PID:g8204 A;Ote: strain Canton S C;Genetics: A;Gene: FlyBase:mam A;Cross-references: FlyBase:FBgn0002643</smo>	
Que Bes Mat	uery Match 12.6%; Score 378; DB 2; Length 1596; lest Local Similarity 30.2%; Pred. No. 8.1e-10; latches 157; Conservative 30; Mismatches 143; Indels 190; Gaps 24;	
Qγ	46 KKSQASYSDPMNALQ-SLTGGPAAGAAGIGMPPRGPGQSLGGMGSFGAMGQPMSLSGQP- 103 	
Qy		
Db	GPNGGTGGAPNACGNGGNSGNLMSEHPLAAQTLKQMAEQHQHKNAMGGMGGEPRPPHGMN 6	
, p	136 -0000000F00000AAAL00	

. 5	Db Db Db Db Db Db Db Db Db	RES T255 C; D, C; D, C; D, C; A, S, N, A, S, A, S, A, S, A, S, A, S, A, S, C, D, A, C,	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
	Query Matches Hest Loc Matches 93 591 651 134 705 705 821	otheti otheti ate: 1 ccessi alson, nitted ascrip ascrip ocessi tatus:	164 710 191 770 242 8825 276 276 2940 3324
. QeQeeeSQALeQvLQQMHHTQHHQPPPQP	Atch 169; C MNALOSLI     :: MOCOONMI MGOPMSLS   ::  MNRPSSQMLQ MNRPSSQMLQ MNGSPHQQ QAQQSAMQ CAQQSAMQ	RESULT 10 725563 hypothetical protein C24A8.3 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000 C;Accession: 72563 R;Nelson, J; Gattung, S. submitted to the EMBL Data Library, December 1996 A;Description: The sequence of C. elegans cosmid C24A8. A;Reference number: 220051 A;Reference number: 220051 A;Reference number: 220051 A;Recession: 72563 A;Status: preliminary; translated from GB/EMBL/DDBJ A;Residues: preliminary; translated from GB/EMBL/DDBJ A;Residues: 1-1307 (NEL) A;Residues: 1-1307 (NEL) A;Cross-references: EMBL:080845; PIDN:AAB37980.1; GSPDB:GN00028; CESP:C24A8.3 A;Coss-references: EMBL:080845; PIDN:AAB37980.1; GSPDB:GN00028; CESP:C24A8.3 A;Emp position: X A;Introns: 42/3; 116/2; 165/1; 200/3; 233/3; 275/1; 318/1; 358/3; 397/3; 590/3; 606/3 A;Introns: 42/3; 116/2; 165/1; 200/3; 233/3; 275/1; 318/1; 358/3; 397/3; 590/3; 606/3	64 QAQQSAM

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: DNA A;Residues: 1-1655 <NEW>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: FlyBase:FBgn0013119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R;Newfeld, S.J.; Tachida, H.; Yedvobnick, B.
J. Mol. Evol. 38, 637-641, 1994
A;Title: Drive-selection equilibrium: homopolymer evolution in the Drosophila gene ma
A;Reference number: Z17850; MUID:94365848
A;Accession: T13998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gene mastermind protein - fruit fly (Drosophila virilis)
C;Species: Drosophila virilis
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 17-Nov-2000
C;Accession: T13998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 11
T13998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 12.5%; Score 377; DB 2; Length 1655; Hest Local Similarity 25.2%; Pred. No. 9.3e-10; Matches 162; Conservative 30; Mismatches 159; Indels 292; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1171 AKSSPDLSQPSTSKQRPPANKADMTVIRDAIVSHVKGSRKMTPEYIE-----YVCEEL 1223
197 LHHQN-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1268 AR 1269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1224 NRLMRELEK-ADMKTDRRYISVRKLLALIQE-----EKLTIIIPP-----RIPMP 1267
                                                               784 QQQQQQHHAQQQQQHPNGPNMGVPMGGAGNFAKQQQQQVPTPQQQQQQQQQQQQQQQYSP 843
                                                                                                                156 QQQQQQFQAQQS-------AMQQQFQAVVQQQQQLQQQQQQQHLIK 196
                                                                                                                                                              727 HLPPQFHQKAPGGGPGMNVQQNFLDIKQELFYSSPNDFDLKHLQQQQAMQQQQ---QQQQ 783
                                                                                                                                                                                                               610 GGPTAGGGGGG----NGPGGLMSEHSLAAQTLKQMAEQHQHKSAMGGMGGFHVPPHGMQQQ 666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1117 APNGLP-----PNNAGPMIQQGKNIAGGYPPNQNKVTPGKNVPKNQQQSRPQQANGKVQ 1170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1057 APKPRYRGKKNPAQEPPPPIQQTNAEDLNNSMSGLPMGAKGERKVMAPSLTTNTFHQQQQ 1116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1001 QQNIPIQ--HQQQQQNMMNQPMQSNNNQNMANIQNQQNLQNPPIIQQQQQQQ--IPPAKV 1056
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   539 HR 540
                                                                                                                                                                                                                                                                                                                    91 ------GAMGQPMSLSGQPPP---GTSGMAPHSMAVVSTATPQTQ- 126
                                                                                                                                                                                                                                                                                                                                                                                                                   64 GGPAAGAAGIGMPPRGPG------90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         481 RRMINKIDKNEDRKKD--LSKMKSLLDILTDPSKRCPLKTLQKCETALEKLKNDMRCPLP 538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           429 ARTPQNFSVPSPGPLNTPVNPS-----SVMSPAGSSQAEEQQYLDKLKQLSKYI-EPL 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          378 TPQSMPPPPQPSPQPGQPSSQPNSNVSSGPAPSPSSFLPSPS------PQPSQSPVT 428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               350 A-----LSSPSPGQQVQ 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              305 AQALPGQMLYTQPPLKFVRAPMV-------VQQPPVQPQVQQQQTAVQTAQA 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            941 NGMQYKLVPQQRQQNQQKMPNQQGQPMQQVHQGGHQEEGFQQQHGPPNNQGQNQQPPMQN 1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             280 ------QQPPVAQNQPSQL------PPQSQ---TQPLVSQ 304
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                    --0001000000LQ-----R 214
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R;Le, T.T.; Kemp, K.; Scheet, P. submitted to the EMBL Data Library, April 1997 A;Description: The sequence of C. elegans cosmid C37A2. A;Reference number: Z20746
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypothetical protein C37A2.2 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT
T30160
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A;Introns: 46/1; 124/1; 159/1; 231/1; 508/3;
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Experimental source: strain Bristol N2; clone C37A2
                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gene: CESP:C37A2.2
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                                                                                                                                                                                                                                                                                            123
587
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   904 ATQQQQQQQQQQQQQQQQQQQQQQATTTTLQMKQTQQLHISQQGGGSHGIQVSAGQHLH
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                                        250
                                                                                                                                                                                                                                                                                                                                                                       71 AGIGMPPRGPG----QSL----GGMGSFGAMGQPMSLSGQPPPGTSGMAPHSMAVVSTAT 122
                                  ------QQPQPPPSQA---LPQQLQQMHHTQHHQPPPQPQQPPVAQNQPSQLPP-
                                                                                                                                                                 LSMQQ--IAAIQQQQQ---
                                                                                                                                                                                                        SAMOQQFQAVVQQQQQQQQQQQQHLIKLHHQNQQQIQQQQQQQQQQQQQQQQQQQQQ
                                                                                                                                                                                                                                                                                        SGSGQPTPVPGTPQPQQITPQPGSLGPMGSLGPPTA----PPGSQPMNP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NNGAMNQLGGPMGGMPGMQMGGPGGVPINPMQMNPNGGAPNAQ 1204
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ----AAAQQQQQQVPPNMRQRQTQAQAAAAAAAAAA----AAQAQAAANANGGPGGNVPLM 1131
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IQRMNSYPGNAQQFRPPPQQSQQPIPPQQQQ-----QPPAPPQQLQQPPVQDTSAVAEPPK
                                                                                                                          QQQQQQQQQA-----
                                                                                 QQQVQQQQQAPPPTTPNPGHPQGFFPTNQAGPPGTPGRPIPPYAMGQPPMYHQAGPQGQM
                                                                                                                                                                                                                                                                                                                                                                                                                     170;
                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                 --QQQRIQQQQAAPSASNSPLLVNLLSNQQPPQQQYMYPGPSAQG 491
                                                                                                                                                                                                                                                                                                                                                                                                                                      12.4%;
25.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -VPSPGPLNTPVNPSSVMSPAGSSQAE 462
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -PVAQNQPSQLPPQSQTQPLVSQAQALPGQMLYTQPPL
                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 372; DB 2;
Pred. No. 1.2e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       from GB/EMBL/DDBJ
                                                                                                                        -LEAQPP-----IQQPPM-----
                                                                                                                                                               ----HQQYQQRILQQQQQ------QAMMQQQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        740/3; 891/1; 931/1; 975/1; 1014/3; 1083/3
                                                                                                                                                                                                                                                                                                                                                                                                                   169;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 1234;
                                                                                                                                                                                                                                                                                                                                                                                                                   Indels 280;
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                                        294
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hypothetical protein 87B1.5 - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 17-Nov-2000
C;Accession: T13606; S23632
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                                                                                                                                                                                                                   C;Superfamily: SAM homology
C;Keywords: DNA binding; nucleus
F;74-80,247-285,411-450,494-650,727-737,775-955,1032-1061/Region: glutamine-rich
F;1510-1576/Domain: SAM homology <SAM>
                                                                                                                                                                                                                                                                                        A;Cross-references: FlyBase:FBgn0004861; FlyBase:FBgn0004860
A;Introns: 12/2; 595/1; 745/2; 1340/1
C;Superfamily: SAM homology
                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: mRNA
A; Residues: 1-1010,'V',1012-1192,'L',1194-1274,'I',1276-1589 <DEC>
A; Cross-references: EMBL:X63672; NID:911056; PIDN:CAA45211.1; PID:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Reference number: S23632; MUID:92146957
A;Accession: S23632
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A; Accession: T13606
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               B
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                                        Вp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Molecule type: DNA
A;Residues: 1-1589 <MUR>
A;Cross-references: EMBL:298269; NID:el355202; PID:el251078;
                                                                                                                                                                                                                                                                                                                                                    A;Gene: FlyBase:ph-p
                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Status: preliminary
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                                                                                                                          Matches
                                                                                                                                              Best
                                                                                                                                                               Query Match
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  51
                                                                                                                                            Local Similarity
                                        ASSVSTQTAQNQSLLKAKMRNKQQPVRPALATLKTEIGQVAGQNKVVGHLTTVQQQQQQAT 733
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SVSDPMNALQSLTGGPAAGAAGIGMPPRGPGQSLGGMGSFGAMGQPMSLSGQPPPGTSGM 110
                                                                                 AHSKSSKDMESHVFLKAKTRDEY - - - -
                                                                                                                          158;
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                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     --- QSQTQPLVSQAQALPGQMLYTQPPLKFVRAP----MVVQQP-
                                                                                                                                              12.1%;
29.7%;
                                                                                                                        57;
                                                                                                                                              Score 365; DB 2; Pred. No. 3e-09;
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                                                                                                                          Mismatches
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                                                                                 --LSLVA----RLIIHFRDIHNKKSQA 50
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                                                                                                                                                               Length 1589
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24;

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transcription activator CAL11 homolog - yeast (Candida albicans)
C;Species: Candida albicans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
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A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-1390 <SAI>
A;Cross-references: EMBL:AB009080; NID:dl228566; PID:dl034109; PIDN:BAA33143.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                trfA protein - slime mold (Dictyostelium discoideum)
c;Species: Dictyostelium discoideum
c;Species: Dictyostelium discoideum
c;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 11-May-2000
C;Accession: T14004
R;Saito | J.; Adachi, H.; Sutoh, K.
J. Biol. Chem. 273, 2465: 24659, 1998
A;Title: Dictyostelium T1:FA homologous to yeast Ssn6 is required for normal growth and A;Heference number: 2178:2; MUID: 98406112
A;Heference number: 2178:2; MUID: 98406112
                                                                                                          RESULT 15 T18235
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   253 QPPPSQALPQQLQQIHHTQHHQPPPQPQQPPV----AQNQPSQLPPQSQTQPLVSQAQA 307
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R;Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, November 1998
A;Reference number: Z18831
A;Accession: T18235
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A;Residues: 1-1145 <BAR>
A;Cross-references: EMBL:AL033501; NID:e1341022; PID:e1341031; PIDN:CAA21993.1
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959 TTPGTANHSHNP 970
                                                        569 TIPCTA-HSFQP 579
                                                                                                                 904 PTPGALPATTPGTLANA---IKTPHNIPTPQIPPQTQSNKNTPSAQS--PAYPVKATPSS 958
                                                                                                                                                                         510 PSK-RCPLKTLQKCEIALEKLKNDMRCPLPHRPRCHRPNSSTYASRSWMPSWPTSAHLSS 568
                                                                                                                                                                                                                                  857 ------QQQQQQQQQPPQRQQSVSKASQKSVAKTNKKGTGQGRKK-----KASISAGTA 903
                                                                                                                                                                                                                                                                                          450 SSVMSPAGSSQAEEQQYLDKLKQLSKYIEPLRRMINKIDKNEDRKKDLSKMKSLLDILTD 509
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         343 AVQTA-----QAAQMVAPGVQVSQSSLPMLSSPSPGQQVQTP---QSMPPPPQPS 389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  698 LEKVRSQYAKYFEYVKEQINLRRQQVLQQGGANMMSSQQQQQQQQQNMTRSQPQSQQQQQ 757
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24.4%; Pred. No. 1.6e-08;
ative 56; Mismatches 191; Indels 261; Gaps
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Search completed: February 28, 2002, 19:39:11 Job time: 303 sec

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Copyright (c) 1993 - 2000 Compugen Ltd.
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DC11_DROME
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SMF1_HUMAN
GDA7_HHEAT
GDA5_WHEAT
GDA5_WHEAT
GDP_MOUSE
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Query Match
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Matches 170; Conserv

44 HNKKSQASVSDPMNALQSLTGGPAAGAAGIGMPPRG-------PGQS-LGG 86 6 HHQGNSSSSSSSSSSSTQTIGGSDLSNISALPLPLPSIFTTAQNQMNPPILFPPTSSLLGG

12.7%; Score 383; DB 1; Length 708; ilarity 24.4%; Pred. No. 1.5e-09; Conservative 57; Mismatches 200; Indels 2

Indels 270; Gaps

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99075; AAA2; ;; T00315; DD02046; ption regu. 339 481 115 115 270 549 708 AA;	the Swiss 1 Lean Bioinformon-profit and this st requires a n email to	INAX3; INAAX3; INE-94170994; PubMed-8125261; itzler G.R., Fischer W.H., Fi: ning and characterization of ntial component of the develop development in Dictyostelium s Dev. 8:502-514(1994). FUNCTION: CAMP-RESPONSIVE TRAI LATE GENE EXPRESSION. ESSENTI. SWITCH BETWEEN EARLY AND LATE CAGGT-RICH GENE REGULATORY ELL CAGGT-RICH GENE REGULATORY EL	(Rel. (Rel. (Rel. (Rel. ) (Rel	8888889999 55788889000111
AAA21021.1; 315; 046; gbfA. regulation; 39 368 81 510 11 21 11 263 70 292 49 557 8 AA; 79268		A., AND PARTIAL S ; PubMed=8125261; Fischer W.H., Fi Fischer W.H., Fi racterization of ent of the devel in Dictyostelium -514(1994). TRESPONSIVE TRE PRESSION. ESSENTI ENE REGULATORY EL LOCATION: NUCLEAN	m ~ m	1028 618 347 395 1531 1531 1468 1023 1142 11081 11556 2414
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är þr	ed through a collaboration and the EMBL outstation en restrictions on its content is in no way ge by and for commercial //www.isb-sib.ch/announce/	factor, an ween early and ATOR REGULATING E DEVELOPMENTAL IS TO A NUMBER OF		p51521 drosophila Q24762 drosophila P18175 sus scrofa Q05738 mus musculu Q94916 homo sapien Q09260 caenorhabdi Q61735 drosophila P13055 drosophila P19659 saccharomyc Q94614 homo sapien

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SEQUENCE FROM N.A.
MEDLINE-88065502; PuɔMed-3316983;
Schultz J., Carlson M.;
Schultz J., Carlson M.;
"Molecular analysis of SSN6, a gene functionally related to the SNF1 protein kinase of Saccharomyces cerevisiae.";
Mol. Cell. Biol. 7:3537-3645(1987).
                                                                                                                                                                                                                                                                                                    GLUCOSE REPRESSION MEDIATOR PROTEIN.

SSN6 OR CYC8 OR YBR112C OR YBR0908.

Saccharomyces cerevisiae (Baker's yeast).

Eukaryota; Fung1; Assomycota; Saccharomycotina; Saccharomycetes;

Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                     SSN6_YEAST STANDARD: PRT; 966 AA. P14922; 01-APR-1990 (Rel. 14, Created) 01-APR-1990 (Rel. 14, Last sequence update) 01-FEB-1995 (Rel. 31, Last annotation update)
                                                                                                                                                                                 Trumply R.J.; "Cloning and characterization of the CYC8 gene mediating glucose
                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDIJINE=89211964; PubMed=2854095;
                                                                                                                                                                                                                                                                                      NCBI_TaxID=4932;
                                                                                                                                              iene 73:97-111(1988)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           640 LNSFSNTGALLSSNGINLANLGNPLSQLNKKQKKRSD 676
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                470 LKQLSK-----YIEPLRRMINKIDKNEDRKKD 496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          580 SSSISQSPLQLNYQTPTCSPNPSLPSIGGNLNSQANSIKPDGGILISGLSPPKSSSSLNN 639
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               420 PQP-SQSPV-----TARTPQNFSVPS-PGPLNTPVN---PSSVMSPAGSSQAEEQQYLDK 469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        520 SPSSPKKKSNITPITTSSTSSSSSTPSIINNNNNNNANSSKNNTPKKQLSPPPSVLQSPS 579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             391 QPGQPSSQPN-----SNVSSGPAPS-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    469 NTLNSLS-----TSVSCPPCPLCRGISSWKHDKKRYFCKECKKPFTPVGAGLSPSS 519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                409 PTQPQNNMNQINHQLLQQQHQQAQLQAHLNLTASNQQVPPQLQQQINGGLPNNNNSLITQ 468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     332 PVQPQ------VQQQ------QTAVQTAQAAQMVAPGVQ------VSQ 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            356 RWWCKECKKAFTPGITKMQQVPQQAQLQPLQNHNQIIP-QLWDSQ-----QNNSSQNTP 408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    291 -----QLPPQSQTQPLVSQAQALPGQMLYTQPPLKFVRAPMVVQQP 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        296 LNNLTLSQNNTSGSNTPSPSTKGKRKHHETSNSEKKDSSGQTIPKCTRCNEAASWKHDKR 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    283 ----PVAQNQPS------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              56 PSOALPOOLOOMHHIOHHOPPPOPOOP------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     87 MGSFGAMGQPMS--LSGQPPPGTSGMAPHSMAVVS-----TATPQTQLQLQQVALQQQQ 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SSLPMLSSPSPGQQVQTPQSMPPPP------99SP 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ----HQHNQQQHQCQQNQIQMYPQQPQSLSNSGNNNNNNNNNNNNNNNNNNNNNNNNNNSHQ 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     \mathsf{HHQLQQHQHQQQCQQQHQQQQHQQQQHHQQQQQHHQHSQPQQQHQHQHQQQQQ--240}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28.1 ОМООННОООООМНООООООННООМООННООМООННООМОООННООМОООННООМОООННООМО
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SSNTPSFLLPPSSIMSSNVFPSHDGQYPDMPNMVDQYQIHPNQNPHYNYQYQLMFMQQQA 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HQNQQQIQ----QQQCQLQRIAQLQLQQQQQQQQQQQQQQQQQALEAQPPIQQPPMQQPQPP 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QQQQFQQQQAALQCQQQQQQQQQQQGSAMQQQFQAVVQQQQQQLQQQQQQQQHLIKLH 198
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                                                                                                                                                                                                                        CONFLICT
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IF FUNCTION: IT IS INVOLVED IN REPRESSION BY A1-ALPHA2 AND ALPHA2 AND IN OTHER SYSTEMS AS A GENERAL REPRESSOR OF TRANSCRIPTION. THIS PROTEIN HAS NO OBVIOUS DNA-BINDING DOMAINS. IT MIGHT NOT INTERACT DIRECTLY WITH DNA BUT WITH DNA-BOUND PROTEINS.

1- SUBCELLULAR LOCATION: NUCLEAR.

1- SIMILARITY: TO YEAST GALL AND CCR4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPRO01440; TPR. Pfam; PF00515; TPR; 10. SMART; SM00028; TPR; 9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; M23440; AAA34545.1; --
EMBL; M17826; AAA35103.1; --
EMBL; X66247; CAA46973.1; --
EMBL; X78993; CAA55615.1; --
EMBL; Z35981; CAA85069.1; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sikorski R.S., Boguski M.S., Goebl M., Hieter P.A.;
"A repeating amino acid motif in CDC23 defines a family of proteins and a new relationship among genes required for mitosis and RNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mannhaupt G., Stucka R., Ehnle S., Vetter I., Feldmann H.; "Molecular analysis of yeast chromosome II between CMD1 and LYS2: the excision repair gene RAD16 located in this region belongs to a novel group of double-finger proteins.";
                                                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                                            REPEAT
                                                                                                                                                                                                                                                                                                                                               REPEAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Transcription regulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TPR REPEATS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            [3]
SEQUENCE FROM N.A.
STRAIN=S288C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nuclear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=92327848; PubMed=1626431;
140 QQQFQQQQQAALQQQQQQQQQQFQAQ------QSAMQQQFQAVVQQQQQLQQQQ 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=90124639; PubMed=2404612;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          reast 8:397-408(1992).
                                                                  447 GNPLNTRISAQSANATASMVQQQHPAQQTPINSSATMYSNGASPQLQAQAQAQAQAQAQAQAQ
                                                                                                     94 GQPMS--LSGQPPPGTSGMAPHSMAVVST------ATPQTQLQLQQVALQQQQQ 139
                                                                                                                                                        Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   S0000316; CYC8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          60:307-317(1990)
                                                                                                                                      al Similarity
145; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                r protein.
15
                                                                                                                                                                                                                          966 AA;
                                                                                                                                        Conservative
                                                                                                                                                                                                                          107202 MW;
                                                                                                                                12.7%; Score 383; DB 1; 27.9%; Pred. No. 1.9e-09; tive 60; Mismatches 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Repressor; Repeat; TPR repeat;
                                                                                                                                                                                                                                                         TPR 10.
30 x 2 AA
POLY-GLN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                POLY-GLN.
                                                                                                                                                                                                                      -> Q (IN REF. 3).
84B509CF3208C5C0 CRC64;
                                                                                                                                                                                                                                                                           AA TANDEM REPEATS OF Q-A.
                                                                                                                                        192;
                                                                                                                                                                   Length 966;
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MAM_DROME
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         unusually rich in amino acid homopolymers.";
Genes Dev. 4:1688-1700(1990)
-i- FUNCTION: MAY HAVE A REGULATORY FUNCTION POSSIBLY IN ASSOCIATION
WITH THE N GENE PRODUCT.
-i- SUBCELLULAR LOCATION: NUCLEAR.
-i- DEVELOPMENTAL STAGE: DURING EARLY NEUROGENESIS MAM PRODUCTS ARE
UBIQUITOUSLY LOCATED. DURING LATER STAGES THEY ACCUMULATE IN THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MAM_DROME STANDARD; PRT; 1596 AA. P21519; 101-MAY-1991 (Rel. 18, Created) 01-MAY-1991 (Rel. 18, Last sequence update) 01-MAR-1992 (Rel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Eukaryota; Metazoa; Arthropoda; Diracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Musc
Ephydroidea; Drosophilidae; Drosophila.
                          use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and for entities requires a license agreement (See http://www.isb-sib
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=CANTON-S;
MEDLINE=91065516; PubMed=1701150;
                                                                                                                    This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the El the European Bioinformatics Institute. There are no rest
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "The Drosophila neurogenic locus mastermind encodes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Yedvobnick B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Smoller D., Friedel C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NEUROGENIC
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   send
                                                                                                                                                                                                                                                                                                                                           MISCELLANEOUS: THE PROTEIN HAS MANY AA HOMOPOLYMERIC I POLY-GLN RUNS (FROM 5 TO 16 AA IN LENGTH), 4 POLY-GLY AA), 3 POLY-ASN (3 X 5 AA), 1 POLY-ALA (10 AA) AND 1 F
                                                                                                                                                                                                                                                                                                                                                                                                                                            CENTRAL NERVOUS SYSTEM.
                                                                                                                                                                                                                                                  SIMILARITY: TO OTHER NUCLEAR PROTEINS OF DROSOPHILA, TO CERTAIN YEAST AND MAMMALIAN REGULATORY PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KLKQLSKYIE--------PLRRMINKIDKNED 492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SPAEEATKAASVSPSTKPLNTEPESSSVQPTVSSESSTTKANDQSTAETIELSTATVPAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QLQPFSTQAMEHPQSSQLPPQQQQLQSVQHPQQLQGQPQAQAPQPLIQHNVEQNVLPQKR 684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TVKEEAKMREEEQTSQEKSPQENTLPRENVVRQVEEDEN 963
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QPSSQPNSNVSSGPAPSPSSFLP-SPSPQPSQSPVTARTPQN------FSVP--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NINKLVNTATSIEENAKSEVSNQSPAVVESNTNNTSQEEKPVKANSIPSVIGAQEPPQEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QAAQMVAPGVQVSQSSLPMLSSPSPG-----QQVQTP---QSMPP--PPQPSPQPG
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   an
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   email to license@isb-sib.ch).
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                                                                                         rmatics Institute. There are no restrictions institutions as long as its content is in
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A36391; A36391.
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                                                                                          GNAGGGYGYGYGYGYGNGGPNPGQQQQQPNQNMSNANVPS
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                                                                                                                                                                        GGNTPNAPQQQQQQQSTTTTL-QMKQTQQLHISQQGGGAQGIQVSAGQHLHLSGDMK-SN
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GLN-RICH.
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ALA-RICH.
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7 x 2 AA TANDEM REPEATS O
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Pred. No. 4.6e-09;
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GLY/ASN-RICH.
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W; B944D86EF359D605
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZN_FING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; X63672; CAA45;11.1;
EMBL; M64750; -; NOT_ANNOT
PIR; S23632; S23632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- SUBCELLULAR LOCATION: NUCLEAR.
-!- TISSUE SPECIFIC:TY: SALIVARY GLANDS.
-!- SIMILARITY: CONVAINS 1 SAM DOMAIN.
-!- SIMILARITY: TO MOUSE EARLY DEVELOPMENT REGULATOR PROTEIN RAE-28.
-!- CAUTION: IT IS (INCERTAIN WHETHER MET-1 OR MET-9 IS THE INITIATOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     peatrick J., Daly M., Randsholt N.B., Brock H.W.;
"The complex genetic locus polyhomeotic in Drosophila melanogaster
potentially encodes two homologous zinc-finger proteins.";
Gene 105:185-195(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Drosophila melanoga:ter (Fruit fly).

Bukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

Pterrygota; Neoptera Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR001660; SAM; 1
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   734 NLQQVVN------AAGNKM-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 199-1584 FROM N.A.
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MEDLINE=92146957; PhbMed=1346609;
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                                                                                                                   674 ASSVSTQTAQNQSLIKAKMRNKQQPVRPALATLKTEIGQVAGQNKVVGHLTTVQQQQQQAT 733
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The polyhomeotic gene of Drosophila encodes a chromatin protein that
hares polytene chromosome-binding sites with Polycomb.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=7227
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                                                                                                                                                                                                                                                                                   Local
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                                                                                                                                                                                                                                                    158;
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                                                                                                                                                                                                                                                                                   Similarity
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29.7%; Pred. No. 1.4e-08;
tive 57; Mismatches 177;
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GLN-RICH.
GLN-RICH.
GLN-RICH.
GLN-RICH.
SER/THR-RICH.
C4-TYPE.
MISSING (IN REF. 2).
D -> A (IN REF. 2).
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------VVMSTTGTPITLQNGQ 762
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1008 AA;

114831 MW;

436D1EBAEA17F7DB CRC64;

DOMAIN DOMAIN Transcription

regulation; Activator; Galactose metabolism 75 84 POLY-GLN.

GLN-RICH. GLN-RICH. POLY-GLN

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                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   p32257;
01-OCT-1993 (Rel. 27, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Dickson R.C., Hopper J., Mylin L.M., Gerardot C.J.;
"Sequence conservation in the Saccharomyces and Kluveromyces GAL11
                                                                                                                                      EMBL; M68870; AAA35254.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   transcription activators suggests functional domains.";
Nucleic Acids Res. 19:5346-5350(1991).
-i-FUNCTION: AUXILIARY TRANSCRIPTION ACTIVATOR FOR GENES ENCODING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       _KLULA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1094 TVSVTSTAVTSSPGQLVLLSTASSGGGGSIPATPTKETPSKGPTATLVPIGS 1145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1049 SATIAGGTQ------QQPQGPPSLTPTTNPILAMTSMMNATVGHLSTAPPV 1093
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=92020226; PubMed=1923818;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kluyveromyces lactis (Yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Kluyveromyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TRANSCRIPTION REGULATORY PROTEIN GAL11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=28985
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    308
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     111 APHSMAVVSTATPQTQLQL---QQVALQQQQQQQQF----QQQQQQAALQQQQQQQ----Q 159
                                                                                                                                                                                                                                                                                                                                                                  GALACTOSE-METABOLIZING ENZYMES. ESSENTIAL FOR NORMAL GROWTH ON KONFERWENTABLE CARBON SOURCES, FOR SPORULATION AND MATING. MISCELLANEOUS: GALL1 LACKS A DNA-DOMAIN, IT PROBABLY COMPLEXES WITH GAL4 THAT HAS THE CAPACITY TO BIND DNA. ASSOCIATION DETWEEN GALL1 AND GAL4 MAY SERVE TO EXPEDITE PHOSPHORYLATION OF GAL4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KLULA
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RESULT 6
FSH_DROME
ID FSH_D
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DE FEMAL
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SEQUENCE FROM N.A.
MEDLINE-89276730; PubMed-2567251;
MEDLINE-89276730; PubMed-2567251;
Haynes S.R., Mozer B.A., Bhatia-Dey N., Dawid I.B.;
"The Drosophila fsh locus, a maternal effect homeot apparent membrane proteins.";
                                                                                                                                                 Drosophila melanogaster (Fruit fly).

Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Ins
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
                                                                                                                                                                                                                            FSH_DROME STANDARD; PRT; 2038 AA.
P13709; P13710;
01-JAN-1990 (Rel. 13, Created)
01-JAN-1990 (Rel. 13, Last sequence update)
01-OCT 1996 (Rel. 34, Last annotation update)
FEMALE STERILE HOMEOTIC PROTEIN (FRAGILE-CHORION MEMBRANE
                                                                                                                                                                                                              FS(1)H OR FSH.
                                                                                                                                    Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              457
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----NTPVNPSSVMSPAGSSQAEEQQYLDKLKQLSKYIEPLRR------MINKID-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PSPNKDKKNPATRAVKGKKNSQSGIPTSNPQSNSNASVVNSRTATPTVIPGSSPMFNNKS
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23.2%;
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                   homeotic
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                                                                                                                                                                     Insecta
                   gene,
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                                                                                                                                                   Muscomorpha;
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                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   TRANSMEM
TRANSMEM
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HSSP: P04002: 1WFA.

F1yBase; FBg00004656; fs(1)h.

InterPro; IPR001487; Bromodomain.
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VARIANT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Dev. Biol. 134:246-257(1989).

-!- FUNCTION: REQUIRED MATERNALLY FOR PROPER EXPRESSION OF OTHER HOMEOTIC GENES INVOLVED IN PATTERN FORMATION, SUCH AS UBX.
-!- SIMILARITY: HIGH, TO HUMAN RING3 PROTEIN.
-!- SIMILARITY: CONTAINS 2 BROWODDMAINS.
-!- SIMILARITY: CONTAINS 1 ET DOMAIN.
                                                                                                            1400
                                                                                                                                                                                                                                                                         1226 HNKNGPNDLSKVQPGGPINAALPPHSFAGGTATVATSQSSGGIRIASNLHKPSGLG----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SMART;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00439; bromodomain;
                                                                                                                                                                                                                    1282 --GGDLGEHHAALAAALTSGINSTGTAGGGINNNGGSNNNANPLGGSHGDAMVNASLASL 1339
                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
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                                                                                                                                    163
                                                                                                                                                                                          121
                                                                                                                                                                                                                                               79
                                                                                                                                                                                                                                                                                                  44 HNKK-----SQASVSDPMNAL---QSLTGGPAAGA-----
 ----MQLQQQHHQQQQQQTHQQQQ---
                                                                                                                                                                                                                                               GPGQSLG-----
                          PSQALPQQLQQMHHTQHHQPPPQPQQPPVAQNQPSQLPPQSQTQPLVSQAQALPGQMLYT
                                                     \verb| MAAAYQQKHPQQQQQQAHNNGFNVADFGMAGFDGLNMTAASFLDLEPSLQQQQMQQ----| \\
                                                                                FQAQQSAMQQQFQAVVQQQQQLQQQQQQQHL----IKLHHQNQQQTQQQQQQQQQQQRIAQLQ 219
                                                                                                                                                                                          ATPQTQLQLQQVALQQQQQQQQF-----
                                                                                                         FGHQQQ-----QQQQQQQQQQQQQQQQHMDYVTELLSKGAENVGGMNGNHLLNFNLD 1449
                                                                                                                                                               ASGLKQTPQFDDPVEQSLASLEFSAGSTGKSGLTDNFLMQQHLMQPAGPQQQQQQQQQQQ
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                                                                                                                                                                                                                                                                                                                                           Similarity
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51 123
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                                                                                                                                                                                                                                                                                                                                                                                                205332 MW;
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POTENTIAL.
POTENTIAL.
G -> A.
H -> RKPYY.
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                                                                                 -----QALEAQPPIQQPPMQQPQPP 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Transmembrane;
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                                                                                                                                                                                          -----QQ--QQQAALQQQQQQQQQQQQ 162
                                                                                                                                                                                                                                                                                                                              192;
ОНОООННООООООГТОООГОО 1546
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SNF5_YEAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1990 (Rel. 16, Created)
01-OCT-1994 (Rel. 36, Last sequence update)
20-AUG-2001 (Rel. 4C, Last sequence update)
TRANSCRIPTION REGULATORY PROTEIN SNF5 (SWI/SNF COMPLEX COMPONENT (TRANSCRIPTION FACTOR TYE4).
SNF5 OR TYE4 OR SWIJO OR YBR289W OR YBR2036.
Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                        "The sequence of a 12,420 bp segment located on the right arm of chromosome II from Saccharomyces cerevisiae.";
Yeast 10:S47-S62(19:4).
'east 10:S47-S62(19:4).
'I FUNCTION: INVOLVED IN TRANSCRIPTIONAL ACTIVATION. THE SWI/SNF COMPLEX IS REQUIRED FOR THE INDUCED EXPRESSION OF A LARGE NUMBER OF GENES. THIS COMPLEX ALTERS CHROMATIN STRUCTURE TO FACILITATE BINDING OF GENES-SPECIFIC DEDICATED TRANSCRIPTION FACTORS.

"I SUBUNIT: COMPONENT OF THE SWI/SNF GLOBAL TRANSCRIPTION ACTIVATOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "The SNF5 protein of Saccharomyces cerevisiae is a glutamine- and proline-rich transcriptional activator that affects expression of broad spectrum of genes.", and cell. Biol. 10:5616-5625(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1547 QQ---
                                                                                   EMBL; M36482; AAA35(62.1; -. EMBL; X76053; CAA53652.1; -. EMBL; Z36158; CAA85254.1; -.
                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SNF5_YEAST
P18480;
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SGD; S0000493; SNF5. Transcription regulation; Activator; Nuclear protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-91042489; PubMed-2233708; Laurent B.C., Treitel M.A., Carlson M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1653 SPQSHTSSS-----SSSSKAKPAMDSFQQFRNKAKER---DRLKLLEAAEKEKKNQK 1701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=94378722; Pt.bMed=8091861;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  485 NKIDKNEDRKKDLSKMKSL 503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  431 TPQNFSVPSPGPLNTPVNPSSVMSPAGSS-----QAEEQQYLDKLKQLSKYTEPLRRMT 484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      376 VQTPQSMPPPPQ-PEPQPGQPSSQPNSNVSSGPAPSPSSFLPSPSPQPSQSP----VTAR 430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         316 QPPLKFVRAPMVVQCPPVQPQVQQQQTAVQTAQAAQMVAPGVQVSQSSLPMLSSPSPGQQ 375
                                                                                                                                                                                                                                                                                                                                               SIMILARITY: BELCINGS TO THE SNF5 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                     SUBCELLULAR LOCATION: NUCLEAR
                                            $44551; RGBYS5.
$39145; $39145.
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SEQUENCE
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                        -i- SUBUNIT: MAY BE COVALENTLY LINKED BY DISULFIDE BONDS TO OTHER POLIFICEPTIDES TO FORM THE 80 KDA ANTIGEN
-i- DEVELOPMENTAL STAGE: PRESENT IN ALL STAGES THROUGHOUT THE
                                                                                                                                                                                          "Identification and characterization of a target antigen of a monoclonal antibody directed against Eimeria tenella merocoites."; Mol. Biochem. Parasitol. 41:53-64(1990).

-i- FUNCTION: UNKNOWN. THE GLN-RICH TANDEM REPEATS MAY BE IMPORTANT FOR AN UNKNOWN ASPECT OF THE PARASITIC LIFE CYCLE. MAY BE AN IMPORTANT IMMUNOGEN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    LP61_EIMTE STANDARD; PRT; 255 AA. P15714.1990 (Rel. 14, Created) 01-APR-1990 (Rel. 14, Last sequence update) 01-FEB-1994 (Rel. 28, Last annotation update) 01-FEB-1994 (Rel. 28, Last annotation update) ANTIGEN LPMC-61 (FRAGMENT).
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                                                                                                                                                                                                                                                                                                   MEDLINE=90348718; PubMed=2200963; Ko C., Smith C.K. II, McDonell M.
                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida; Eimeriidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  64 QQQQQQTSPPPQTHQS-------PPPPPPQQS-----QPIANQSATST 98
                                                                                                          EXCYSTATION
                                                                                                                          SPORULATION OF THE OCCYSTS AND IN THE SPOROZOITES FOLLOWING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q------QQQQQQQQQIPQSQQVP-QVRSM-----SGQPPTNVQPTI--GQLPQLPKL 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VNAITVAQQQVQRQIEQQKGQQTAQTQLEQQRQLLVQQQQQQQQLRNQIQRQQ----QQQFR 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PPPPP---APHNLHPQIGQVPLAPAPINLPPQIAQLPLATQQQVLNKLRQQAIAKNNPQV 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QALEAQPPIQQPPMQQPQPPPSQALPQQLQQMHTQHHQPPPQPQQPPVAQNQPSQLP---
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E -> D (IN REF. 1).
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ASP/GLU-RICH (ACIDIC).
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Q93074;
01-NOV-1997 (Rel. 3
01-NOV-1997 (Rel. 3
01-NOV-1997 (Rel. 3
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                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; vo
Mammalia; Eutheria; Primates; Catarrhini;
                                     Nagase T., Seki N., Ishikawa K.-I., Tanaka A., Nomura N.; Prediction of the coding sequences of unidentified human The coding sequences of 40 new genes (KIAA0161-KIAA0200) c analysis of cDNA clones from human cell line KG-1."; DNA Res. 3:17-24(1996).
                                                                                                                                                                                 KIAA0192
                                                                                                                                                                                           HYPOTHETICAL PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
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                                                                                                  TISSUE=Bone marrow;
MEDLINE=96281124; PubMed=8724849;
                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                         NCBI_TaxID=9606;
                                                                                                                                                                      Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                     140
                                                                                                                                                                                                                                                                                                                                                                                              168
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                                                                                                                                                                                                                                                                                                                                                       QQQQQQQQQQQQQALEAQPPIQQP---PMQQPQPPPSQALPQQLQQMHHTQHHQPPPQPQQ
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an email to license@isb-sib.ch).
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Best Local
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                                                                                                                                                                                                                                                                            Pitts E.G., Rafalski J.A., Hedgcoth C.;

"Nucleotide sequence and encoded amino acid sequence of a genomic gene region for a low molecular weight glutenin.";

Nucleic Acids Res. 16:11376-11376(1988).

-I- FUNCTION: GLUTENINS ARE THE HIGH MOLECULAR WEIGHT SEED STORAGE PROTEIN OF WHEAT ENDOSPERM. THOUGHT TO BE RESPONSIBLE FOR THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P10385;
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                       the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commer
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MEDLINE=89083577; P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAR-1989 (Rel. 10, Last sequence update) 15-JUL-1999 (Rel. 38, Last annotation update)
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                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
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                                                                                                                                                                                                        VISCO-ELASTIC PROPERTY OF WHEAT DOUGH.
SUBUNIT: DISULFIDE-BRIDGE LINKED AGGREGATES.
MISCELLANEOUS: GLUTENINS ARE CODED BY SEVERAL GENES ON EACH OF THE
                                                                                                                                                                                   GROUP 1 CHROMOSOMES OF WHEAT.
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GIP4_WHEAT STANJARD; ....,

P08489;

01-AUG-1988 (Rel. 03, Created)

01-AUG-1988 (Rel. 03, Last sequence update)

15-JUL-1999 (Rel. 3à, Last annotation update)

15-JUL-1999 (Rel. 3à, Last annotation pw212 PRECURSOR.

Triticum aestivum (Wheat).

Eukaryota; Viridiplintae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Lillopsida; Poales; Poaceae; Pooideae;

Triticeae; Triticum.
NUCLEIC ACIDS Res. [13:8729-8737(1985).

-I- FUNCTION: GLUTENINS ARE THE HIGH MOLECULAR WEIGHT SEED STORAGE PROTEIN OF WHEAT ENDOSPERM. THOUGHT TO BE RESPONSIBLE FOR THE VISCO-ELASTIC PROPERTY OF WHEAT DOUGH.

-I- SUBUNIT: DISULFIDE-BRIDGE LINKED AGGREGATES.

-I- MISCELLANEOUS: GLUTENINS ARE CODED BY SEVERAL GENES ON EACH OF THE
                                                                                                                                                        STRAIN=CV. YAMHILL;
MEDLINE-86093674; PubMed=3001648;
MEDLINE-86093674; PubMed=3001648;
Suglyama T., Raffalski A., Peterson D., Soll D.G.;
Suglyama T., Raffalski A., Peterson D., Soll D.G.;
T. Wheat HMW glutenin subunit gene reveals a highly repeated
                                                                                                                                            structure.
                                                                                                                                                                                                                                                     SEQUENCE FROM N.A
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Seed storage protein; Repeat; Multigene family; Signal.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 341 TTTSVPLG 348
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            286 LGQCVSQPLQQLQQ2LGQQPQQQQLAHQIAQLEVMTSIALRT-----LPTMCNVNVPLYE 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       393 -GQPSSQPNSNVSS--GPAPSPSSFLPSPSPQPSQSPVTARTPQNFSVPSPGPLNTPVNP 449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               226 HVMQQQCCQQLRQIPEQSRHESIRAIIYSIILQQQQQQQQQQQQQQQQQQGQSIIQYQQQQPQQ 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               178 SRQQQIP-----VIHPSVLQQLNPCKVFLQQQCIPVAMQRCLARSQMLQQSIC 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 QQPPFSQQQQQPPFTQQQQQQQQQQPFTQQQQ-PPFSQQPPISQQQ--QPPFLQQQRPPF 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         134 LQQQQQQQQFQQQQQAALQQQQQ----QQQQQQF--QAQQSAMQQQFQAVVQQQQQLQQQ 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               245 QQPP--MQQPQPPPSQALPQQLQQMHHTQHHQPPPQPQQPPVAQNQPSQLPPQSQTQPLV 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ------QVSQSS------LPMLSSPSPGQQVQTPQSMPPPPQPSPQP 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SQAQALPGQMLYTQPPLKFVRAPMVVQQ-PPVQPQVQQQ--QTAVQTAQA-AQMVAPGV- 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ISQQQQAPPFSQQQQPPFSQQQQPPFSQQQQSPFSQQQQPPFAQQQQPPFSQQPPISQQ 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IPR003612; AAI. IPR001954; Glia_glutenin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10.2%; Score 308; DB 1; Length 356; 31.8%; Pred. No. 9.5e-07; tive 30; Mismatches 137; Indels 84; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GLUTENIN, LOW MOLECULAR WEIGHT SUBUNIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AA2613FC0DD4DCA5 CRC64;
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P29617; 09U6A2; 09VGP8; 01-APR 1993 (Rel. 25, Created) 01-FEB-1996 (Rel. 33, Last sequence update) 20-AUG-2001 (Rel. 40, Last annotation update)

PROTEIN PROSPERO. PROS OR CG17228.

Drosophila melanogaster (Fruit fly)

Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

PRO\_DROME

PRO\_DROME

STANDARD;

PRT;

1403 AA.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
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-!- MISCELLANBOUS: THE MATURE PROTEIN IS CHARACTERIZED BY A LARGE NUMBER OF WELL PRESERVED REPEATS OF THE TWO MOTIFS: GOOPGO AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; X03346; CAA27052.1; -.
                                                             549 QQPGQGQQPGQLQQPAQGQQGQQ 571
                                                                                                      441 GPLNTPVNPSSVMSPAGSSQAEE 463
                                                                                                                                             491 GQQPG--QGQPGYYPTSPQQSGQGQPGQWQQPGQGQPGYYPTSPLQPGQGQPGYDPTSP 548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  130 QQVAL-QQQQQQQQQQQQAALQQQ--QQQQQQQQQFQAQQSAMQQQFQAVVQQQQ---- 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Seed storage protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PIR; A24107; EEWTHW
                                                                                                                                                                                       385 PPQPSPQPGQPSSQPNSNVSSGPAPSPSSFLPSPSPQPSQSPVTARTP----QNFSVPSP 440
                                                                                                                                                                                                                                 444 ----TSPQQSGQGQPGQLQQSAQGQKGQQPG-QGQQ-----PGQGQQGQQPGQGQQPGQGQQ 490
                                                                                                                                                                                                                                                                          325 PMVVQQPPVQPQVQQQTAVQTAQAAQMVAPGVQVSQSSLPMLSSPSPGQQVQTPQSMPP 384
                                                                                                                                                                                                                                                                                                                    402 QQVGQGQQAQQPGQQQP--GQGQPGYYP----TSPLQS-GQGQPGYYL------ 443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               183 -QLQQQQQQQHLIKLHHQNQQQIQ------QQQQQLQRIAQLQLQQQQQQQ 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         178 PQQPGQLQQPAQGQQPGQGQQGR-----QPGQGQPGYYPTS------SQLQPGQL 221
                                                                                                                                                                                                                                                                                                                                                             265 QQMHHTQHHQPPPQPQQPPVAQNQPSQLPPQSQTQPLVSQAQALPGQMLYTQPPLKFVRA 324
                                                                                                                                                                                                                                                                                                                                                                                                     342 QQPGQGQQGQQPGQGQQPGQGQPGYYPTSPQQSGQGQPGYYPTSSQQPTQSQQPGQGQQG 401
                                                                                                                                                                                                                                                                                                                                                                                                                                            228 QQ--QQQQQQQALEAQPPIQ-QP-----PMQ--QPQP---PPSQALP------QQL 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     282 TSLQQSGQGQFGYYPTSLQQLGQGQSGYYPTSPQQPGQGQQPGQLQQPAQGQQPEQGQQG 341
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   77 PRGPGQ----SLGGMGSFGAMGQPMSLSGQPPPGTSGMAPHSMAVVSTATPQTQL---QL 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Sin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GOOPGOGOOGYYPTS.
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44; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              o; IPR001419; Glutenin.
PR00210; GLUTENIN.
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838 AA; 89174 MW;
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32.5%; Pred. No. 4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REPEATS.
; 71D715B7BDF0722D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GLUTENIN, HIGH MOLECULAR WEIGHT SUBUNIT
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RA Beeson K.Y. Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y. Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Gubart W. M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Gubart P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Chiu X., Rathang T. Simeson M. Skunski M. D. Smith T.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chu-Lagraff Q., Wright D.M., McNeil L.K., Doe C.Q.; "The prospero gene encodes a divergent homeodomain controls neuronal identity in Drosophila.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=92171948; PubMed=1540176;
Matsuzaki F., Koizumi K., Hama C., Yoshioka T., Nabeshima Y.;
"Cloning of the Drosophila prospero gene and its expression ir ganglion mother cells.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=92069760; PubMed=1720353;
Vaessin H., Grell E., Wolff E., Bier E., Jan L.Y., Jan Y.N.;
"Prospero is expressed in neuronal precursors and encodes a nuclear
                     Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T., Spier E., Spradling A.C., Stapleton M., Strong R., Sun E., Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X., Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J., Walliams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zhang Ye J., Zhong F.N., Zhong W., Zhan W., Zhau S., Zhu X., Smith H.O., Shong X.H., Zhong F.N., Zhong W., Zhou X., Zhu X., Smith H.O., Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Xu C., Kauffmann R.C., Zhang J., Kladny S., Carthew R.W.;
"Overlapping activators and repressors delimit transcriptional
response to receptor tyrosine kinase signals in the Drosophila eye.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Drosophila.";
Cell 67:941-953(1991).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=20503846; PubMed=11051550;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=93083413; PubMed=1842358;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=20196006; PubMed=10731132;
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genome sequence of Drosophila melanogaster.";
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                                     CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           entities requires
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Trends Biochem. Sci. 19:70-71(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Science 287:2185-2195(2000).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; M81389; AAA28841.1; -. EMBL; D10609; BAA01464.1; -. EMBL; Z11743; CAA77802.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This
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                                                                                                                                                                                   CONFLICT
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               SEQUENCE
                                                                                   CONFLICT
                                                                                                       CONFLICT
                                                                                                                                   CONFLICT
                                                                                                                                                                                                                                CONFLICT
                                                                                                                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                                                                                       DNA_BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nuclear protein; Transcription regulation; DNA-binding; Homeobox;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FOR THE SPECIFICATION OF IDENTITY, PROSPERO PROTEIN MAY REGULATE TRANSCRIPTION BY BINDING TO DNA.
SUBCELLULAR LOCATION: NUCLEAR.
ALTERNATIVE PRODUCTS: 2 ISOFORMS; PROS-L (SHOWN HERE) AND PROS-S; ARE PRODUCED BY ALTERNATIVE SPLICING. THEY HAVE DIFFERENT N-TERMINAL AMINO ACIDS OF THE HOMEODOMAIN.
TISSUE SPECIFICITY: NEURONAL PRECURSORS. EXPRESSED IN THE TISSUE SPECIFICITY: NEURONAL PRECURSORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DEVELOPING CNS, LENS-SECRETING CONE CELLS OF THE EYE, DEVELOPMENTAL STAGE: EXPRESSED IN NEURONAL PRECURSORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENES AS WELL AS AXONAL OUTGROWTH AND PATHFINDING OF NUMEROUS CENTRAL AND PERIPHERAL NEURONS. IT IS PROBABLY GENERALLY REQUIRED FOR PROPER NEURONAL DIFFERENTIATION OF MOST OR ALL NEURONS & THEIL PRECURSORS IN THE CENTRAL AND PERIPHERAL NERVOUS SYSTEMS, BUT NOT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FUNCTION: INVOLVED IN THE CONTROL OF OTHER NEURONAL PRECURSOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FORMATION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A41089;
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                 153569
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H -> Q (IN REF
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9 MW; 9EFB9973E;
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IGSLNSTSKLLQQQHNNNSIAPANS -> NLALQFHVQVAA
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NUCLEAR LOCALIZATION SIGNAL
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                                                                                                                                                                                                                                   AKMLNELFGRQMKQAQDATSGLP ->
                                                                                                                                                                                                                                                       MISSING (IN ISOFORM PROS-S)
                                                                                                                                                                                                                                                                                   PROSPERO-LIKE
                                                                                                                                                                                                                                                                                                       HOMEOBOX (ATYPICAL).
                                   > S (IN REF. 1)
> S (IN REF. 1)
> QQQQQ (IN REF
                 9EFB9973E24E238E CRC64;
                                                                                                         Q (IN REF. 2).
C (IN REF. 1).
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Query Match Best Local Similarity

9.9%;

Score 298; DB 1; Pred. No. 7.4e-06;

Length 1403;

Matches

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Conservative

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A RANGE REPORTED TO THE REPORT OF THE REPORT
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Biochemistry 32:9532-9538(1993)
                           "An unusual catalyti: subunit for the cAMP-dependent protein kinase of Dictyostelium dispoideum.";
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01-FEB-1994 (Rel. 28, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
                                                                                                                                                                                                                                                                                                                       MEDLINE-91323730; PubMed-1864510;
Buerki E., Anjard C., Scholder J.-C., Reymond C.D
"Isolation of two genes encoding putative protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Dictyostelium discoideum (Slime mold).
Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium
                                                                                                                                           MEDLINE=93385090; PubMed=8373760;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PKAC OR PK2 OR PK3
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                                                                                                           Anjard C.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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                                                                                                       Etchebehere L., Pinaud
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                                                                                                       Veron M., Reymond C.D.;
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Pfam; PF00433; pkinase_C; 1.
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-1- CATALYTIC ACTIVITY: ATP + A PROTEIN - ADP + A PHOSPHOPROTEIN.
-1- SUBUNIT: IN DICTYOSTELIUM THE HOLDSKYME IS A DIMER COMPOSED OF
A REGULATORY (R) AND A CATALYTIC (C) SUBUNIT. IN THE PRESENCE OF
CAMP IT DISSOCIATES INTO THE ACTIVE C SUBUNIT AND AN R MONOMER.
-1- DEVELOPMENTAL STAGE: CAPK ACTIVITY IS LOW IN VEGETARIVELY GROWING
ANGEBAE, INCREASES DURING DEVELOPMENT OF AGGREGATION AND REACHES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS00107;
PROSITE; PS00108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR000961; pkinase_C.
InterPro; IPR002290; Ser_thr_kin_actsite.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DictyDb; DD02030; pkaC.
InterPro; IPR000719; Euk_pkinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mann S.K.O., Yonemoto W.M., Taylor S.S., Firtel R.A.; "DdPK3, which plays essential roles during Dictyostelium development, encodes the catalytic submit of CAMP-dependent protein kinase."; Proc. Natl. Acad. Sci. U.S.A. 89:10701-10705(1992).
                                                                                                                                                                                                                           147
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; M38703; -; NOT_ANNOTATED_CDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the European Bioinformatics Institute. There are no rest use by non-profit institutions as long as its content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This
254 TSGL--SLQHAHSS--YTPSNVLHSPTHFQ---SSLPTRLDTNPITT--
                                                     257 SQALPQQIQQMHHTQHHQPPPQPQQPPVAQNQPSQLPPQSQTQPLVSQAQALPGQMLYTQ 316
                                                                                                                                                                                                                                                                                                                                                  114 LNSFGNFKVPSTFSLTPP------EPNKQQQPQQQPQQQPQQQQPQQQPQQQ 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-AX3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CHARACTERIZATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=93066311; PubMed=1332055;
                                                                                                                                                                                                                                                                                                                                                                                                     87 MGSFGAMGQPMSLSGQPPPGTSGMAPHSMAVVSTATPQTQLQLQQVALQQQQQQQQQQFQQQ 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                QQQQQ------QQQQQKQQKQQQQQQQHLHQDGIVNTPSTTQTSTTTTTTTTTNPH
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                                                                                                                                                                      QQQQQLQRIAQLQLQQQQQQQQQQQQQQQQQALEAQPPIQQPPMQQPQP------pp 256
                                                                                                                                                                                                                                                                                       QQAALQQQQQQQQQQQFQAQQSAMQQQFQAVVQQQQQQLQQQQQQQQQHLIKLHHQNQQQIQ 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JQ1150; JQ1150.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A MAXIMUM AT CULMINATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation een the Swiss Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Serine/threonine-protein kinase; ATP-binding; cAMP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROTEIN_KINASE_ATP; 1.
PROTEIN_KINASE_ST; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROTEIN_KINASE_DOM;
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223
250
590
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355
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 296.5; DB 1,
Pred. No. 4.5e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PHOSPHORYLATION (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROTEIN KINASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    THR-RICH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GLN-RICH.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       D0F9B3A48C58D084 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Usage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 648;
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                                                                                                                                Query Match
Best Local
                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Anderson O.D.;

Submitted (FEB-1997) to the EMBL/GenBank/DDBJ databases.

-I- FUNCTION: GLUTENINS ARE THE HIGH MOLECULAR WEIGHT SEED STORAGE PROTEIN OF WHEAT ENDOSPERM. THOUGHT TO BE RESPONSIBLE FOR THE VISCO-ELASTIC PROPERTY OF WHEAT DOUGH.

-I- SUBUNIT: DISULFIDE-BRIDGE LINEAD AGGREGATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-89098419; PubMed-2563152;
MEDLINE-89098419; PubMed-2563152;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAR 1989 (Rel. 10, Created)
01-NOV-1997 (Rel. 35, Last seque
15-JUL-1999 (Rel. 38, Last annot
GLUTENIN, HIGH MOLECULAR WEIGHT
GLU-1D-1D OR GLU-D1-1B.
                                                                                                                                                                                                                                  DOMAIN
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidea Triticeae; Triticum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WHEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; X12928; CAA31395.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-CV. CHEYENNE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REVISIONS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nucleic Acids Res. 17:461-462(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=4565;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Triticum aestivum (Wheat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P10388;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GLT5_WHEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Malpica-Romero J.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Nucleotide sequences of the two high-molecular-weight glutenin genes from the D-genome of a hexaploid bread wheat, Triticum aestivum L. cv
                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    294
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128
                                                   49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MISCELLANEOUS: THE MATURE PROTEIN IS CHARACTERIZED BY A LARGE NUMBER OF WELL PRESERVED REPEATS OF THE TWO MOTIFS: GQQPGQ ANI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GROUP 1 CHROMOSOMES OF WHEAT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MISCELLANEOUS: GLUTENINS ARE CODED BY SEVERAL GENES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GOOPGOGOOGYYPTS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 S02262;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SWISS-PROT entry is copyright. It is produced through a collaboration en the Swiss Institute of Bioinformatics and the EMBL outstation -
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                                                                                                                                                                                                                                                                                                                                                                  storage protein; Repeat; Multigene
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QASPQRPGQGQQ-----PGQGQQGYYPTSPQQPGQWEEPEQGQQGYYPTSPQQPGQLQQP 182
                                              QASVSDPMNALQSLTGGPAAGAAG-IGMPPRGPGQ----SLGGMGSF-----GAMGQP 96
                                                                                                       149;
                                                                                                                                                                                                                                                                                                                                                                                              PR00210; GLUTENIN.
                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                   52; S02262.
IPR001419; Glutenin.
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                                                                                                                                                                                                                                                                131
                                                                                                       Conservative
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Last annotation updat
                                                                                                                                                                                                                                     MW,
                                                                                                    16;
                                                                                                  Score 296; DE
Pred. No. 5.9e
L6; Mismatches
                                                                                                                                                                                                                                                                                                              GLUTENIN,
                                                                                                                                                                                                                                                           REPEATS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
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                                                                                                                                                                                                                                                                                                              HIGH
                                                                                                                                                                                                                                                                                                                                                                  family; Signal.
                                                                                                                          DB 1;
.9e-06;
                                                                                                                                                                                                                                                                                                              MOLECULAR WEIGHT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRECURSOR
                                                                                                    205;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Shewry P.R.,
                                                                                                                                                      839;
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                                                                                                  114;
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01-NOV-1990
01-NOV-1990
20-AUG-2001
                                                                                                                                                                                                                 "Cloning and analysis of the Drosophila eggshell."; required for proper assembly of the Drosophila eggshell."; Genes Dev. 2:341-349(1988).

-i- function: The DEC-1 FEMALE-STERILE LOCUS PROTEIN IS REQUIRED FOR PROPER ASSEMBLY OF THE DROSOPHILA EGGSHELL.

FOR PROPER ASSEMBLY OF THE DROSOPHILA EGGSHELL.

FOR PROPER ASSEMBLY OF THE DROSOPHILA EGGSHELL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
MEDLINE-91032553; PubMed-1699826;
Warring G.L., Hawley R.J., Schoenfeld T.;
"Multiple proteins are produced from the dec-1 eggshell
Drosophila by alternative RNA splicing and proteolytic c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
DEFECTIVE CHORION-1 PROTEIN, FC125 ISOFORM PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                  Hawley R.J., Waring G.L.;
"Cloning and analysis of the dec-1 female-sterile locus,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  events
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Pterygota;
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                                                                                                                                                                                                  ALTERNATIVE PRODUCTS: 3 ISOFORMS; FC106 HERE) AND FC177 (AC P18171); ARE PRODUCE
                                                                                                                   DEVELOPMENTAL STAGE: EXPRESSION PEAKS AT EMBRYONIC STAGE 1 SLIGHTLY REDUCED BY STAGE 10B, AND UNDETECTED IN STAGE 11.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Drosophilidae; Drosophila
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FlyBase; FBgn0000427 dec-1
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                                                                               982 RV-----HKSPSSAPSETEIENAPSS 1002
                                                                                                             426 PYTARTPONESVPSPGPLNTPVN--PSS 451
                                                                                                                                              929 NDEVDEMLRQHQTMARTINPKQPGEVGGSESQKSNSN-----PPTTLTPAPQEQPQEH 981
                                                                                                                                                                            374 -----QQVQTPQ;;mPPPPQPSPQPGQPSSQPNSNVSSGPAPSPSSFLPSPSPQPSQS 425
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58 11 (APPROXIMATE).
88 12 (APPROXIMATE).
127959 MW; FOREEEE771066
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12 X 26 AA APPROXIMATE TANDEM REPEATS, GLU, MET-RICH.
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1: sp_archea:*
2: sp_bacteria:
3: sp_fungi:*
      473505 seqs, 146272329 residues
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Gapop 10.0 , Gapext 0.5
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sp_invertebrate:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	% Query Match Length		DB	ID	Description
μ,	3010	100.0	579	4	Q9P1T3	Q9p1t3 homo sapien
2	1780	59.1	349	4	015413	homo
ω	469.5	15.6	749	ப	Q9Y149	Q9y149 drosophila
4	460.5	15.3	1069	σı	Q9VF64	Q9vf64 drosophila
51	456.5	15.2	2123	ഗ	Q9U9S7	Q9u9s7 dictyosteli
Ø	447	14.9	796	υ	045322	045322 caenorhabdi
. 7	439	14.6	4957	4	014687	014687 homo sapien
8	439	14.6	5262	4	014686	014686 homo sapien
9	423	14.1	2285	σ	Q9VP17	Q9vp17 drosophila
, 10	419	13.9	1542	σ	Q9VE07	Q9ve07 drosophila
11	415.5	13.8	1798	σı	Q9VUB6	Q9vub6 drosophila
12	414.5	13.8	900	G	Q9VK09	Q9vk09 drosophila
13	400	13.3	455	10	Q9FR41	Q9fr41 secale cere
14	399	13.3	1893	Ω	Q24279	Q24279 drosophila
15	398	13.2	926	σ	Q9W3G1	Q9w3g1 drosophila
16	397	13.2	2251	ഗ	Q22190	Q22190 caenorhabdi
17	395.5	13.1	1013	ப	Q9VYT7	Q9vyt7 drosophila
18	395.5	13.1	2703	σ	Q9VPL9	Q9vp19 drosophila
19	395.5	13.1	5322	G	Q9NI64	Q9ni64 drosophila

je U	n i	44	43	42	41	40	39	38	37	36	ω 5	34	ω u	32	31	30	29	28	27	26	25	24	23	22	21	20
304.0	э л	357	358.5	360	362	365	365	367	367	367.5	372	372	372	374	377	379	380.5	382.5	382.5	382.5	382.5	383.5	383.5	383.5	389.5	394.5
11.0	110	11.9	11.9	12.0	12.0	12.1	12.1	12.2	12.2	12.2	12.4	12.4	12.4	12.4	12.5	12.6	12.6	12.7	12.7	12.7	12.7	12.7	12.7	12.7	12.9	13.1
121/	1017	2977	3080	2309	3502	4823	1589	1624	1359	929	1234	1165	1165	1164	1655	539	1004	5560	5554	5533	5476	1594	1366	1012	5533	1954
Ĺ	л	σ	σ	σ	U	13	ű	σı	σ	5	S	10	10	10	U	9	4	σ	σ	σ	U	σ	G	11	5	υ
7 0 10 0 1	P91094	O9VAP9	Q9VRY3	Q9W2U7	Q9VYJ9	093321	046097	Q9W523	Q9NF31	Q9BLX2	001505	Q9LCZ5	Q9SBK4	Q9SYQ6	Q24754	Q9GM67	P78364	Q9VPL1	Q9NHN1	Q9VPL2	Q9NJ17	Q9V6W7	Q9V6W8	Q64028	Q906C3	Q9VN82
		Q9vap9 drosophila	Q9vry3 drosophila		Q9vyj9 drosophila	093321 fugu rubrip	046097 drosophila	09w523 drosophila		Q9blx2 dictyosteli	001505 caenorhabdi	Ç	Q9sbk4 arabidopsis	Q9syq6 arabidopsis	Q24754 drosophila		P78364 homo sapien	Q9vpl1 drosophila	_	_	_	Q9v6w7 drosophila	Q9v6w8 drosophila	Q64028 mus musculu	Q9u6c3 drosophila	Q9vn82 drosophila

## ALIGNMENTS

Qy	Qy	Qy Db	Qy Db	W B O	RESULT QUELTI AC DT DT OC DT OC	
181 QQQLQQQQQQHLIKLHHQNQQQTQQQQQQLQRTAQLQLQQQQQQQQQQQQQQQQQQQQAALEA 240	121 ATPQTOLOLQQVALQQQQQQQFQQQQQAALQQQQQQQQQQQQQFQAAQQSAMQQQFQAVVQQ 180 121 ATPQTQLQLQQVALQQQQQQQQQQQAALQQQQQQQQQQQQQQQ	61 SLTGGPAAGAGIGMPPRGPGOSIGGMGSFGAMGQPMSLSGQPPPGTSGMAPHSMAVVST 120	1 MRKAGVAHSKSSKDMESHVFLKAKTRDEYLSLVARLIIHERDIHNKKSQASVSDPMNALQ 60 	Query Match 100.0%; Score 3010; DB 4; Length 579; Best Local Similarity 100.0%; Pred. No. 1.9e-215; Matches 579; Conservative 0; Mismatches 0; Indels 0; Gaps	PRELIMINARY; PRT; 579 AA.  (199173 PRELIMINARY; PRT; 579 AA.  (199173; O1-CCT-2000 (TrEMBLrel. 15, Last sequence update)  (10-CCT-2000 (TrEMBLrel. 17, Last annotation update)  (1-UN-2001 (TrEMBLrel. 17, Last annotation update)  (2-UN-2001 (TrEMBLrel. 15, Last sequence updat	

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01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-97369492; PubMed-9225980;
Margolis R.L., Abraham M.R., Gatchell S.B., Li S.H., Kidwai A.S.,
Breschel T.S., Stine O.C., Callahan C., Mcinnis M.G., Ross C.A.;
"CDNAs with long CAG trinucleotide repeats from human brain.";
Hum. Genet. 100:114-122(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
TISSUE=CEREBRAL CORTEX;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota;
183 QTAVQTAQAAQMVAPGVQVSQSSLPMLSSPSPGQQVQTPQSMPPPPQPSPQPGQPSSQPN 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9606
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    015413
                                                                    341 QTAVQTAQAAQMVAFGVQVSQSSLFMLSSFSFGQQVQTFQSMFFFFQPSFQFGQFSSQFN 400
                                                                                                                                        123 QPPVAQNQPSQLPPQ3QTQPLVSQAQALPGQMLYTQPPLKFVRAPMVVQQPPVQPQVQQQ 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             161 QQFQAQQSAMQQQFQAVVQQQQQLQQQQQQQQQHLIKLHHQNQQQIQQQQQQQQLQRIAQLQL 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     541 PRCHRPNSSTYASREWMPSWPTSAHLSSTIPCTAHSFQP
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                                                                                                                                                                                                                                                                                                                                             QQQQQQQQQQQQQQQALEAQPPIQQPPMQQPQPPPSQALPQQLQQMHHTQHHQPPPQPQ 280
                                                                                                                                                                                                                                                                                                                                                                                                                     QQFQAQQXAMQQQFQAVVQQQQQQQQQQQQQQQHLIKLHHQNQQQIQQQQQQQQQQIQRIAQLQL 62
                                                                                                                                                                                                                                                                                QQQQQQQQQQQQQQQQALEAQPPIQQPPMQQPQPPPSQALPQQLQQMHHTQHHQPPPQPQ 122
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99.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 1780; DB 4;
Pred. No. 1.8e-124;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 349;
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RESULT Q9Y149

AC Q9 Y149

AC Q9 DT 011

DT 011

DT 011

DT 010

DE BC OC Pt O
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Rubin G.M., Wan K.H., Harvey D., Lewis S.E., Brokstein P., Tsang G., Agbayani A., Arcaina T.T., Baxter E., Blazej R.G., Butenhoff C., Champe M., Chavez C., Chew M., Doyle C.M., Farfan D.E., Frise E., Galle R., George R.A., Harris N.L., Hoskins R.A., Evans-Holm M., Houston K.A., Hummasti S.R., Kim E., Li P., Moshrefi M., Pacleb J.M.,
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09Y149; O1-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
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ARC105 OR BCDNA:GH03922 OR CG4184.
Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Musc
                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=20196006; PubMed=10731132;
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CG5166 PROTE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Park S., Sequeira A., Sethi H., Snir E., Svirskas R.R., Weinburg Celniker S.E.;
                       Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; MuscEphydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                     Q9VF64;
                                                                                                                                                                                                                                                                                                                                               Q9VF64
                                                                                                                      Drosophila melanogaster (Fruit fly).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          533 RVPLETLLKCEKALEKM 549
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30 TKNAGVMENHIFRKSRTKDEYLGLVAKLFMHYKDMSRKSQQQQQQQQQQQQGGPPPNAEMGG
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                                                                                                                                                                                        PROTEIN.
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                                                                                                                                                                                                                  ) (TrEMBLrel.) (TrEMBLrel.)
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                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
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27.6%; Pred. No. 5.
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                                                                                                                                                                                                                                                                                                                                                   1069 AA.
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                                                           Brachycera; Muscomorpha;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 749;
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RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottler P.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottler P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Renriaz C., Ferriaz S., Fleischmann W.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Spier E., Sgradling A.C., Stapleton M., Strong R., Sun E.,
RA Zheng X.H., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Zheng X.H., Kohng F., Rabin G.M., Venter J.C.,
RA Zheng X.H., Kohng F., Rabin G.M., Venter J.C.,
RA Zheng X.H., Kohng R., Rabin G.M., Venter J.C.,
RA Scholland R., Rabin G.M., We
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches 158;
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Best Local :
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    P---
                                        PQQAP----LPQQQHVPHHMQQKAQQQQLVETQHQHVQKQHQSQPQVQQPPPQLLQDPSQQ
                                                                                                                                                                                                    QQFQAQQSAMQ------QQFQAVVQQ----QQQLQQQQQQQQHLIKLHHQN
                                                                                                                                                                                                                                                                                       NSPP------LQTAGPQQQ------QQQQQQQQQQQQQQQPPQQQQHQNIQ
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                                                                                                                                                                                                                                                                                                                                                                                                         NKKSQASVSDPM--NALQSLTGGPAAGAAGIGMPPRGPGQSLGG--MGSFGAMGQPMSLS 100
                                                                                PQPPPSQALPQQLQQMHH-
                                                                                                                                                            QQQIQQQQQLQRIAQLQLQQQQQQQQQQQQQQQQALEAQP-----PIQQP---PMQQ
                                                                                                                      --QVQQQQ----QRALQQSASPPQQQQQQQQQQQQHVVLHQVPQTHLHQAALSQPHYVPQQQ
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----PQSQTQPLVSQAQALPGQMLYTQPPLKFVRAPMVVQQPPVQPQ---VQQQQTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 460.5; DB 5
Pred. No. 3.8e-26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches 150;
                                                                              ---TQH-----HQPPPQPQQPPVAQNQ-PSQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       B9D774F4DDBCEACO CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 1069;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels 129;
      343
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                                                                                                                                                                                                                                                                                           561
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                                                                                                                                                                                                                                                                                                            Matches 132;
                                                                                                                                                                                                                                                                                                                                                 Query Match
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Q9U9S7;
Q9U9S7;
Q1-MAY-2000 (TrEMBL::el. 13, Created)
O1-MAY-2000 (TrEMBL::el. 13, Last sequence update)
O1-JUN-2001 (TrEMBL::el. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00211; Guanylate_cyc; 1.
Pfam; PF00211; HATPE/Se_c; 1.
Pfam; PF0072; response_req; 1.
Pfam; PF00744; BCTRLSENSOR.
SMART; SM00044; CYC(; 1.
SMART; SM00087; HATPEASe_c; 1.
SMART; SM00087; REC; 2.
PR0SITE; PS50125; GLANYLATE_CYCLASES_2; 1.
SMART; PS50125; GLANYLATE_CYCLASES_2; 1.
PROSITE; PS50387; PFASE; UNKNOWN_1.
Phosphorylation; Sersory transduction.
SEQUENCE 2123 AA; 243039 MW; 744247140BC342FA CRC64;
1946 QQQQQQQQPQQQQQIQQQQ----HQQQKQPSPQQQQQP-----QQPQQQQQQQQQQQIQNQ- 1994
                                                                                                                                                      EMBL; AF153362; AAD50121.1; HSSP; P19754; LAWK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (MAY-1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Soderbom F., Anjard C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Dictyostelium disco:deum (Slime mold).
Eukaryota; Mycetozon; Dictyosteliida; Dictyostelium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR000410; Bctrl_sensor.
InterPro; IPR001054; Guanylt_cyclase.
InterPro; IPR003594; HAPPase_c.
InterPro; IPR001596; Pyrophosphatase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: THE N-TERMINAL REGION IS SIMILAR TO THAT OF OTHER REGULATORY COMPONENTS OF SENSORY TRANSDUCTION SYSTEMS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=44689;
                                  306 QALPGQMLYTQPPLKFVRAPMVVQQPPVQPQVQQQQTAVQTAQAAQMVAPGVQVSQS--- 362
                                                                                                            246 QPPMQQPQPPPSQALPQQLQQMHTQHHQPPPQPQQPPVAQNQPSQLPPQSQTQPLVSQA 305
                                                                                                                                                                                      187 QQQQQQHLIKLHHQNQQQIQQ-QQQQLQRIAQLQLQQQQQQQQQQQQQQQQQQQQQALEAQPPIQ 245
                                                                                                                                                                                                                                                                127 ΕΦΕΦΟΥΑΕΦΟΦΟΦΟ ΦΕΦΦΟΦΟΦΑΑΕΦΟΦΟΦΟΦΟΦΟΡΟΑΦΟSAMOΦΟΕΦΑΥΥΘΡΟΦΕΙΟΦ 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Soderbom F., Anjard C., Iranfar N., Loomis W.F.; An adenylyl cyclase that functions during late development of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     826 AATAGGATGTTPVVKKHVLNPSAKPFTPRGP---STPNPSRPHTPQTP 870
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        402 NVSSGPAPSPSSFLPSPSPSPSPSPSPSTARTPQNFSVPSPGPLNTPVNP 449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           767 -QLATPKPEVSPAPI'SSNTTTPTGIASTPTAGVIASAGSEKTTPAAPTPTSNSATVPTGT 825
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                344 VQTAQAAQMVAPGVQVSQSSLP--MLSSPSPGQQVQTPQSMPPPPQQPSPQPGQPSSQPNS 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     726 PLPIYHTMPPPQTS:?VV---------VTSPVLLEQPPPQPMPVVQQQQTQ 766
                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IPR001440;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IPR001789;
                                                                                                                                                                                                                                                                                                     15.2%; Score 456.5; DB 5; Length 2123; illarity 41.5%; Pred. No. 1.5e-25; Conservative 12; Mismatches 133; Indels 41; Gaps
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Best Local :
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Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
Lightning J., Lloyd C., Mcmurray A., Mortimore B., O'Callaghan M.,
Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Showkeen R.
Smaldon N., Smith A., Sonnhammer E., Staden R., Sulston J.,
Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.;
"2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-JAN-1999 (TrEMBLrel. 09, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
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DY3.5.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              569 QIPTHSTSYGNHEDSVIEEEPHGSVISQQQ------VVP------PRPVQPV 608
                                       323 RAP-----MVVQQPPVQPQVQQQQTAVQTAQAAQMVAPGVQVSQSSLPMLSSPS 371
                                                                                511 APAPQAP--APMQPQQPPKQYVTQPPTYKNNYQTAALGQVNTYSGQSKPQVYTYPGPSQV 568
                                                                                                                       277 -PQPQQPPVAQNQPSQLPPQSQTQP-----LVSQAQALPGQ---MLYTQPPLKFV 322
                                                                                                                                                                                                                                                       407 IAQQQ------QLAEQIAAQQAQQREAARLAQQQAQQAQQAQQLQQQIRQQQLQQ 455
                                                                                                                                                                                                                                                                                              361 PPTQTYSGYPQNVA-------QPQPQQIA-----QQQQLQQQQQLAAEQQKQQQQQQQ 406
                                                                                                                                                                                                                                                                                                                                                                                   104 PP-GTSGMAPHSMAVVSTATPQTQLQLQQVALQQQQQQQFQQQQQAALQQQQQQQQQQQQQQ 162
                                                                                                                                                                                                                                                                                                                                                                                                                             303 AKYSQYLDILQKAYGIQLPGE--MSMQPNTAATNAGGYQTSQQQQVANQVPQTYGQSQQP 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         417 SPSPQPSQSPVTARTPQN 434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     363 -----SLPMLSSPSPGQQVQTPQSMPPPPQPSPQPGQPSSQPNSNVSSGPAPSPSSFLP 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         50 ASVSDPMNALQSLTGGPAAGAAGIGMPPRGPGQSLGGMGS-----FGAMGQPMSLSGQP 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local
                                                                                                                                                                      QQQQQQQNQYGGMQPNPYVQPQAPVQQ---QIAQPPPPQQPAPQ--QPMNFLPAPQAPIIQ 510
                                                                                                                                                                                                             QQQQQQQQQ---QQQQQALEAQPPIQQPPMQQPQPPPSQALPQQLQQMHHTQHHQPP--- 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   163;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Z96047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 h 14.9%; Score 447; DB 5; Similarity 32.0%; Pred. No. 2.8e-25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  796 AA; 88783 MW; 4FDEFCBBB5461059 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           47; Mismatches 171; Indels 128;
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR002965; IInterPro; IPR003616; IInterPro; IPR003888; InterPro; IPR003889; InterPro; IPR003889; I
                                                                                                                                                                                                                                                                                                                                                                                                                                                            trithorax.";
Oncogene 15:549-560(1997).
EMBL; AF010404; AAC51735.1; -.
EMBL; AF010404; HMC_12_box.
                                                                                                                                                                                                                                                      pdam; pr00628; PHD; 3.
pffam; pr00856; SET; 1.
prints; pr01217; pr1CHEXTENSN.
pr051TE; pS00398; RECOMBINASES_2; UNKNOWN_1.
pr0SITE; pS00398; SET; 2.
SMART; SM00542; FYRN; 1.
SMART; SM00541; FYRN; 1.
SMART; SM00541; FYRN; 1.
                                                                                                                                                                                                                    SMART;
SMART;
SMART;
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Eukaryota; Metazoa; (
Mammalia; Eutheria; E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Structure and expression pattern of human ALR, a novel gene with strong homology to ALL-1 involved in acute leukemia and to Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Prasad R., Zhadanov A.B., Sedkov Y., Bullrich F., Druck T., Rallapalli R., Yano T., Alder H., Croce C.M., Huebner K., Mazo A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. MEDLINE=97388474; PubMed=9247308;
                                                                                  3214 PPQGPQGMLG-----PAQVAVLQQQHPGALGPQGPHRQVLMTQSRVLSSPQLAQQGQG 3266
                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Canaani E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9606
                            3267 LMGHRLVTAQQQQQQQQHQQQGSMAGLSHLQQSLMSHSGQPKLSAQPMGSLQQLQQQQQL
                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro;
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  158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           372 PGQQVQTPQSMPPPPQPSPQPGQPSS--QPNSNVSSGPAPSPSSFLPSPSPQPSQSPVTA
                                                                                                            76 PPRGPGQSLGGMGSFGAMGQPMSLSGQPPPGTSGMAPHSMAVVSTATPQTQLQLQQ---- 131
                                                                                                                                                    Local Similarity
                                                      -----VALQQQQQQQFQQQQQAA-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RTPQNFSVPS-PGPLNTPVNPSSVMSPAGSSQAEEQ-----
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QQQQQFQAQQSAMQQQFQAVVQ-QQQQLQQQQQQQHLIKLHHQNQQQIQQQQQQQQQLQRIA 216
                                                                                                                                       180;
                                                                                                                                                                                                                     SM00508;
SM00317;
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IPR001214;
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                                                                                                                                       Conservative
                                                                                                                                                                                                7 AA;
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Primates;
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27.7%;
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PostSET.
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05,
17,
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Last sequence update)
Last annotation update)
                                                                                                                                                    Score 439; DB 4;
Pred. No. 6.8e-24;
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                                                                                                                                       Mismatches 163;
                                                                                                                                                                                                        1026562E1419CE8D CRC64;
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                                                                                                                                                               Length 4957;
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                                                       -----LQQQQQQ 157
                                                                                                                                       Indels 268;
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RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SKGLGPWDPPDNLAETQKPEQSSLVPGHLDQVNGQVVPEASQLSIKQEP 3839
                                                                                                                                                                                                                      \texttt{LLGCQPQLGGFPGPQTGPLQELGAGPRPQGPPRLPAPPGALSTGPVLGPVHPTP----PP}
                                                                                                                                                                                                                                                    SL---PMLSS-PSP------GQQVQTPQSMPPPP------QPSPQPGQPS 396
                                                                                                                                                                                                                                                                                                                      FVRAPM--VVQQPP----VQPQVQQQ-----QTAVQTAQAAQMV----APGVQVS--QS
                                                                                                                                                                                                                                                                                                                                                        {\tt SLGDQPGSMTQNLLGPQQPMLERPMQNNTGPQPP--KPGPVLQSGQGLPG--VGIMPTVG}
                                                                                                                                                                                                                                                                                                                                                                                                                            PQPQPQPSSLQLQPPLRLPGQQQQQVSLLHTAGGGSHGQLGSGSSSEASSVPHLLAQPSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LLTGKEQNTVDPAVSSEATEGPSTHQGGPLAIGTTPESMATEPGEVKPSLSGDSQLLLVQ 3499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QLQLQQQQQQQQ------QQQQQQQALEAQPPIQQPPMQ-----
                                                                                                                                                  SSPQEPKRPSQLPSPSSQLPTEAQLPPTHPGTPK-PQGPTLEPPPGRVSPAAAQLADTLF
                                                                                                                                                                                    SQPNSNVSSGPAPSPSSFLPSPSPQPSQSPVTARTPQNFSVPSP------
                                                                                                                                                                                                                                                                                                                                                                                        -----HTQHHQPPPQPQQPPVAQNQPSQLPPQSQTQPLVSQAQALPGQMLYTQPPLK 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                               -QPQPPPSQ-----ALPQQLQQ----MH----
                                                                                                                   GPLNTPVNPSSVMSPAGSS-----QAEEQQYLDKLKQLSKYIEP
PRELIMINARY;
5262
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014686;
                                                                                                      InterPro;
InterPro;
                                                                                                                                                                                                                        SEQUENCE FROM N.A.

MEDLINE-97388474; PubMed-9247308;

Prasad R., Zhadanov A.B., Sedkov Y., Bullrich F.,

Rallapalli R., Yano T., Alder H., Croce C.M., Hue
                                                                                                                                                                                                                                                                                               Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutherla; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                       01-JAN-1998 (TrEMBLrel.
01-JAN-1998 (TrEMBLrel.
01-JUN-2001 (TrEMBLrel.
           Pfam; PF00628; PHD; Pfam; PF00856; SET; PRINTS; PR01217; PR
                                                                                                                                                     Oncogene 15:549-560(1997)
EMBL; AF010403; AAC51734.
                                                                                                                                                                                                                                                                                   NCBI_TaxID=9606;
PROSITE;
                                             InterPro;
                                                        InterPro;
                                                                     InterPro;
                                                                                InterPro;
                                                                                            InterPro;
                                                                                                                               InterPro;
                                                                                                                                          InterPro;
                                                                                                                                                                              trithorax."
                                                                                                                                                                                     "Structure and expression pattern
strong homology to ALL-1 involved
                                                                                                                                                                                                               Canaani E.
PS00398; RECOMBINASES_2;
                                                                             IPR001965; E
                                             IPR003889;
                                                      IPR002965; P_rich_extensn.
IPR003616; PostSET.
IPR003888; FYrich_N.
                                                                                                      IPR001822; Recombinase
IPR001841; Znf_ring.
                                                                                                                              IPR000910; HMG_12_box.
IPR001214; SET.
            PRICHEXTENSN.
                                                                                            PHD.
                                               FYrich_C.
                                                                                                                                                                                                                                                                                                                                                         05,
05,
                                                                                                                                                                                                                                                                                                                                                         Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                Created)
                                                                                                                                                                                        of human ALR, a novel gene with in acute leukemia and to Drosophila
UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                         update)
                                                                                                                                                                                                                         Huebner K.,
                                                                                                                                                                                                                                       Druck T.
                                                                                                                                                                                                                                                                                                             Euteleostomi;
                                                                                                                                                                                                    gene with
                                                                                                                                                                                                                            Mazo A.,
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RESULT 9
09VP17
ID 09VP17
AC 09VP17
DT 01-MAY
DT 01-JUN
DE CG7117
GN CG7177
OS Drosop
OC Pteryg-
OC Pteryg-
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS50280; SNIT; 2.
SMART; SM00542; FYRC; 1.
SMART; SM00541; FYRI; 1.
SMART; SM00349; HMG 1.
SMART; SM00398; HMG 1.
SMART; SM00508; POST.SET; 1.
SMART; SM00184; RING; 3.
SMART; SM00184; RING; 3.
SMART; SM00184; RING; 3.
SMART; SM00317; SET; 1.
SEQUENCE 5262 AA; 564181 P.
               Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
  Ephydroidea; Drosophilidae; Drosophila
                                                                                                                     CG7177 PROTEIN.
                                                                                                                                  01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                  Q9VP17;
                                                                                                                                                                                                                                                                                                                                            4096 SKGLGPWDPPDNLAETQKPEQSSLVPGHLDQVNGQVVPEASQLSIKQEP 4144
                                                                                                                                                                                                                                                                                                                                                                                                                                       4037 SSPQEPKRPSQLPSFSSQLPTEAQLPPTHPGTPK-PQGPTLEPPPGRVSPAAAQLADTLF 4095
                                                                                                                                                                                                                                       Q9VP17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3981 LLGCQPQLGGFPGPCTGPLQELGAGPRPQGPPRLPAPPGALSTGPVLGPVHPTP----pp 4036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3921 QLRAQLQGVLAKNPÇLRHLSPQQQQQLQALLMQRQLQQSQAVRQTPPYQEPGTQTSPLQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3865 SLGDQPGSMTQNLLCPQQPMLERPMQNNTGPQPP--KPGPVLQSGQGLPG--VGIMPTVG 3920
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3805 PQPQPQPSSLQLQP1LRLPGQQQQQVSLLHTAGGGSHGQLGSGSSSEASSVPHLLAQPSV 3864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3572 LMGHRLVTAQQQQQQQQQQQBAQQGSMAGLSHLQQSLMSHSGQPKLSAQPMGSLQQLQQQQQL 3631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3519 PPQGPQGMLG------PAQVAVLQQQHPGALGPQGPHRQVLMTQSRVLSSPQLAQQGQG 3571
                                                                                                                                                                                                                                                                                                                                                                                            441 ----GPLNTPVNPSSVMSPAGSS-----QAEEQQYLDKLKQLSKYIEP 479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         363 SL---PMLSS-PSP------GQQVQTPQSMPPPP----------QPSPQPGQPS 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      321 FVRAPM--VVQQPP----VQPQVQQQ-----QTAVQTAQAAQMV----APGVQVS--QS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  158 QQQQQFQAQQSAMQCQFQAVVQ-QQQQLQQQQQQQHLIKLHHQNQQQIQQQQQQQQQLQRIA 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               132 -----VALQQQQQQQQFQQQQQAA------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          76 PPRGPGQSLGGMGSIGAMGQPMSLSGQPPPGTSGMAPHSMAVVSTATPQTQLQLQQ---- 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SQPNSNVSSGPAPSESSFLPSPSPQPSQSPVTARTPQNFSVPSP------ 440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LLTGKEQNTVDPAVSSEATEGPSTHQGGPLAIGTTPESMATEPGEVKPSLSGDSQLLLLVQ 3804
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QQQQQFQQQQQQQMGLLNQSRTLLSPQQQQQQQQVALGPGMPAKPLQHFSSPGALGPTL 3744
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QLQLQQQQQQQQ----------QQQQQQQALEAQPPIQQPPMQ------ 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----HTQHHQFPPQPQQPPVAQNQPSQLPPQSQTQPLVSQAQALPGQMLYTQPPLK 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -QPQPPPSQ------ALPQQLQQ----MH------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       564181 MW; 26B7C74CAD417E44 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14.68;
27.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    38; Mismatches 163; Indels 268; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 439; DB 4; Length 5262; Pred. No. 7.2e-24;
                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                  2285 AA
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RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Barandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Barlew R.M., Basu A., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Ballew R.M., Basu A., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Ballew R.M., Basu A., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Borkova D., Botchan M.R., Bouck J., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Broktsin P., Brottier P.,
RA Bortis K.C., Blazen R.G., Ergrag C., Ferrag C., Ferrag S., Fleischmann W.,
RA Geraphos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
Charry J.M., Cawley S., Dahlke C., Davenport L.B., Davkes P.,
RA Hodson K., Doup L.E., Downes M., Dugan Rocha S., Dunkov B.C., Dunn P.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibeywam C.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Heiman T.J., Wei M.-H., Ibeywam C.,
RA Kinmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Kinmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Merkulov G., Malishna N.V., Mobarry C., Morris J., Moshrefi A.,
RA Merkulov G., Malishna N.V., Mobarry C., Morris J., Moshrefi A.,
RA Merkulov G., Milshna N.V., Mobarry C., Morris J., Moshrefi A.,
RA Merkulov G., Milshna N.V., Mobarry C., Morris J., Moshrefi A.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA New B.C., Stapleton K.A., Nixon K., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA New B.C., Shen-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Shen B.C., Shen P., Shen H.,
RA Shen B.C., Shen R., Shen R., She
                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                               1105 YAQAMPQQQHQQLVTGSQVMAPHQHQQPIQIPVQMQVPPTSVAPPIQHTYNQQGGQVTLS 1164
                                                                                                                                             ATP-binding; ....
2285 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00069; pkinase; 2.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
ATP-binding; Transferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FlyBase; FBgn0037098; CG7177.
InterPro; IPR000719; Euk_pkinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
285 -AQNQ------PSQLPP--QSQTQ------PLVSQAQALPGQMLYTQP------ 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=7227;
                                                                                              256 PSQALPQQLQQ-----MHHTQHHQP-----PPQPQQPPV--
                                                                                                                                                                                            200 QNQQQIQQQ--QQQLQRIAQLQLQQQQQQQQQQQQQQQQALEAQPPIQQPPMQQPQ--PP 255
                                                                                                                                                                                                                                           999 QQAQQYFQQQQQQPQQAVNMQQAYAMQQAGQQQQLSQPLQIQQQILQQQQ-----VAVSH 1053
                                                                                                                                                                                                                                                                                             145
                                                                                                                                                                                                                                                                                                                                       945 PQQVQVQQPQTVLPPQPHEQ-----QPQQQQQPLQQQLMHTNVQAPDLTQQQQMAQ 998
                                                                                                                                                                                                                                                                                                                                                                                   96 PMSLSGQPPPGTSGMAPHSMAVVSTATPQTQLQLQQVALQQ-------QQQQQQQFQ 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                        QQQQAALQQQQQQQ-----QQQFQAQQSAMQQQFQAVVQQQQQQQQQQQQQQQQQHLIKLHH 199
                                                                                                                                                                                                                                                                                                                                                                                                                                        181;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    252559 MW; 0E94A907CA01C3BA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         14.1%; Score 423; DB 5; Length 2285; 30.0%; Pred. No. 4.8e-23;
                                                                                                                                                                                                                                                                                                                                                                                                                                  56;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                Indels 192; Gaps
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RESULT OF COMMENT OF C
RX MEDLIND=20195006; PubMed=10731132;
RX MEDLIND=20195006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfelffer B.D.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfelffer B.D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beesson K.Y., Benos P.V., Bernan B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Bolshakov S.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Dunkov B.C., Dunn P.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Kimmel B., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Melson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ã.
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Drosophila melanogaster (Fruit fly).

Drosophila melanogaster (Fruit fly).

Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Eukaryota; Metazoa; Arthropoda; Diptera; Brachycera; Musc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAR-2001 (TrEMBLrel. 01-JUN-2001 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CG6026 PROTEIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1483 SSSS 1486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=7227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1436
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QQQQPLVQQQQLPLVQQQPPL----VQQQQPLVQHQQ----PSVQHQQ----PLVQQPQ- 1267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DAQQQQHPGFSAVPQQAAPFIQQPTQQPIQLSMPLEQQLQ----QLLHSQPAQQQQAMSQ 1220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TDPSKRCPLKTLQKCEIALEKLKNDMRCPLPHRPRCHRP--NSSTYASRSWMPSWPTSAH 565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QPIQVNKDANVATDAMS-LNSAHGALEPAPKTEPQNSADAEKQQKQTGTGTRSQKPRRSN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SPVTARTPQNFSVPSPGPLNT---PVNPSSVMSPAGSSQAEEQQ---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GQQVQTPQSMPPPP-----QPSPQPGQPSSQPNSNVSSGPAPSPSSFLPSPSPQPSQ 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ----PL-KFVRAPMVVQQPPVQPQVQQQQTAVQTAQAAQMVAPGVQVSQSSLPMLSSPSP 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RSGNERIPKLSVTSVDEGSVINCHMENKLKTITFKFDIGDRDETASDITKMFEPTIHGVE
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16,
17,
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Muscomorpha;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1435
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RESULT
Q9VUB6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                             Q9VUB6;
01-MAY-2000
01-MAY-2000
01-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H., Shue B.C., Siden-Klamos I., Sinpson M., Skupski M.P., Smith T., Spier E., Spradling A.C., Stapleton M., Strong R., Sun E., Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X., Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J., Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng Y. Yeh R.-F., Zaveri J.S., Zhan M., Zhu S., Zhu X., Smith J. The genome sequence of Drosophila melanogaster."; Science 287:2185-2195(2000).
                           Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Musc
                                                                                  CG8797
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AE003724; AAF55629.2; -
FlyBase; F9gn038676; CG6026.
InterPro; IPR002965; P_rich_extensn.
PRINTS; PR01217; PRICHEXTENSN.
                                                                                                 CG8797 PROTEIN.
                                                                                                                                                                                  9впл6
               Ephydroidea;
                                                                                                                                                                                                                                                                    739
                                                                                                                                                                                                                                                                                                     454
                                                                                                                                                                                                                                                                                                                                      683
                                                                                                                                                                                                                                                                                                                                                                       402
                                                                                                                                                                                                                                                                                                                                                                                                        624
                                                                                                                                                                                                                                                                                                                                                                                                                                        362
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                                                                                                                                                                                                                                                                    PPQQSSTPQKPQ 750
                                                                                                                                                                                                                                                                                                   SPAGSSQAEEQQ 465
                                                                                                                                                                                                                                                                                                                                      FHQNGNVATSGAPGTISYQEPPPEAPTPYQQLPLIGSNKR----PSKKPVTKPEQPSHSY 738
                                                                                                                                                                                                                                                                                                                                                                                                     VSVGHPSIEKEPLFAKDTPGVQYGQVINEDIGNIKRPLKEPLPPPPNFQQ-MPSIQQNSN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AEEESNVAQNYQQNQGFDAQGNLIQPIAPSKPSPFAMQQPGTQQQPGTQQPAPHQRPSPN 565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QQQLQRIAQLQLQQQQQQQQQQQQQQQQQQALEAQPPIQQPPMQQPQPP-PSQALPQQL---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AFSPIPGTGIPNLDPADVYHTLGQKNTQAEEQQQLQL-----EKQQQMQKQQQIQHQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HHATPQAAIFPTEPVTTTKMYTTSSTSAPVVFTEGPTPPP-----
                                                                                                                                                                                                                                                                                                                                                                  ----NVSSGPAPSPSSFLPSPSPQPS---QSPVTARTPQNFSVPSPGPLNTPVNPSSVM 453
                                                                                                                                                                                                                                                                                                                                                                                                                                    SSL-----PMLSSPSPGQQ------VQTPQSMPPPPQPSPQPGQPSSQPNS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EQKYISGSQENYSNEYVSYQVQQPNMMQYRPVPGQI--NNVVISPGQQSASFVLGSQVQQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QAQALPG-QMLYTQPPLKF-VRAPMVVQQPPVQPQVQQQQTAVQTAQAAQMVAPGVQVSQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QQQHQ-----QHQQQHIQQQHQHQQQHQPL---PPTLQ----QQPSPPKPPMTLSDIFNSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QYQEQQQQLYEQQQYQLQLEKQHLDKQKHPYQQQLEKQQQQQQQQQQQQHHQQQHQQQHQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QQQQQQQQFQAQQSAMQQQFQAVVQQ----QQQLQQQQQQQQQHLIKLHHQNQQQIQQQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SLSGQPPPGTSGMAP----HSMAVVST-ATPQTQLQLQQVALQQQQQQQQQQQQQQQAALQ 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ---QMHHTQHHQ-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              146;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1542 AA;
                                                                                                               (TrEMBLrel.
                                                                                                                                               (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                  PRELIMINARY;
             Drosophilidae; Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13.9%;
29.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              168644 MW;
                                                                                                             13,
13,
17,
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                                                                                                             Last sequence update)
Last annotation update)
                                                                                                                                                Created)
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Pred. No. 6.5e-23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches 170;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27C06E61A73FF016 CRC64;
                                                                                                                                                                                  1798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       - PPPQPQQPPVAQNQPSQLPPQSQTQPLVS
                             Brachycera; Muscomorpha;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 1542;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels 116;
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Qγ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RX
MEDLINES—20196006; Phoymed=10731132;
RX
Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA
Adams M.D., Celniker S.E., Holt R.M., Hoskins R.A., Galle R.F.,
RA
Amanatides P.G., Scharer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA
Amanatides P.G., Scharer S.E., Richards S.A., Ashburner M., Henderson S.N.,
RA
Sutton G.G., Wortman J.R., Yannell M.D., Zhang Q., Chen L.X.,
RA
Brandon R.C., Rogers Y.H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA
Abril J.F., Agbayani A., An H.-J., Andrews Pfannkoch C., Baldwin D.,
RA
Abril J.F., Agbayani A., An H.-J., Andrews Pfannkoch C., Baldwin D.,
RA
Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA
Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA
Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Devitter A., Chandra I.,
RA
Cherry J.M., Cawley S., Dahlke C., Davenport I.B., Davies P.,
RA
Borito J.M., Cawley S., Dahlke C., Davenport I.B., Davies P.,
RA
Glodek R., Doup L.E., Downes M., Dugan Rocha S., Dunkov B.C., Dunn P.,
Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA
RA Glodek A., Gong F., 3orrell J.H., Gu Z., Gunn P., Harris M.,
RA
Adrialli M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA
Alaris N.L., Harvey D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA
Adrialli M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA
Adrialli M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA
Adrialli M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA
Adrialli M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA
Adrialli M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA
Adrialli M., Kalush R., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA
Adrialli M., Kalush R., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA
Adrialli M., Kalush R., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA
Adrialli M., Kalush R., Karpen G.H., Ke Z., Kennison J.A., Naliz D.,
RA
Adrialli M., Kalush R., Manda R., Barti S., Kulp D., Lin X.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                          Matches 163;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; iPR001357; BRCT.
Pfam; PF00533; BRCT; 4.
SMART; SM00292; BRCT; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                   336 QPQQQQQQPQQQHTPSPRQSPLQQQPTTPTLQQQPNQQNAQQIQQQQQQQQQQQQQQQQQQ
185
                                                                                                                                                                                                                                                                       144 QQQQQAALQQQQ----QQQQ----
                                                                                                                                                                                                                                                                                                                                                               95 QPMSLSGQPPPGTSGMAPHSMAVVSTATPQT-----QLQLQQVALQQQQQQQQQF 143
                                           TIQRPPTNVQQQQQVPQQQQQIIGQFPQQQQLQQQPQQQISGVQQPQQQQQQQQQKTFIIS 575
                                                                                                                                   QQQPQQQQCITQVQQLPPAQQQQQLPQQHQVQQQQPQQVQFTQQQQIALGAGGQVRIIQQ
                                                                                                                                                                               QQQQQQQQHLIKLHH----QNQQQTQQQQQ-QLQRTAQLQLQQQQ--
                                                                                                                                                                                                                           QQQQQQVLTQQQPQPGQQQQVITQRHVINTSTAQGQQIIQSHMSLALQKQQQLLHVQQQA 455
                                                                                       -----QQQQQQQQQQQALEAQPPIQQPPMQQPQPPPSQA-LPQQLQQMHHT----
                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PS50172; BRCT;
1798 AA; 20
                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                          13.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         205695 MW; 64E4963B1181B6E9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      . 4
2
                                                                                                                                                                                                                                                                                                                                                                                                        42; Mismatches 172; Indels 151; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                             Score 415.5; D
Pred. No. 1.4e-
                                                                                                                                                                                                                                                                    --QQQFQAQQSAMQQQFQAVVQQQQQL 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 5; Length 1798;
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RA Adams M.D. (Calniker S.E., Holt R.A., Evans C.A., Gocayne J.D., RA Adams M.D.) (Calniker S.E., Lit P.W., Hoskins R.A., Galle R.F., RA Adams M.D.) (Calniker S.E., Lit P.W., Hoskins R.A., Galle R.F., RA Adams M.D.) (Calniker S.E., Richards S., Ashburner M., Henderson S.N., RA George R.A., Levis S.E., Richards S., Ashburner M., Henderson S.N., RA George R.A., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D., RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D., RA Brandon R.C., Moyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G., RA Burtis V.G., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., RA Beeson K.Y., Benos P.V., Berman B.P., Bhadari D., Bolshakov S., RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., RA Borkvoa D., Botchan M.R., Bouck J., Brokstein P., Brottier P., Cadieu E., Center A., Chandra I., RA Gerbalos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M., RA Gerbalos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M., RA Golock R., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Pieischmann W., RA Glock A., Gong F., Gorrell J.H., Gal Z., Glabart M.M., Glasser K., RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J., RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J., RA Harris N.L., Levitsky A.A., Li J. Li Z., Liang Y., Lin X., RA Liu X., Mattel B., McIntosh T.C., McLeod M.P., McPherson D.L., RA Liu X., Mattel B., McIntosh T.C., McLeod M.P., McPherson D.L., RA Liu X., Mattel B., McIntosh T.C., McLeod M.P., McPherson D.L., RA RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G., RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G., RA Ra Mang Z.-Y., Wassarman D.A., Weinstock G.M., Weinstock G.M., Wang X., Smith T., Ra Schien B.C., Stapleton M., Strong R., Sun E., Ra Kennight D.A., Ratchulov G.M., Pittman R., Sun E., Ra Kennight J., Ratchulov
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09VK09;

01-MAY-2000 (Tri

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CG6043 PROTEIN.
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Drosophila melanogaster (Fruit fly)
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=20196006; PubMed=10731132;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  431 TPQNFSVP----SPGPLNTPVNPSSVMSPAGSSQ-AEEQQYLDKLKQL 473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                754 QSPQHHPQMQQQHWSPQSPAGGQMASSTPGTPTSVGMQSPLPGGPTTPQPQPQQQFVPRG 813
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   305 AQALPGQMLYTQ-----PPLKFVRAPMVVQ-QPPVQPQVQQQQTAVQTAQAAQMVAPGV 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        576 QQHFNQLSVQQQQQILAQNPQSQNVYVVNQTQQQLVQQQQMLQQQQIIPQQQQQRM--Q 633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q---VSQSSLPM-----LSSPSPGQQV-----QTPQSMPPP---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (TrembLrel. 13, Created)
(TrembLrel. 13, Last sequence (TrembLrel. 17, Last annotation)
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Last annotation update)
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RESULT
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Best Local Similarity
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Q9FR41;
01-MAR-2001 (TIEMBLITEL 1
01-MAR-2001 (TIEMBLITEL 1
01-JUN-2001 (TIEMBLITEL 1
           STRAIN-CV. IMPERIAL;
What was a seried J.H., Appels R.;
"A gene from the Sec2 (Gli-R2) locus of a wheat 2RS.2Bl translocation line.";
Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases EMBL; AF201084; AAG35598.1; -.
                                                                                                                                     Secale cereale (Rye).
Eukaryota; Viridiplantae; Stre
Spermatophyta; Magnollophyta;
Triticeae; Secale.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AE003639; AAF53274.1;
FlyBase; FBgn0032497; CG6043.
InterPro; IPR002965; P_rich_extensn.
PRINTS; PR01217; PRICHEXTENSN.
                                                                                                                                                                                              GSEC2-1.
                                                                                                                                                                                                         SECALIN PRECURSOR.
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                                                                                                                       NCBI_TaxID=4550;
                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                625 PVSAAPI---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10 KSSKDMESHVFLKAKTRDEYLSLVARLIIHFRDIHNKKSQASVSDPMNALQSLT-----
                                                                                                                                                                                                                                                                                                        13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           SLYTAPLAQPTEPQAQRILLQQQQQQSSARDSPMRQLPQQQPQTNQPMRWLSSQPASKEQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QQQDSHPQPIYNNVQQQQQRSRDVFSPARNETSAANTFNSQ----QQQNQFGGAAKPTNVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QPQPPPSQALPQQLQQMHTQHHQPPPQPQQPPVAQNQPSQLPPQSQTQ---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PATRPEFRSVPMPTSPAVNVYTRQSDSPRSPFEPQQQQQQQQQQPQRSTESPFRFAQQQQQQQ 342
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GPRPSAASVESSYSPYTPTPQVPPV----AKSPPVQYQQPTPPAT---PPQQQQQQQSEQQ 282
                                                                                                                                                                                                                                                                                                                                                                                                                                PGVQVSQSS--LP-MLSSPSPGQQVQTPQSMPPPPQPSPQPGQPS-SQPNSNVSSGPAPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----PLVSQAQALPGQMLYTQPPLKFVRAPMVVQQPPVQPQVQQQQQTAVQTAQAAQMVA
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IPR001954; Glia_glutenin
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30.8%;
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                                                                                                                                                  Streptophyta; Embryophyta; Tracheophyta;
yta; Liliopsida; Poales; Poaceae; Pooidea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      42;
                                                                                                                                                                                                                                                Created)
                                                                                                                                                                                                                     Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                             PRT;
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                                                      2RS.2Bl chromosomal
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01-NOV-1996
01-JUN-2001
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Q24279;
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PRINTS; PR00208; GLIADGLUTEN.
PRINTS; PR01217; PRICHEXTENSN.
CHAIN 20 455 SECALIN
                                                                                                                                                                                                                                                                        Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Musc
Ephydroidea; Drosophilidae; Drosophila.
           InterPro; IPR002710; DIL.
InterPro; IPR000253; FHA_domain.
InterPro; IPR0004778; PDZ.
InterPro; IPR000159; RA.
Pfam; PF01843; DIL; 1.
                                                                                                         Genes Dev. 9:612-625(1995).
EMBL; D49534; BAA08478.1; -
                                                                                                                                                                                         Miyamoto H., Nihonmatsu I., Kondo
                                                                                                                                                                                                        STRAIN=CANTON-S;
MEDLINE=95212910; PubMed=7698650;
                                                                                                                                                                                                                                                                                                                                   CNO OR CG2534.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                               FlyBase; FBgn0000340; cno.
                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                    Drosophila."
                                                                                                                                                 "canoe encodes a novel protein containing functions with Notch and scabrous in commo
                                                                                               ISSP;
                                                                                                                                                                              lkegamı
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              341
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    115 MAVVSTAT---POTOLOLOCVALOCOCOCOCOCOCOAALOCOCO----COCOCOCF--CACC 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7 LAILAMATTIATANMQVNPSGQVQCPQQQPFPQPQQSSPQQPQQPFPQQSQQPFPQQPQQ
                                                                                                                                                                                                                                                                                                                                                                                                                                              14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QTAVQTAQAAQMVAPGVQVSQSSLPMLSSPS---PGQQVQTPQSMPPPPPQPSQPGQPSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QQQQQQQQQQQQALEAQPPIQQPPMQQPQPPPSQALPQQLQQMHHTQHHQPPP---QPQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SAMQQQ----FQAVVQQQQQLQQQQQQQHLIKLHHQNQQQ1QQQQQQQQQQQQQQQQQQQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SKIFPQSECQVMQQQCCQQLAQIPQQLQCAAIHSVVHAIIMQQEQRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QSQEQFPQVHQPQ------QPSPQQQQPSIQLSLQQQLN-PCKNVLLQQCSPVALVSSLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q----PYPQEPQQLFPQSQQPQQPFPQPQQPFPQPQPQTQQSIPQPQQPFPQPQQPFP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QPFPQPQQPQQLFPQTQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QPPVAQNQPSQLPPQSQTQPLVSQAQALPGQMLYTQPPLKFVRAPMVVQQPPVQPQVQQQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PQQPVPQQPLQQFPQQPRPQQPLQQFPQQPQQPFPQQPQQPVPQQSQQPFPQTQQPQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SSPQPQQPYPQQPFPQQPQQPYPQQPPQQ----PFPQQPQQPYPQQPQQ-----QFPQQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QPNSNVSSGPAPSPSSFLPSPSPQPSQSPVTARTPQNFSVPSPGPLNTPVNPSSVMS----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 135;
                                                                                             Q12923;
                                                                                                                                                                              Y., Yamamoto D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -PAGSSQAEEQQYLDKLKQLSKYIE--PLRRMINKIDKNEDRKK 495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   455 AA;
                                                                                                                                                                                                                                                                                                                                                            (TrEMBLrel. (TrEMBLrel. )
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                               3PDZ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   455 ;
51731 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              33.2%;
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01,
17,
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                                                                                                                                                                                                                                                                                                                                                            Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -QSSPQQPQQVTSQPQQPFPQA----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SECALIN.
; C1A4176DD045D927 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 400; DB 1
Pred. No. 5e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                           s.,
                                                                                                                                                                                                                                                                                                                                                                                                                    1893
                                                                                                                                                  common
                                                                                                                                                                                           Ueda
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                                                                                                                                                                                                                                                                                                                                                                                                                    A
                                                                                                                                                               a GLGF/DHR motif
                                                                                                                                                                                      R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 175;
                                                                                                                                                  developmental
                                                                                                                                                                                           Togashi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 455;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -QPPQQSSPQSQ
                                                                                                                                                                                         s.,
                                                                                                                                                                                                                                                                                           Muscomorpha;
                                                                                                                                                  pathways
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 58;
                                                                                                                                                                                           Hirata
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340 175 280 115 223 66

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                                                                                                                                                                                                          RESULT 15
Q9W3G1
                                                                                                                                                                                                                                                                                                             Db.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                    Q9W3G1
Q9W3G1
Q9W3G1
Q1-MAY-2000 (TrEMBLr:1.13, Created)
Q1-MAY-2000 (TrEMBLr:1.13, Last sequence update)
Q1-UN-2001 (TrEMBLr:1.17, Last annotation update)
CG10555 PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1406 SYVASNQGNNRPLHSESNPWEREEREKDLEMRREHIRQWREQQISELSQIVSRSPMQEEQ 1465
                                                                                                                                                                                                                                                                                                             1621 NNNE 1624
                                                                                                                                                                                                                                                                                                                                                                                                              1562 SILKHNRYSEGGVGP3GAPSSPSKSQKSASFANERHLHTEHPISNLAKELNQL-TMLDKD 1620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1521 ---YRQTEIKLAEMP-------DSNSLVDSVP-PQP----PAPTAQPLSSNTQQPK 1561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1466 LKTLILERDFERRAQ3LQEQ--EEQDQEQQYDKENVQELFRLAGGGQQVSAIQTPITS--- 1520
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1111 AMNAYNGSSPLAPQQ PPQQQQQSPYQQQQQQQHMQANANLPPTRPVSAYYHSQQSAQQQL 1170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1010 AHLPNSKSVPA---LHHHTGSGTISLA-----NSKSRST-----HSLHNNTSGM 1050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Prodom; PD003376; DIL; 1.

SMART; SM002240; FHA; 1.

SMART; SM00228; PD2; 1.

SMART; SM00314; RA; 2.

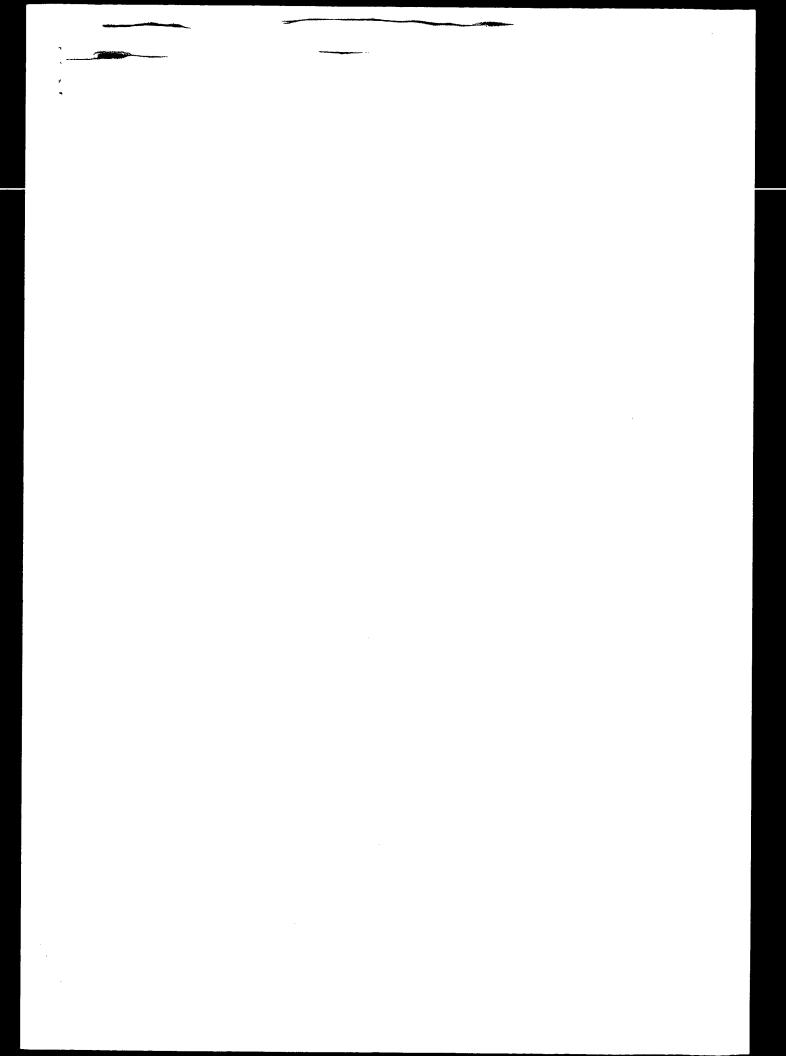
PROSITE; PS50106; PDZ; 1.

SEQUENCE 1893 AA; 210186 MW; E958E3470783CDDA CRC64;
Drosophila melanogas:er (Fruit fly)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1346 VPPSTAPKPQQQQQRYLGQSLPAEDKPPLPPTATHPLFKATQQIAPGMNYVASTLDPPKG 1405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1171 QQQQQQQQ----QHSLQQQQFALSSGNLNGQQQQQQQQHQHQLTLNNRTKSQQNFQHTLRMQ 1227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1051 GGTGGAAAGGMLGQPNGSQNNANGNGNGNEQGFYQNLSVYRAQNQSQPTLNERPPTAAHA 1110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00595; PDZ; 1. Pfam; PF00788; RA; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1288 YRRSQLHDPSTLYEI 2QQQLQQQQQQQQQQQQQQASPNFIALPPKPLGSLQSP--NKPN 1345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1228 QMMAPSMPNISNMYH3QQQHQQQLPLQQQQQQQQQPLMSSSQSMQNVNDFAGGYQNGSLE 1287
                                                                                                                                                                                                                                                                                                                                                               488 DKNE 491
                                                                                                                                                                                                                                                                                                                                                                                                                                                             428 TARTPONESVPSPGPENTPVNPSSVMSPAGSSQAEEQQYLDKLKQLSKYIEPLRRMINKI 487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                372 PGQQVQTPQSMPPPP PSPQPGQPSSQPNSNVSSGPAPSPSSFLPSPSPQP----SQSPV 427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       284 -- VAQNQPSQLPPQS 2TQP--------LVSQAQALPGQMLYTQPP 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        254 PPPSQA-LPQQLQQMHHTQ----HHQPPPQP------QQ------PP-- 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             155 QQQQQQQQFQAQQSAMQQQF-----QAVVQQQQQLQQQ------QQQQQHLIKL- 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          111 APHSMAVVSTATPQT?LQLQQVALQQQQQQQQQQQFQQ------QQQAALQQQ 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              67 A--AGAAGIGM--PPRGPGQSLGGMGS-----FGAMGQPMSLSGQPPPGTSGM 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7 AHSKSSKDMESHVFLKAKTRDEYLSLVARLIIHFRDIHNKKSQASVSDPMNALQSLTGGP 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LK-----FVRAPM/VQQPPVQPQVQQQQTAVQTAQAAQMVAPGVQVSQSSLPMLSSPS 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----IAQLQLQQQQQQQQQQQQQQQA--LEAQPP----IQQPPMQQPQ 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   182;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13.3%; Score 399; DB 5; Length 1893; 27.4%; Pred. No. 2.4e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             58; Mismatches 196; Indels 228; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30;
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RA Addams M.D., Celniker S.E., Lichards S. Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y. H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Man K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Glodek A., Gong F., Correll J.H., Gul Z., Glan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Duuck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Kinmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris S., Kulp D., Lai Z.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris D.M., Peacleb J.M.,
RA Melson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Melson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Melson D.R., Nelson K.A., Sampson M., Skupski M.P., Saith T.,
RA Reinert K., Remington K., Sampson M., Skupski M.P., Saith T.,
RA Reinert E., Spradling A.C., Stapleton M., Strong R., Sin E.,
RA Men M., Shang S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Zheng X.H., Wang S.N., Zhon M., Zhon X., Zhu X., Smith H.O.,
RA Zheng X.H., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Zheng X.H., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Zheng R. R., Shang R. R
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 154;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AE003443; AAF46366.1; -.
FIYBASC; FB9n0030034; CG10555.
InterPro; IPR002965; P_rich_extensn.
PRINTS; PR01217; PRICHEXTENSN.
SEQUENCE 926 AA; 93004 MW; 6FD5B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila. NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=20196006; PubMed=10731132;
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                                                                                          243 PVPGQPGQGPPQMGMQQHGGDPQGPPVQMPPYGAQQQPQPHPGLPPGAQQQSQQQQQQQQ 302
                                                                                                                                                                           103 PPPGTSGMAPHSMAVV------STATPQTQLQLQQVALQQQQQQQQQQQQQQQQQQQ
                                                                                                                                                                                                                                                                189 AQLADPAMNISQILPPPHILQTQAMQQGGQQTPPTGPHGMLGG------PPQQQQQQPGQG 242
                                                                                                                                                                                                                                                                                                                                                 50 ASVSDPMNALQSLTGGP-----AAGAAGIGMPPRGPGQSLGGMGSFGAMGQPMSLSGQ- 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local
QQQAALQQQQQQQQQQQQFQAQQSAMQQQFQAVVQQQQQQLQ------QQQQQQQQHLIKLHH 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                  13.2%; Score 398; DB 5; Length 926; 30.7%; Pred. No. 1.4e-21; Indels 130; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6FD5B9F77C36C006 CRC64;
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Sea1 Job	Дb	Qy	ф	Qy :	ДЬ	Qy	Вβ	οy	<b>-</b> Db	Q, T
Search completed: February 28, 2002, 19:39:50 Job time: 202 sec	Db 630TSSAQSPYQAYQQQQQQ 646	444		··· <del>-</del>	511					
9:39:50			571 QQPPPGPPQSQYGPPPPQNSAGGPPPMGYAGYPPNPGQYGQAGAGGGPPPSGYWPPPPP- 629	-SPQPGQPSSQPNSNVSSGPAPSPSSFLPSPSPQPSQSPVTARTPQNFSVPSPGPL 443	PPVPGQQQPPP	342 TAVQTAQAAQMVAPGVQVSQSSLPMLSSPSPG-QQVQTPQSMPPPPPQP 388	476 YQPQGAYPYGPPTQGYGPPPPGPPNAAQGGYHHGP 510	287 NQPSQLPPQSQTQPLVSQAQALPGQMLYTQPPLKFVRAPMVVQQPPVQPQVQQQQ 341	420 NQQQQQQTGPGGPGPQPGAGGPGVPPPQSPYRVSYQQQQQQHSHYPGYPPQPQTQ 475	244 IQQPPMQQPQPPPSQALPQQLQQMHHTQHHQPPPQPQQPPVAQ 286



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gb_est2:BF14300
gb_est2:BF1089323
gb_est2:BG982754
gb_est2:BG982761
gb_est2:BF382761
gb_est1:BF382464
gb_est1:BF387483
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gb_est2:BG421322
lgb_est1:BE251464
gb_est2:BI024741
                                                                                                                             gb_est1:AW747905
gb_est1:AI787536
                                                                                                                                                                                                                                                                         gb_est2:BG122694
gb_est2:BG177319
gb_est1:AW227792
                                                                                                                                                                                                                                                                                                                                                                                      gb_est2:BG335275
gb_est1:BE391135
gb_est1:AA664125
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Query length: 579
                                                                                                                                                                                                                                          gb_htc:BC003221
gb_est1:BE284329
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gb_est2:BI151303
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gb_est1:AW603679
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Database length: 1077921985
                                                                                                                                                                                                                           gb_est2:BF584530
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gb_lest2:BG386117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gb_est1:AL046886
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gb_est2:BG281923
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gb_est2:BG766214
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Search time (sec): 1388.280000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Database:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Search information block:
Query: US-09-668-119-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Command line parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    About: Results were produced by the GenCore software, version 4.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Date: Feb 28,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OM of: US-09-668-119-3 to: EST:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -MODEL=frame+_p2n.model -DEV=xlp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Copyright (c) 1993-2000 Compugen Ltd.
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1010.96
997.14
 out_format :
                                              9.6e-22
6.2e-21
6.3e-20
1.5e-19
1.2e-18
6.5e-18
8.9e-18
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2.9e-28
6.3e-28
1.5e-26
2.0e-26
3.0e-26
3.0e-25
1.7e-23
1.5e-22
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4.6e-36
5.2e-34
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3.8e-47
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7.7e-32
1.3e-31
4.0e-31
2.9e-30
3.1e-29
6.4e-29
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4.4e-22
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8.7e-33
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3.9e-43
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1.2e-41
! Documentation
                                                         | BC00527 Homo Sapiens, clone | BC281923 602403104F1 NIH_MGC_20 | AL04686 DKFZp586E2117_r1 586 | BG386117 602455292F1 NIH_MGC_11 | BG386117 602455292F1 NIH_MGC_11 | BG386117 602455292F1 NIH_MGC_21 | BG38611602509947F1 NIH_MGC_21 | BG468341 602509947F1 NIH_MGC_11 | BG468341 602509947F1 NIH_MGC_11 | BG01526 ba83f05.y1 NIH_MGC_11 | BG01526 ba83f05.y1 NIH_MGC_21 | BG01526 60248567F1 NIH_MGC_21 | BE01956 ba83f05.y1 NIH_MGC_21 | BG915202 602814508F1 NIH_MGC_21 | BG915202 602814508F1 NIH_MGC_21 | BG2335275 602403785F1 NIH_MGC_21 | BG335275 602403785 | BG375785 | BG3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BG750043 602708813F1 NIH_MGC_4
BG766214 602737942F1 NIH_MGC_4
I BC005027 Homo sapiens, clone
             BI389244 UMN30B11 Canine Brain AA982166 ua21h02.r1 Soares_mamm BE387483 601273695F1 NIH_MGC_20
                                                                                                                                                                                                                                                                                                                                                                                                     BE391135 601286095F1 NIH_MGC_4
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gb_est2:BF600990
gb_est2:BG982938
gb_est2:N49344
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ORGANISM
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                                                                                                                                                                               alignment_block:
                                                                                                                                                                                                                                                              alignment_scores:
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                                                                                                                                                                                                                                                                                                                                BASE COUNT
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LOCUS BG750043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gb_est2:BI011820
                                                                                                                               Align seg 1/1 to: BG750043
                                                                                                                                                                US-09-668-119-3 x BG750043
                                                                                                                                                                                                            Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                JOURNAL
               145 nGlnGlnAlaAlaLeuGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnG
                                                                                              129 LeuGlnGlnValAlaLeuGlnGlnGlnGlnGlnGlnGlnPheGlnGl 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               source
52 GCAGCAGCAGCGGCGCTACAGCAGCAGCAGCAGCAGCAGCAACAGCAGC
                                                               2 CTCCAGCAGGTGGCGCTGCAGCAGCAGCAGCAGCAGCAGCTTCCAGCA
                                                                                                                                                                                                            Quality: 1223.50
Ratio: 4.855
milarity: 97.674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 776)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Plate: LLCM1684 row: j column: High quality sequence stop: 743.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BG750043 776 bp mRNA EST 15-MAY-2001 602708813F1 NIH_MGC_43 Homo sapiens cDNA clone IMAGE:4845411 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BG750043.1 GI:14060696
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CDNA Library Preparation: Ling Hong/Rubin Laboratory
                                                                                                                                                                                                                                                                                                                                  207
                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /db_xref="taxon:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
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538.
533.
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455.40
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435.47
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3.3e-16
4.7e-16
4.3e-15
                                                                                                                                                                                                                              Length:
Gaps:
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487
382
313
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| BF600990 265840 MARC 3BOV Bo
| BG982938 PM0-CN0150-050301-0
| N49344 yy23e10.rl Soares mel
                              162
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162 lnPheGlnAlaGlnGlnSerAlaMetGlnGlnGlnPheGlnAlaValVal

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REFERENCE
                                      COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           seq_documentation_block:
LOCUS BG766214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               seq_name: gb_est2:BG766214
                                                                                                                                                                                                                                                                                                                                       KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                    ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DEFINITION
                                                                                                      TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        702 GCAGTCT.CCCATGCTGTCCTCGCCGTCACCGGGCCAGCAGGTTGCAAGA 750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            312 etLeuTyrThrGlnProProLeuLysPheValArgAlaProMetValVal 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           245 nGlnProProMetGlnGlnProGlnProProProSerGlnAlaLeuProG 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   152 CAGCAGCAGCAGCTCCAGCAGCAGCAGCAGCAGCAGCAGCATCTAAT 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                179 GlnGlnGlnGlnLeuGlnGlnGlnGlnGlnGlnGlnGlnHisLeuII 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       751 CCCCGCATCGGAATGGCCCCTCCC 774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 379 ProGln...SerMetFroProPro 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          362 erSerLeuProMetLeuSerSerProSerProGlyGlnGlnValGlnThr 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          652 GACAGCTCAGGCTGCCCAGATGGTGGCTCCCGGAGTCCAGGTCAGCCAGA 701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    345 nThrAlaGlnAlaAlaGlnMetValAlaProGlyValGlnValSerGlnS 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          552 TGTTGTATACCCAAGCACCACTGAAATTTGTCCGAGCTCCGATGGTGGTG 601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           502 GTCGCAGACCCAGCCTTTGGTGTCACAGGCGCAAGCTCTCCCCTGGACAAA 551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         452 CCCCAGCAGCCTCCAGTTGCTCAGAACCAATCATCACAACTCCCGCCACA 501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        279 ProGlnGlnProProValAlaGlnAsnGlnProSerGlnLeuProProGl 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           262 InGlnLeuGlnGlnMetHisHisThrGlnHisHisGlnProProProGln 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            352 GCAGCCACCGATGCAGCCACAGCCTCCGCCCTCCCAGGCTCTGCCCC 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              302 CAGCAGCAGCAGCAGCAGCAGCGCGTTGCAGGCCCAGCCAATTCA 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         202 TAAATTGCATCAACAAATCAGCAACAGATACAGCAGCAGCAGCAACAGCAGC 251
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        602 CAGCAGCCCCCAGTGCAGCCCCAGGTGCAGCAGCAGCAGCAGCAGTACA 651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     329 GlnGlnProProValGlnProGlnValGlnGlnGlnGlnThrAlaValGl 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        295 nSerGlnThrGlnProLeuValSerGlnAlaGlnAlaLeuProGlyGlnM 312
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                              Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 730)
11 (bases 1 to 730)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                      BG766214.1 GI:14076867
                                                                                                                                                                                                                                                                                                                                                                                                                                   mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BG766214 730 bp mRNA EST 15-MAY-2001 602737942F1 NIH_MGC_49 HOMO sapiens cDNA clone IMAGE:4862938 5',
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alignment_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         402 snValSerSerGlyProAlaProSerProSerSerPheLeuProSerPro 418
                                            354 CCCCCAGGCGTCCCCGCCAGCCCGGCCAGCTCACAGCCCAACTCCA 403
                                                                                         385 oProGlnProSerProGlnProGlyGlnProSerSerGlnProAsnSerA 402
                                                                                                                                        304 TCGCCGTCACCGGGCCAGCAGGTGCAGACCCCGCAGTCGATGCCCCCTCC 353
                                                                                                                                                                369 SerProSerProGlyGlnGlnValGlnThrProGlnSerMetProProPr 385
                                                                                                                                                                                                                                  254 TGGTGGCTCCCGGAGTCCAGGTCAGCCAGAGCAGCCTCCCCATGCTGTCC 303
                                                                                                                                                                                                                                                                            352 etValAlaProGlyValGlnValSerGlnSerSerLeuProMetLeuSer 368
                                                                                                                                                                                                                                                                                                                        204 CCAGGTGCAGCAGCAGCAGCAGCAGTACAGACAGCTCAGGCTGCCCAGA 253
                                                                                                                                                                                                                                                                                                                                                   335 oGinvalGinGlnGlnGhrhrAlaValGhrhrAlaGhnAlaAlaGhm 352
                                                                                                                                                                                                                                                                                                                                                                                                                    154 CTGAAATTTGTCCGAGCTCCGATGGTGGTGCAGCAGCCCCCAGTGCAGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                               319 LeuLysPheValArgAlaProMetValValGlnGlnProProValGlnPr 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 285 aGlnAsnGlnProSerGlnLeuProProGlnSerGlnThrGlnProLeuV 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        269 HisThrGlnHisHisGlnProProProGlnProGlnGlnProProValAl 285
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Quality: 1206.00
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      http://image.llnl.gov
Plate: LLCM1724 row:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CDNA Library Preparation: Ling Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) CNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ratio:
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/db_xref="taxon:9606"
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DEFINITION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ### AGCTGAAGCAGCTGTCGAAGTACATCGAGCCCCTGCGCCCCATGATCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SerProGlnProSerGlnSerProValThrAlaArgThrProGlnAsnPh 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TCATGAGCCCAGCTGGCTCCAGCCAGGCTGAGGAGCAGCAGTACCTGGAC
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                                                               This clone has the following problem: frame shifted.

Coration // Analysia.
                                                                                                                                                                                                                                                   Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield, Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin, Letticia Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven Ness, Pawan Pandoh, Anna-Liisa Prabhu, Parvaneh Saeedi, Jacqueline Schein, Duane Smailus, Michael Smith, Lorraine Spence, Jeff Stott, Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy,
                                                                                                                                                                                                                                                                                                                                                                                                                           cDNA Library Preparation: Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Genome Sequence Centre, BC Cancer Agency, Vancouver, BC, Canada
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
                                                                                                                                                                                                                                     George Yang, Scott Zuyderduyn, Marco Marra.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (26-MAR-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1. (bases 1_to 2752)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                       info@bcgsc.bc.ca
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                                                     Location/Qualifiers
           /organism="Homo sapiens"
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alignment_block:
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Percent Similarity:
                          405 erGlyProAlaProSerProSerSerPheLeuProSerProSerProGln 421
                                                                                                                                                                                                                                               372 ProGlyGlnGlnValGlnThrProGlnSerMetProProProProGlnPr 388
                                                                                                                                                 388 oSerProGlnProGlyGlnProSerSerGlnProAsnSerAsnValSerS
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                                                                                                                                                                                                                                                                                                   700 TCCACTTCCAGGTCAGCCAGAGCAGCCTCCCCATGCTGTCCTCGCCGTCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         244 eGlnGlnProProMetGlnGlnProGlnProProProSerGlnAlaLeuP 261
CTGGCCCTGCCCCATCTCCCAGTAGCTTCCTGCCCAGCCCCTCACCGCAG
                                                                                                GTCCCCGCAGCCCAGCCCAGCTCACAGCCCAACTCCAACGTCAGCT 849
                                                                                                                                                                                                   laLeuProGlyGlnMetLeuTyrThrGlnProProLeuLysPheValArg
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Ratio: 4.041
milarity: 78.191
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905 c 791 g
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/clone_lib="NIH_MGC_7"
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/clone="IMAGE:2822900"
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Gaps: 10
Identity: 67.287
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seq_name: gb_est2:BG281923
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1300 TCCTGGATGCCGTCCNGGCCAACATCCGCTCACCTGTCTTCAACCATTCC 1349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1250 CCCACCGCCCCGGTCCCACCGACCAAACAGCAGTACCTATGCCAGCCGC 1299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1200 TGTGAGATCGCCCTGCAGAAACTCAAGAATGACATGGCGGTGCCCACTCC 1249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         505 spileLeuThrAspProSerLysArgCysProLeuLysThrLeuGlnLys 521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            488 pLysAsnGluAspArcLysLysAspLeuSerLysMetLysSerLeuLeuA 505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                900 CCCTCCCAGAGCCCAGTGACGGCGCGGGACCCCCACAGAACTTCAGTGTCCC 949
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      538 roHisArgProArgCysHisArgProAsnSerSerThrTyrAlaSerArg 554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            522 CysGluIleAlaLeuCluLysLeuLysAsnAspMet.ArgCysProLeuP 538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    472 GlnLeuSerLysTyrlleGluProLeuArgArgMetIleAsnLysIleAs 488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          455 roAlaGlySerSerGlnAlaGluGluGlnGlnTyrLeuAspLysLeuLys 471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                950 CTCACCTGGACCTTTAAACACACCTGTGAACCCCCAGCTCTGTCATGAGCC 999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          438 oSerProGlyProLeuAsnThrProValAsnProSerSerValMetSerP 455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       555 SerTrpMetProSerTrpProThrSerAlaHisLeuSerSerThrIlePr 571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              571 oCysThrAlaHisSerPheGlnPro 579
                                                                                                                                                     source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Matazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eucheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 :0 886)
                                                                                                                                                                                                       Plate: LLCM1230 row: g column: 02 High quality sequence stop: 876.
                                                                                                                                                                                                                                                                                                                                                                                                                   Email: cgapbs-r@mail.nih.gov
Tissue Procucement: ATCC/DCTD/DTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BG281923.1 GI:13030849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BG281923 886 bp mRNA EST 21-FEB-2001 602403104F1 HIH_MGC_20 Homo sapiens cDNA clone IMAGE:4545433 5',
                                                                                                                                                                                                                                      found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov plate: LLCM1230 row: g column: 02
                                                                                                                                                                                                                                                                                            cDNA Librar/ Preparation: Ling Hong/Rubin Laboratory CDNA Librar/ Arrayed by: The I.M.A.G.E. Consortium (LLNL) CDNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be
/or yanism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4545433"
/clone_lib="NIH_MGC_20"
/tissue_type="melanotic melanoma"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (1999)
                                                                                                                                                                                on/Qualifiers
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COMMENT

SOURCE

VERSION

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alignment_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Align seg 1/1 to: BG281923 from: 1 to: 886
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Quality: 1136.50
Ratio: 4.209
Percent Similarity: 89.109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-668-119-3 x BG281923
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       153 CAGGCGGCGCTACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGTTCCA 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            148 GlnAlaAlaLeuGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnPheGl 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          114 rMetAlaValValSerThrAlaThrProGlnThrGlnLeuGlnLeuGlnG 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    181 lnGlnGlnLeuGlnGlnGlnGlnGlnGlnGlnHisLeuIleLysLeu 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        164 nAlaGlnGlnSerAlaMetGlnGlnPheGlnAlaValValGlnGlnG 181
296 SerGlnThrGlnProLeuValSerGlnAlaGlnAlaLeuProGlyGlnMe 312
                                                                                           552 CCAGCAGCCTCCAGTTGCTCAGAAGCAAGCATCACAAACTCCCGCCAAAG 601
                                                                                                                                                                                                                                                                                                                                  246 lnProProMetGlnGlnProGlnProProProSerGlnAlaLeuProGln 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                             403 AGCAGCAAGCGAGCGAGGCTTTGCGAGGCCCAGCCAATTCAGCC 452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            231 lnGlnGln...GlnGlnAlaLeu.GluAlaGlnProProIleGln.G 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    353 AATAGCACAGCTGCAGCTCCAACAACAGCAACAGCAGCAGCAGCAGCAGC 402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    303 CATCATCAAAATCAGCAACAGATACAGCAGCAGCAACAGCAGCTGCAGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    198 HisHisGlnAsnGlnGlnGlnIleGlnGlnGlnGlnGlnLeuGlnAr 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               253 AGCAGCAGCAGCAGCAGCAGCAGCAGCAGCATCTAATTAAATTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   203 GGCTCAGCAGAGTGCCATGCAGCAGCAGTTCCAAGCAGTAGTGCAGCAGC
                                                                                                                                                      279 oGlnGlnProProValAlaGlnAsnGlnProSerGln.LeuProProGln 295
                                                                                                                                                                                                              503 CAGCTGCAGCAGATGCATCACACACAGCACCAGCCAGCCGCA.CCACAGCC 551
                                                                                                                                                                                                                                                                       263 GlnLeuGlnGlnMetHisHisThrGlnHisHisGlnProProProGlnPr 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               53 CATGGCTGTCGTGTCTACGGCAACTCCACAGACCCAGCTGCAGCTCCAGC 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98 SerLeuSerGlyGlnProProProGlyThrSerGlyMetAlaProHisSe 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 TCTCTCAGGTCAGCCGCCTCCTGGGACCTCGGGGATGGCCCCTCACAG 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /lab_host="DH10B (phage-resistant)"
/note="Organ: skin; Vector: DOTB7; Site_1: XhoI; Site_2:
Const; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
a 299 c 231 g 122 t
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Align seg 1/1 to: AL046886

from: 1

to: 757

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VERSION
KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACCESSION
us-09-668-119-3 x AL046886
                                                                                                                                                 alignment_scores
                                                                                                                                                                                                                                                     BASE COUNT
                                                                         Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  _name: gb_est1:AL046886
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         375 InValGlnThrProGlnSerMetProProProProGlnProSerPro 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        802 GGAAGCTTGGCCAAGGTGGGATGCACATAAGAGCCCGGTCCCGTCTACAA 851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        361 nSerSerLeuProMetLeu.....SerSerProSerProGlyGlnG 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           329 GlnGln.ProProVal.GlnProGlnValGlnGlnGlnGlnThrAlaVal 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             652 GTTGTATACCCAAGCACCAATGAAATTTGTCCGAGCTCCTGATGGTGGTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GlnThrAlaGlnAlaAlaGlnMetValAlaProGlyValGlnValSerGl 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CAGCAGGCCCCCAGTGCCAGCACCAGGTGCAGCAGCAGCAGAGACAGCAGTA 751
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CAGACCTGCTCAGGCTGCCAGATGGTGGCTCCCGGAATCCAGATGATCAC 801
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AL046886 757 bp mRNA EST 29-FEB-2000 DKFZp586E2117_r1 586 (synonym: hutel) Homo sapiens cDNA clone DKFZp586E2117 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  No s1 sequence available. This clone (PKFZp886E2117) is available at the RZPD in Please contact the RZPD: Ressourcenzentrum, Heubnerweg Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This is the observed to the control of the General Cancer Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s.wiemann@dkfz- heidelberg.de; sequenced by BMFZ (Biomedical Research Center at the Charite, parlia //carmanv) within the cDNA sequencing consortium of the Ge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Koehrer, K., Beyer, A., Mewes, H.W., EST (Koehrer, et al.)
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genome Project.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Berlin/Germany) within the cDNA sequencing consortium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Am Klopfersp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Koehrer K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
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                                                                                                                         Quality: 1129.00
                                                                                                    Ratio:
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                                                                                                                                                                                                                                                     199
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                                                                                                                                                                                                                                                                                                                                              /clone="DKFZp586E2117"
/clone_lib="586 (synonym:
/tissue_type="uterus"
                                                                                                                                                                                                                                                  /note="Vector: pSport1; Site_1: Not1; Site_2: SalI/MluI"
233 c 208 g 116 t 1 others
                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                         4.552
96.124
                                                                                                                                                                                                                                                                                                  /lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                         /dev_stage="adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .TGTCCGCATCCCGTAAGCTCCAATCCT 883
                                                                            Percent
                                                                            Identity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gassenhuber, J. and
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                                                                               94.961
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seq_name: gb_est2:BG386117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           34 laArgLeuIleIleHisPheArgAspIleHisAsnLysLysSerGlnAla 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17 rHisValPheLeuLys&laLysThrArgAspGluTyrLeuSerLeuValA 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  53 CCATGTTTTCCTGAAGGCCAAGACCCGGGACGAATACCTTTCTCTCGTGG 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 ATGAGGAAAGCTGGTGTGGCACACAGTAAATCCAGCAAGGATATGGAGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MetArgLysAlaGlyValAlaHisSerLysSerSerLysAspMetGluSe 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        aAlaGlyAlaAlaGlyIleGlyMetProProArgGlyProGlyGlnSerL 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GGGCAGCCGCCTCCTGGGACCTCGGGGGATGGCCCCTCACAGCATGGCTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GlyGlnProProProGlyThrSerGlyMetAlaProHisSerMetAlaVa 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               euGlyGlyMetGlySerPheGlyAlaMetGlyGlnProMetSerLeuSer 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TGCGGGAGCCGCTGGAATTGGCATGCCTCCTCGGGGCCCGGGACAGTCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SerValSerAspProMetAsnAlaLeuGlnSerLeuThrGlyGlyProAl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CCAGGCTCATTATCCATTTTCGAGACATTCATAACAAGAAATCTCAAGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                  nGlnLeuGlnGlnGlnGlnGlnGlnGlnHisLeuIleLysLeuHisH 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        lValSerThrAlaThrProGlnThrGlnLeuGlnLeuGlnGlnValAla. 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TGGGCGGGATGGGTAGCCTTGGTGCCATGGGACAGCCAATGTCTCTCA
                                                                                                                                                                oMetGlnGln 251
                                                                                                                                                                                                                                      lnGlnGlnGlnAlaLeuGluAlaGlnProProIleGlnGlnPro.Pr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CGCTACAGCAGCAGCAGCAGCAGCAACAGCAAGCAGTTCCAGGCTCA 502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CTGCAGCAGCAGCAACAGCACGCAGTTCCAGCAGCAGCAGCAGCAGCGG
                                                                                                                                                                                                  AGCACAGCTGCAGCTC.....CAACAACAGCAACAGCAGCAGCAGCAGC
                                                                                                                                                                                                                                                                                                                 eAlaGlnLeuGlnLeuGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnG
                                                                                                                                                                                                                                                                                                                                                       ATCAAAATCAGCAACAGATACAGCAGCAGCAACAGCAGCTGCAGCCGAAT
                                                                                                                                                                                                                                                                                                                                                                                           isGlnAsnGlnGlnGlnIleGlnGlnGlnGlnGlnGlnLeuGln.ArgIl 215
                                                                                                                                                                                                                                                                                                                                                                                                                                GCAGCTCCAGCAGCAGCAGCAGCAGCAGCATCTAATTAAATTGCNTC
                                                                                                                             GATGCAGCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            252
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                                                                                                                                                                                                                                            248
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sequence.

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alignment_block:
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Quality: 1103.50
Ratio: 4.294
Percent Similarity: 70.604
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TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Align seg 1/1 to: BG386117 from: 1 to: 878
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-668-119-3 x BG386117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KEYWORDS
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                                                                             204 GGGACAGCCAATGTCTCTCAGGGCAGCCGCCTCCTGGGACCTCGGGGA 253
                                                                                                                                                                                                                                                   110 etAlaProHisSerMe:AlaValValSerThrAlaThrProGlnThrGln 126
                                                                                                                                                                                                                                                                                                                                                                                                                        104 AGAGCCTGACTGGCGGACCTGCGGGAGCCGCTGGAATTGGCATGCCT 153
                                                                                                                              93 tGlyGlnProMetSerSeuSerGlyGlnProProProGlyThrSerGlyM 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         60 inSerieuThrGlyGlyProAlaAlaGlyAlaAlaGlyIleGlyMetPro 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27 AspGluTyrLeuSerLeuValAlaArgLeuIleIleHisPheArgAspIl 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4 GACGAATACCTTTCTCTCGTGGCCAGGCTCATTATCCATTTTCGAGACAT 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CDNA Library Preparation: Ling Hong/Rubin Laboratory CDNA Library Preparation: Ling Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: NIH Intramural Sequencing Center Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image llnl.gov Plate: LLCMI:07 row: h column: 24 High quality sequence stop: 742. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: cgapb::-r@mail.nih.gov
Tissue Procumement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Matazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eucheria, Primates, Catarrhini, Hominidae, Homo. 1 (bases 1 :0 878)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BG386117.1 5I:13279563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /or;anism="Homo.sapiens"
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/clone_lib="NH_MGC_15"
/ti;sue_type="adenocarcinoma cell line"
/lat_host="brid B (phage-resistant)"
/lat_host="brid B (phage-resistant)"
/note="Organ: colon; Vector: pOTB7; Site_1: XhoI; Site_2:
/note="Organ: colon; Vector: poTB7; Site_2: XhoI; Site_2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Percent Identity: 67.857
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	name: gb_est1:BE384305	na
	lnGlnVal :::    ACCACGTG	ν ω
371 787	359 ValSerGlnSerSerLeuProMetLeuSerSerProSe 3 :::	~1 (a)
358 737	2 rAlaValGlnThr.AlaGlnAlaAlaGlnMetValAlaProGlyValGln	<b>O</b> (1)
342 687	326 tValValGln.GlnProPro.ValGlnProGlnValGlnGlnGlnGlnTh :	<b>a</b> (1)
326 637	310 lyGlnMetLeuTyrThrGlnProProLeuLys.PheValArgAlaProMe:	15 (1)
310 588	3 oProGlnSerGlnThrGlnProLeuValSerGlnAlaGlnAlaLeuProG 	
293 539	277 ProGlnProGlnGlnProProValAlaGlnAsnGlnProSerGlnLeuPr	
276 489	260 euProGlnGlnLeuGlnGlnMetHisHisThrGlnHisHisGlnProPro	
260 439	InGlnProProMetGlnGlnProGlnProProProSerGlnAlaL 	
243 389	nGlnGlnGlnGlnGlnGlnAlaLeuGluAlaGlnProPr	
354	554	
226	10 lnGlnLeuGlnArgIleAlaGlnLeuGlnLeuGlnGlnGlnGlnGlnGln	
354		
ب شر	93 sLeuIleLysLeuHisHisGlnAsnGlnGlnGlnIleGlnGlnGlnGln	
UT U	54	
35 <b>4</b>	354	
176	60 lnGlnGlnPheGlnAlaGlnGlnSerAlaMetGlnGlnGlnPheGlnA	
354		
160	143 eGlnGlnGlnGlnAlaAlaLeuGlnGlnGlnGlnGlnGlnGlnGlnG	
143 353	127: LeuGlnLeuGlnGlnValAlaLeuGlnGlnGlnGlnGlnGlnGlnGlnGlnPh 	
303		
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seq\_documentation\_block:
LOCUS BE384305 620 bp mRNA EST 21-JUL-2000
DEFINITION 601272684F1 NIH\_MGC\_20 Homo sapiens cDNA clone IMAGE:3613868 5',

mRNA sequence.

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REFERENCE
AUTHORS
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KEYWO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    alignment_scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Align seg 1/1 to reverse of: BE384305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Percent Similarity: 100.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   source
                                                                                                                                                                                  238|uGluAlaGlnProProIleGlnGlnProProMetGlnGlnProGlnProP 255
                                                                                                                                                                                                                                                                                                                                                                                                               222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          520 TACAGCAGCAGCAACAGCAGCTGCAGCGAATAGCACAGCTGCAGCTCCAA 471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       570; GCAGCAGCAGCATCTAATTAAATTGCATCATCAAAATCAGCAACAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   188 nGlnGlnGlnHisLeuIleLysLeuHisHisGlnAsnGlnGlnGlnI 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   620 CAGCAGTTCCAAGCAGTAGTTCAGCAGCAGCAGCAGCTCCAGCAGCAGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          172 GlnGlnPheGlnAlaValValGlnGlnGlnGlnGlnLeuGlnGlnGlnGl 188
                                                                                                                                      420 GCAGGCCCAGCCAATTCAGCAGCCACCGATGCAGCAGCCACAGCCTC
                                                                                                                                                                                                                                                                                                                        255 roProSerGlnAlaLeuProGlnGlnLeuGlnGlnMetHisHisThrGln
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 leGlnGlnGlnGlnGlnLeuGlnArgIleAlaGlnLeuGlnLeuGln 221
                                                                                                                                                                                                                                                                                                                                                                                                               GlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnAlaLe 238
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov plate: LLCM275 row: g column: 21 High quality sequence stop: 620.
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Ratio: 5.141
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (1999)
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National Institutes of Health, Mammalian Gene Collection (MGC)
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
CDNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
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/tissue_type="melanotic melanoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: skin; Vector: pOTB7; Site_1: Xho1; Site_2: EcoR1; cDNA made by oligo-dT priming. Directionally EcoR1; cDNA made by oligo-dT priming. Directionally eloned into EcoR1/Xho1 sites using the following 5'
adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the Laboratory of Gerald M. Rubin (University of the laboratory 
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/db_xref="taxon:9606"
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REFERENCE
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602405533F1 NIH_MGC_21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (1999)
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National Institutes of Health, Mammalian
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/tissue_type="choriocarcinoma"
/lab_host="DHIOB (phage-resistant)"
/lab_host="DHIOB (phage-resistant)"
/note="Organ: placenta; Vector: pOTB7; Site_1: XhoI;
/note="Organ: placenta; Vector: pOTB7; Site_1: XhoI;
Site_2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by
Ling Hong in the laboratory of Gerald M. Rubin (University
of California, Berkeley) using ZAP-cDNA synthesis kit
                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                             /clone="IMAGE:4542993"
                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
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                                                                                                                                                                                     600 TGGGTGCAGCAGCCCCAGTGCAAGCCCCAGGTGCAGCAGCAGCAGA 649
                                                                                                                                                                                                                                                                                                                                              310 GlyGlnMetLeuTyrThrGlnProProLeuLysPheValArgAlaPro.. 325
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359 ValSerGlnSerSerLauProMetLeuSerSerProSerProGlyGlnGl 375
                                                            650 CAGCAGTA.....GCITATGCAGCGCTCCTGGATGCC.....GTCCTG 687
                                                                                                                     342 hrAlaValGlnThrAlaGlnAlaAlaGlnMetValAlaProGlyValGln 358
                                                                                                                                                                                                                                                     326 MetValValGlnGlnProProValGln.ProGlnValGlnGlnGlnGlnT 342
                                                                                                                                                                                                                                                                                                              551 GGACAAATGTTGTATACCCAAGC.ACACTGAAATTTGTCCGAGCTCCGAA 599
                                                                                                                                                                                                                                                                                                                                                                                                                                      501 CGCCACAGTCGCAGACCCAGCCTTTGGTGTCACAGGCGCAAGTTCTCCCT 550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               293 roProGlnSerGlnThrGlnProLeuValSerGlnAlaGlnAlaLeuPro 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            451 ACCACAGCCCCAGCCTCCAGTTGCTCAGAACCAACCATCACAACTCC 500
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    260 LeuProGlnGlnLeuClnGlnMetHisHisThrGlnHisHisGlnProPr 276
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        193 sLeu IleLysLeuHisHisGlnAsnGlnGlnGlnIleGlnGlnGlnGln 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         151 GTAGTGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCA 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        210 GlnGlnLeuGlnArglleAlaGlnLeuGlnLeuGlnGlnGlnGlnGlnGl 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    201 TCTAAATTAAATTGC&TCATCAAAATCAGCAACAGATACAGCAGCAGCAA 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  177 ValValGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnHi 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  101 AGCAGCAGTTCCAGGCTCCAGCAGTGCCATGCAGCAGTTCCAAGCA 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           160 lnGlnGlnPheGlnAlaGlnGlnSerAlaMetGlnGlnGlnPheGlnAla 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                143 eGlnGlnGlnGlnAlaAlaLeuGlnGlnGlnGlnGlnGlnGlnGlnG 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       51 CCAGCAGCAGCAGCAGCGCGCGCTACAGCAGCAGCAGCAGCAGCAGCAAC 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 CTGCAGCTCCAGCAGCTGCAGCGGGAGCAGCAACAGCAGCAGTT 50
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                                                                                                                                                        Quality:
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Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 914)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: NIH Intramural Sequencing Center
Clone distribution: MGC clone distribution information can be
                                                                                                                           Ratio:
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/clone_lib="NIH_MGC_15"
/clone_lib="NIH_MGC_15"
/tissue_type="adenocarcinoma cell line"
/tissue_type="adenocarcinoma cell line"
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/note="Organ: colon; Vector: poTB7; Site_1: XhoI; Site_2:
/cloned into EcoRI/XhoI sites using the following 5'
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDWA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)"
25 a 305 c 229 g 155 t
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99.441
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/db_xref="taxon:9606"
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                                                                                                                                                                       Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                               NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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cDNA Library Preparation: Ling Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: NIH Intramural Sequencing Center Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
                                                                                                                            Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 roSerProGlyProLeuAsnThrProValAsnProSerSerValMetSer 454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GCCCTCCCAGAGCCCAGTGACGGCGCGGACCCCACAGAACTTCAGTGTCC
CTCCTGGATGCCGTCCTGGCCAACATCCGCTCACCTGTCTTCAACCATTC
                                 gSerTrpMetProSerTrpProThrSerAlaHisLeuSerSerThrIleP 571
                                                                                       CCCCACCGCCCCGGTGCCACCGACCAAACAGCAGTACCTATGCCAGCCG
                                                                                                                               ProHisArgProArgCysHisArgProAsnSerSerThrTyrAlaSerAr 554
                                                                                                                                                                                 GTGTGAGATCGCCCTGGAGAAACTCAAGAATGACATGGCGGTGCCCACTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Plate: LLCM1708 row: p column: High quality sequence stop: 756.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /tissue_type="adenocarcinoma cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: colon; Vector: poTB7; Site_1: XhoI; Site_2:
ECORI, cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following: 5'
adaptor: GGCACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)"
79 a 264 c 186 g 126 t 1 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     919.00
5.251
99.432
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/db_xref="taxon:9606"
/clone="IMAGE:4857083"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone_lib="NIH_MGC_15"
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                                                                                                                                                                                                                                                                      357
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roCysThrAlaHisSerPheGlnPro 579

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alignment_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Align seg 1/1 to: BE019568 from: 1 to: 526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -09-668-119-3 x BE019568
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                                                         183 lnLeuGlnGlnGlnGlnGlnGlnGlnHisLeuIleLysLeuHisHis 199
                                                                                                                                                                                                                                                                                                                                                                                                               150 AlaLeuGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnDheGlnAlaG1 166
102 AGCTCCAGCAGCAGCAGCAGCAGCAGCATCTAATTAAATTGCATCAT 151
                                                                                                                                                                                                                              166 nGlnSerAlaMetGlnGlnGlnPheGlnAlaValValGlnGlnGlnGlnGlnG 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   508 CCTGTACCGCACATTGGTTCCAGCCA 533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    source
                                                                                                                                                                                52 GCAGAGTGCCATGCAGCAGCAGTTCCAAGCAGTAGTGCAGCAGCAGCAGC 101
                                                                                                                                                                                                                                                                                                                                                                2 GCGCTACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGTTCCAGGCTCA 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Quality:
Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BE019568 526 bp mRNA EST 06-JUN-200 ba83f05.yl N.H_MGC_21 Homo sapiens cDNA clone IMAGE:2907009 similar to TR:015413 015413 CTG7A ; mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  High quality sequence stop: 463.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           image.llnl.gov/image/html/iresources.shtml
Seq primer: ~40RP from Gibco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cDNA Library Preparation: Ling Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NIH-MGC http:
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Mammalia; Eukheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 526)
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/clime_tipe="NAGE:2907009"
/clime_tipe="riboriocarcinoma"
/tissue_type="riboriocarcinoma"
/lal_host="DH10B (phage-resistant)"
/note="Organ: placenta; Vector: pOTB7; Site_1: xhoI;
/note="Organ: placenta; Vector: pOTB7; Site_size using the following of the 
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Institutes of Health, Mammalian Gene Collection (MGC)
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5.166
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Percent Identity: 99.429
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FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        seq_name: gb_est1:BE390284
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   502 ACCACCACTGAAATTTGTCCGAGCT 526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              452 CCTTTGGTGTCACAGGCGCAAGCTCTCCCTGGACAAATGTTGTATACCCA 501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          300 ProLeuValSerGlnAlaGlnAlaLeuProGlyGlnMetLeuTyrThrGl 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          352 GATGCATCACACACAGCCACCAGCCGCCACCACAGCCCCAGCAGCCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             302 CAGCAGCCACAGCCTCCGCCCTCCCAGGCTGCCAGCAGCTGCAGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          200 GlnAsnGlnGlnGlnIleGlnGlnGlnGlnGlnGlnLeuGlnArgIleAl 216
                                                                                                                                                                                                                                                                                                                                                                               source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               316 nProProLeuLysPheValArgAla 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  402 CAGTTGCTCAGAACCAACCATCACAACTCCCGCCACAGTCGCAGACCCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  283 roValAlaGlnAsnGlnProSerGlnLeuProProGlnSerGlnThrGln 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   266 nMetHisHisThrGlnHisHisGlnProProProGlnProGlnProP 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             250 GlnGlnProGlnProProProSerGlnAlaLeuProGlnGlnLeuGlnGl 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             252 AGCAGCAGCCAGCCTTTGCAGGCCCAGCCAATTCAGCAGCCACCGATG 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         233 lnGlnGlnAlaLeuGluAlaGlnProProIleGlnGlnProProMet 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                202 ACAGCTGCAGCTCCAACAACAGCAACAGCAGCAGCAGCAGCAGCAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            216 aGlnLeuGlnLeuGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnG 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            152 CAAAATCAGCAACAGATACAGCAGCAGCAGCAGCAGCAGCGAATAGC 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 656)

NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BE390284 656 bp mRNA EST 21-JUL-200-601285167F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3606905
                                                                                                                                                                                                                                                                                                                                                                                                                                               High quality sequence stop: 588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             http://image.llnl.gov
Plate: LLCM257 row:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     found through the I.M.A.G.E. Consortium/LLNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cDNA Library Preparation: Ling Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         numan
/Clone_lib="NIH_MGC_44"
/tissue_type="endometrium, adenocarcinoma cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: uterus; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of
                                                                                                                                                                                                                                                                      /db_xref="taxon:9606"
/clone="IMAGE:3606905"
                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
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alignment_scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              180 GlnGlnGlnLeuGlnGlnGlnGlnGlnGlnGlnHisLeuIleLy 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 CAGCGGCAGCAGCTCCAGCAGCAGCAGCAGCAGCAGCATCTAATTAA
                                                                                                                                                                                                                                                                                                                                                                                                                                  GlnGlnProProValAlaGlnAsnGlnProSerGlnLeuProProGlnSe 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CAGCAGCAGCAGCAGCAGCCAGCCAGCCAATTCAGCA
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                                                                                                                  CCCGAAGAAAAATGGCCCACATTCCCCCAGGCAGCCGAAGACCGGCCAGC
                                                                                                                                                       rProGlnSerMetProProProGlnProSerProGlnProGlyGlnP
                                                                                                                                                                                                GAGCAGCCTCCCATGCTGTCCTCGCCGCA.CCGGGCCAGCAGTTGACAAA
                                                                                                                                                                                                                                                                                                   CAGCAGCCTCCAGTTGCTCAGAACCAACCATCACAACTCCCGCCACAGTC
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                                      CA
                                                                           ro 395
                                                                                                                                                                                                                                   SerSerLeuProMetLeuSerSerProSerProGlyGlnGlnValGlnTh 378
                                                                                                                                                                                                                                                                              AGACAGCTCAGGCTGCCCAGATGGTGGCTCCCGGAGTCCATGGTCAGCCA 550
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REFERENCE
AUTHORS
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                                                                                                                                                                          source
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TCTGTCAGTGACCCCATGAATGCAACTGCAGAGCCCTTACTGGTGACCCA 579
                   SerValSerAspProMetAsnAla.LeuGlnSerLeuThrGlyGlyProA 67
                                                                                        CCCGACTCATTACCAGTTTCCGAGATATTCATAACAAGAA.TCCCAAGCT 629
                                                                                                         laArgLeuIleIleHisPheArgAspIleHisAsnLysLysSerGlnAla 50
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleosto

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;

1 (bases 1 to 795)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D.,
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BG915202
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a 193 c
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Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert 2.5 kb. Library constructed by Life
Technologies, catalog # 12018-016. Investigators providing
samples: Lothar Hennighausen/Priscilla Furth, NIH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 887.00
3.823
86.245
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /tissue_type="tumor, gross tissue"
/lab_host="DH10B"
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COMMENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6 CC 5
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Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                               BE279307 723 bp mRNA EST 13-JUL-2000 601157640F1 \text{HIH\_MGC\_21} Homo sapiens cDNA clone IMAGE:3504608 5',
                                                                                                        NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                     Unpublished (1999)
                                                                                                                                                                      Ebkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 723)
                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                            human
                                                                                                                                                                                                                                                                                                                                                BE279307.1 GI:9154297
                                                                                                                                                                                                                                                                                                                                                                                                     mRNA sequence.
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alignment_block:
US-09-668-119-3 x BE279307
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                          134 euGlnGlnGlnGlnGlnGlnGlnPheGlnGlnGlnGlnGlnAlaAla 150
                                                                                                                                                                    117 lValSerThrAlaThrProGlnThrGlnLeuGlnLeuGlnGlnValAlaL 134
                                                                                                                                                                                                                                                                                                                                                                                                     357
457 CGTGTCTACGGCAACTCCACAGACCCAGCTGCAGCTCCAGCAGGTGGCGC 506
                                                                                                                                                                                                                                                                   407 GGGCAGCCGCCTCCTGGGACCTCGGGGATGGCCCCTCACAGCATGGCTGT 456
                                                                                                                                                                                                                                                                                                                            101 GlyGlnProProGlyThrSerGlyMetAlaProHisSerMetAlaVa 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       307 TGCGGGAGCCGCTGGAATTGGCATGCCTCCTCGGGGCCCCGGGACAGTCTC 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 257 TCCGTCAGTGATCCTATGAATGCACTCCAGAGCCTGACTGGCGGACCTGC 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  207 CCAGGCTCATTATCCATTTTCGAGACATTCATAACAAGAAATCTCAAGCT 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    157 CCATGTTTTCCTGAAGGCCAAGACCCGGGACGAATACCTTTCTCTCGTGG 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  107 ATGAGGAAAGCTGGTGTGGCACACAGTAAATCCAGCAAGGATATGGAGAG 156
                                                                                                                                                                                                                                                                                                                                                                                                                                       84 euGlyGlyMetGlySerPheGlyAlaMetGlyGlnProMetSerLeuSer 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17 rHisValPheLeuLysAlaLysThrArgAspGluTyrLeuSerLeuValA 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  51 SerValSerAspProMetAsnAlaLeuGlnSerLeuThrGlyGlyProAl 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MetArgLysAlaGlyValAlaHisSerLysSerSerLysAspMetGluSe 17
                                                                                                                                                                                                                                                                                                                                                                                                 Quality:
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//lab_host="hHl0B (phage-resistant)"
/note="organ: placenta; vector: pOTB7; Site_1: XhoI;
/note="organ: placenta; vector: pOTB7; Site_1: XhoI;
/note="organ: placenta; vector: pOTB7; Sites using the Directionally cloned into EcoRI/XhoI sites using the following 5 adaptor: GGCACGAGG(9). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of Callifornia, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
a 208 c 224 g 114 t
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/db_xref="taxon:9606"
/clone="IMAGE:3504608"
/clone_lib="NIH_MGC_21"
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alignment_block:
US-09-668-119-3 x BG335275
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                                                                                                                                                                                           Percent Similarity:
                                                                                    Align seg 1/1 to: BG335275
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TITLE
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                      127 LeuGlnLeuGlnGlnValAlaLeuGlnGlnGlnGlnGlnGlnGlnGln...Gl
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CTGCAGCTCCAGCAGGTGGCGCGCTGCAGCAGCATGCAACAGCATGCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       nSerAlaMetGlnGlnGlnPheGlnAlaValValGlnGlnGlnGln.Gln 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CTACAGCAGCAGCAGCAGCAGCAGCAGCAGTC. CAGGCTCAGCA
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                                                                                                                                                                                                                                      Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cDNA Library Preparation: Ling Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at: http://lnage.llnl.gov plate: LLCM1219 row: b column: 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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BG335275.1 GI:13141713
EST.
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602403789F1 NIH_MGC_21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
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                                                                                                                                                                                                                  Ratio:
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                                                                                                                                                                                                                                                                                                                                    /lab_host="DH10B (phage-resistant)"
/note="Organ: placenta; Vector: pOTB7; Site_1: XhoI;
Site_2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
a 325 c 238 g 157 t 1 others
                                                                                                                                                                                         873.50
4.200
88.136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="taxon:9606"
/clone='IMAGE:4541110"
/clone_lib="NIH_MCC_21"
/tissue_type="choriocarcinoma"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
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                                                                                                                                                                                  Length: 236
Gaps: 4
Identity: 83.051
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                                                                                                        342 ThrAlaValGInThrAlaGInAlaAlaGInMetValAlaProGlyValGl
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                                                                                                                                                                                                                       CCCTTGACAAATGTAGTATACCCAACA.CCACTGAAATTTGTCCGAGCTC
                                                                                                                                                                                                                                                                                                 CTCCCGCAACAGTCGCAGAC.CAGCCTTTGGTGTCACAGGCGCAAGCTCT
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                                                                       . GAAGACAGGCAGTACTTAATGCCAGCCGCTCCTGGAATTGC
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Isolation and characterization of a novel gene from the digeorge chromosomal region that encodes for a mediator subunit Genomics 74 (3), 320-332 (2001)
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Berti,i., Mittler,G., Przemeck,G.K.H., Stelzer,G., Guenzler,B.,
Amati,F., Conti,E., Dallapiccola,B., Hrabe' de Angelis,M.,
Novelli,G. and Meisterernst,M.
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1212	CAGAGCAGCCTCCCCATGCTGTCCTCGCCGTCACCGGGCCAGCAGCAGCAGCCCGCAG	1153	рb
1140	agagcagcctccccatgctgtcctcgccgtcaccgggccagcaggtgcagaccccgcag	1081	Qy
1152	GGTGGCTCCCGGAGTCCAGGTCAG	1093	ДD
1080	agacagcagtacagacagctcaggctgcccagatggtggctcccggagt	1021	Qy
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720	gcagcagcagcagcagcagcagcagcagcaggctttggaggcc	661	Qy
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Institute of Molecular Immunology-GSF, Marchionini Str. 25, Munich
81377, Germany
                                                                                                                                                  2 (bases 1 to 3295)
Berti, L., Mittler, G., Przemeck, G.K.H., Stelzer, G., Guenzler, B., Amati, F., Conti, E., Dallapiccola, B., Hrabe' de Angelis, M., Novelli, G. and Meisterernst, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Musinae; M
                                                                                                                                                                                                                                                                                                                                                                                                              Novelli,G. and Meisterernst,M.

Isolation and characterization of a novel gene from the digeorge chromosomal region that encodes for a mediator subunit
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                                                                                                                   Direct Submission
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                                                                                                                                                                              559 CAGCAGCAACAGCAACAGCAGTTCCAGGCACAACAGAATGCCATGCAGCAACAGTTC
                                                                                                                                                                                                                                                                                                                                                             439 ACAACTCCACAGACTCAGCTGCAGCTCCAGCAAGTGGCCATTGCAGCAACAGCAGCAGCGG 498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          361 gcaactccacagacccagctgcagctccagcaggtggcgctgcagcagcagcagcag----- 414
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                181 agcctgactggcggacctgctgcgggagccgctggaattggcatgcctcctcgggggcccg 240
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                                                                                                                                                                                                                                                           cagcagcagcagcagcagcagttccaggctcagcagagtgccatgcagcagcagttc 522
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SMPPPPQPSQPGSQPNSNVSSGPAPSPSSFILPSPSPQPSQSPVTARTPQNRSVPSPS
PLNTPVNPSSVWSPAGSSQAEEQQYLDKLKQLSKYIEPLRMINKIDKNEDRKKDLSK
MKSLLDILTDPSKRCPLKTLQKCEIALEKLKNDMAVPTPPPPPVLPTKQQDLCQPLLD
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/protein_id="AAK58424 1"
/protein_id="AAK58424 1"
/db_xref="G1:14276859"
/translation="MDVWGQETDWRSAAFRIKIVSQIEDAMRKAGVAHSKSSKDMESH
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                                                                                     GACAAGCTGAAGCAATTGTCCAAGTACATCGAGCCCCTGCGACGCATGATCAACAAGATC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (02-DEC-1996) Psychiatry, Johns Hopkins Univ. Sch. of Med., 600 N. Wolfe Street, Meyer 2-181, Baltimore, MD 21205, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Margolis, R.L., Breschel, T.S.,
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388 c
                                                                                                                  /note="polymorphic"
/rpt_type=tandem
                                                                                                                                                                                QTPQSMPPPPQPSPQPGQPSSQPNSNVSSGPAPSPSSFLPSPSPQPSQSPVTARTPQN
FSVPSPGPLNTPVNPSSYMSPAGSSQAEEQQYLDKLKQLSKYIEPLRRMINKIDKNED
                                                                                                                                                                                                                                                                                                                             /gene="CTG7a"
/note="glutamine
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                                                                                                                                                                 RKKDLSKMKSLLDGI"
                                                                                                                                                                                                                                                                                                                  /codon_start=!
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                                                                                                                                                                                                                                                                                                                                                                                                                        /chromosome="20"
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/db_xref="taxon:9606"
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99.7%;
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                 Score 1035.8; DB 9
Pred. No. 1.2e-148;
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Similarity

37.9%; 99.1%;

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Score 659; DB 9; Length 2106; Pred. No. 2.7e-91;

1063 cccggagtccaggtcagccagagccatccccatgctgtcctcgccgtcaccgggccag 1122

51 CCCATGGCACAGGTCAGCCAGAGCCTCCCCATGCTGTCCTCGCCGTCACCGGGCCAG 110

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Letticia Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven Ness, Pawan Pandoh, Anna-Liisa Prabhu, Parvaneh Saeedi, Jacqueline Schein, Duane Smailus, Michael Smith, Lorraine Spence, Jeff Stott, Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy, George Yang, Scott Zuyderduyn, Marco Marra.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cDNA Library Preparation: Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Co DNA Sequencing by: Genome Sequence Centre,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (10-MAY-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield,
Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: MGC
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REPROSSQPMSAGSSQAESQQYLDKLKQLSKYIEDLERNPPPPPPPPPPROSVICOPILL
SKMKSLDDITIDESKCPLKKTLQKCETALEELKENDANVTEPPPPPPPPPPPROSVICOPILL
DAVLANTRSPVENHSLYRTEVPAMTAHBGPPTTAPVCTTRKRLEDDERQSIPSVLOG
EVARLDFKFLVNLDPSHCSNNGTVHLICKLDDKDLPSVPPDLELSVPADYPADSPLWID
ROWOYDANPFLQSVHRCKTSRLLQLPDKHSVTALLNTWAQSVHQACLSAA"
719 c 553 g 378 t
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                                                                   Submitted (28-APR-2000) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. MO 63108, USA
On Apr 10, 2001 this sequence version replaced of 12421762
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chemistry: Dye-primer ET; 2% of reads
Chemistry: Dye-terminator Big Dye; 58% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 153264 bases at least Q40
Consensus quality: 156105 bases at least Q30
Consensus quality: 157587 bases at least Q30
Consensus quality: 157587 bases at least Q20
Insert size: 168000; agarose-fp
Insert size: 169020; sum-of-contigs
Quality coverage: 9.85 in Q20 bases; sum-of-contigs
Quality coverage: 9.85 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     * NOTE: This is a 'working draft' sequence. It currently consists of 6 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence this as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequencing vector: M13; 38% Sequencing vector: plasmid; 22%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           be preserved.
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9273
17588
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39186
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273 17587: contig of 8315 bp in length
588 17687: gap of unknown length
688 39085: contig of 21398 bp in length
986 39185: gap of unknown length
1186 61924: contig of 22739 bp in length
11925 62024: gap of unknown length
11925 107416: contig of 45392 bp in length
117 107516: gap of unknown length
1186 115 contig of 48799 bp in length
11927 156315: contig of 48799 bp in length
11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11928 11
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107517. .156315
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39186. .61924
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         clone_end:T7
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/db_xref="taxon:9606"
/chromosome="2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="assembly_name:Contig71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="assembly_name:Contig69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="assembly_name:Contig67"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="assembly_name:Contig66"
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77.0%;
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                                                                                                                                                                                                                                                                                                                  Score 560; DB 2; I
Pred. No. 1.4e-76;
0; Mismatches 210;
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                                                                                                                                                                                                                                                                                                                                                                                               DB 2; Length 156315;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        504 others
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                                                                                                                                                                                                                                                                                                                      Gaps
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Db 153327 -GCAGTCCTGAACCANTCCCTGCACCGCGCCTTGGTGCTGCCCA 153285
                                         AL359452
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Qy
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                                                                                                                                                                                                                                                                                           Db 153387 CACGCAGCACCTTGGCGCCTGCCGCTCCTGGACACAGTCCTGGCCCGCATCTGCTC 153328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Db 153623 CCTGGACAAGCTAAA3CCGCTGCCCAAGTACAGGGAGCCCCTGCGCCGCCTGAGCAACGG 153564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Db 153683 TATGAAACGCGGCTCAGTCATGAGCCCAGCGGGCTCCAGCCGGGCCGAGCAGCAGCAGTG 153624
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Db 153797 GCCCCAGCGCCCAGTGGCTAGCTTCCTGCCCAGCCCCTCGCCGAAACCCTCCCAGAGCCC 153738
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Db 153737 AGGGATGGCG-----CACCAGAACTTCAGAGTCCCATGACCCGGATCTTTAAACGCCCC 153684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Db 153917 CTCGCCGTCGCAGGGCCAACAGGTGCAGACCCTGCAGTCGATGTCCCCTCCCCGACTGCC 153858
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Db 153977 GCCTCCCAGGTGGTGGCTCCCGGAGTCCATGGTAGCCAGAGCAGCCTCCCCATGATGTC 153918
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Qy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Db 154037 AGCCCCGCTGCAGCCGGTGCAGTCCTGGACGCAGTAGCTGACAGTGGTGCGGACCGCTGA 153978
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Db 154097 ATGCCCAACAACAGCTGCAATTTGTCTGAGCTCCAAGGGTAGTTCAGCAGCTGCAAGTGC 154038
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Db 154274 CCCCTCCCAGGTCCTGCCCCAGCAGCTGCAGCAGATACGTCAACCACCACCACCAGCA 154215
                                                                                                                                                                                                                                                                                                                                                                                                                           153447 GGAGAAACGCAAGCATGACCTGGAGGTGCCCAAGCCCCGACTGCACCTGGTGCCGCTGAC 153388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        153563 GATCCACGGGAACCAAGACAGCAAAAAGGG----CTGCGGTAAGACGAGCCTTCTGGACGC 153508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           153857 GTCCTCACAACCCGACTAGCCCCGGTCTCACAGCCCCAACTCCAACATCAGCTCCGGCCCT 153798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              154214 GCTGCCATAGTCCCGGCAACCTCCAGCTGCTCAGAACCATTGCAGCTGCCGCCACA 154155
                                                                                                                                                                                                1694 acctgtcttcaaccautccctgtaccgcacattcgttccagcca 1737
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1518 totgacagaccocto:jaagcggtgtcccctgaagaccttgcaaaagtgtgagatcgccct 1577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1222 gccccatctcccag----tagcttcctgcccagcccttcaccgcagccctcccagagccc 1277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1278 agtgacggcgcggaccccacagaacttcagtgtcccctcacctggacctttaaacacacc 1337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1164 gtccccgcagcccggccagcccag--ctcacagcccaactccaacgtcagctctggccct 1221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1104 ctcgccgtcaccgggccagcagttgcagaccccgcagttgattgccccctcccccccagcc 1163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1044 ggctgcccagatggtggctcccggagtccaggtcagccagagcagcctcccccatgctgtc 1103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  941 atacccaaccaccactgaaatttgtccgagctccgatggtggtgcagcagcagccccagtgc 1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   883 --cagtcgcagacccagcctttggtgtcacaggcgcaagctctccctggacaaatgttgt 940
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              825 gccaccacagccccegcagcctccagttgctcagaaccaaccatcacaactcccgcca-- 882
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                caaacagcagtacct atgccagccgctcctgg--atgccgtcctggccaacatccgctc 1693
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ggagaaactcaagaa::gacat-gcggtgcccactcccccaccgccccggtgccaccgac 1636
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cctggacaagctgaajcagctgtcgaagtacatcgagcccctgcgccgcatgatcaacaa 1457
       AL359452
64:231 bp
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13-JUN-2001
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COMMENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Assembly program: XGAP4; version 4.5 sequencing vector: plasmid; L08752; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Consensus quality: 52454 bases at least Q40 consensus quality: 57767 bases at least Q30 consensus quality: 59753 bases at least Q20 Insert size: 62331; sum-of-contigs Insert size: 190157; 8.2% error; agarose-fp Quality coverage: 2.09x in Q20 bases; sum-of-cont coverage: 1.09x in Q20 bases; agarose-fp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            * NOTE: This is a 'working draft' sequence. It currently consists of 20 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence some as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Center project name: bA422P18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: humquery@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (12-JUN-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 153, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequestesanger.ac.uk On Aug 27, 2000 this sequence version replaced gi:9864141.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens chromosome 1 clone RP11-422P18, *** SEQUENCING IN PROGRESS ***, 20 unordered pieces.
AL359452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Web site:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Center: Sanger Centre
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Center code:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AL359452.4 GI:9930964
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 be preserved.

1 2992: contig of 2992 bp in length
2993 3092: gap of 100 bp
3093 5136: contig of 2094 bp in length
5137 5236: gap of 100 bp
7850: contig of 2614 bp in length
7851 7950: gap of 100 bp
7951 9976: contig of 2626 bp in length
30912 31011: gap of 100 bp

31012 35721: contig of 4710 bp in length

35722 35821: gap of 100 bp

35822 38454: contig of 2633 bp in length

38455 38554: gap of 100 bp

41226 41225: contig of 2671 bp in length

41226 4125: contig of 6741 bp in length

41326 48066: contig of 6741 bp in length

48067 48166: gap of 100 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (bases 1 to 64231)
                                                                                                                                                                                                                                                                                   24902 2703:
27604 27703:
                                                                                                                                                                                                                                                                                                            21785 21884: gap of 100 bp
21885 24801: contig of 2917 bp in length
24802 24901: gap of 100 bp
24802 24901: gap of 2702 bp in length
                                                                                                                                                                                                                                                                                                                                                                                           18057 18156: gap of 100 bp
18157 21784: contig of 3628 bp in length
21785 21884: gap of 100 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14689 14788: gap of
14789 18056: con
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12632 146
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     http://www.sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                v/o: gap of 100 bp in length
12531: contig of 2455 bp in length
531: gap of 100 bp
16688: contig of
                                                                                                                                                                                                                                                                30911:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7850: contig of 2614 bp in length
0: gap of 100 bp
9976: contig of 2026 bp in length
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                                                                                                                    Conservative
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/note="assembly_fragment:00888"
a 15771 c 16128 g 15446 t 1
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27704. .30911
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31012. .35721
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/clone_lib="RPCI-11.2"
1. .2992
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/db_xref="taxon:9606"
/chromosome="1"
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fragment_chain:1"
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fragment_chain:1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                         note="assembly_fragment:00517"
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                                                                                                                  Score 353.4; DB Pred. No. 5e-45; O; Mismatches
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Assembly program: XGAP4; version 4.5
Assembly program: XGAP4; version 4.5
Sequencing vector: plasmid; LU8752; 100% of reads
Chemistry: Dye-terminator ET-amersham; 100% of reads Consensu
quality: 152367 bases at least Q40
Consensus quality: 153799 bases at least Q20
Consensus quality: 154743 bases at least Q20
Insert size: 155980; sum-of-contigs
Insert size: 155980; sum-of-contigs
Quality coverage: 5.20x in Q20 bases; sum-of-contigs Quality
coverage: 4.91x in Q20 bases; agarose-fp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (09-JUL-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 15A, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requestes clonerequest@sanger.ac.uk on Aug 22, 2000 this sequence version replaced gi:9214244.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens chromosome 1 clone RP11-4G23,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: humquery@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Web site: http://www.sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           numan
                                                                                                                                                                                         NOTE: This is a 'working draft' sequence. It currently consists of 12 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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                                3464 3563; gap of 100 bp
3564 13200; contig of 937 bp in length
13201 13300; gap of 100 bp
13201 13300; gap of 100 bp
13301 59189; contig of 45889 bp in length
59190 59289; gap of 100 bp
59290 85824; contig of 26535 bp in length
85825
85925
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85924: gap of 100 bp
88142: contig of 2218 k
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bp in length
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*** SEQUENCING IN
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                                              75446 AACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCCTTTGCAGGCCCAGCCACCAA 75387
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                                                                  671 aacagcagcagcagcagcagcagcagcagcagcaggctttggaggcccagccaccaa 730
                                                                                                                                                      611 agatacagcagcagcaacagcagctgcagcgaatagcacagctgcagctccaacaacagc 670
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731 ttcagcagccaccgatgcagccacagcctccgccctcccaggctctgccccagcagc 790
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37302 a 35841 c 39467 g 39369 t 1101 others
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95034 95133: gap of 100 bp
95134 100091: contig of 4958 bp in length
100092 100191: gap of 100 hp
100192 117376:
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139310 139409: gap of 100 bp
139410 157080: contig of 17671 bp in length.
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85925...8
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139410. .157080
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fragment_chain:3"
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fragment_chain:2"
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/db_xref="taxon:9606"
/chromosome="1"
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fragment_chain:2"
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fragment_chain:1"
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fragment_chain:1"
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fragment_chain:1"
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fragment_chain:1"
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Submitted (01-SEP-1999) Department Of Chemistry And Biochemistry,
The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
OK 73019, USA
                                                                                                                                                                                                                                                                                                          Chen, F., Hu, X., Budarf, M., Emanuel, B. and Roe, B.A.
Direct Submission
Submitted (29-JUL-1999) Department Of Chemistry And Biochemistry,
The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
                                                                                                           OK 73019, USA
8 (bases 1 to 163908)
                                                                                                                                                           Submitted (26-AUG-1999) Department Of Chemistry And Biochemistry, The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
                                                                                                                                                                                                                      Chen, F., Hu, X., Budarf, M., Emanuel, B. and Roe, B.A. Direct Submission
                                                                                                                                                                                                                                                            OK 73019, USA
7 (bases 1 to 163908)
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S (bases 1 to 163908)

Chen, F. Hu, X., Budarf, M., Emanuel, B. and Roe, B.A.

Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4 (bases 1 to 163908)
Chen, F., Hu, X., Budarf, M., Emanuel, B. and Roe, B.A.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (07-JUL-1999) Department Of Chemistry And Biochemistry, The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (09-MAR-1999) Department Of Chemistry And Biochemistry, The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman, OK 73019, USA
3 (bases 1 to 163908)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chen, F., Hu, X., Budarf, M., Emanuel, B. and Roe, B.A. Direct Submission
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11 (bases 1 to 163908)
12 (bases 1 to 163908)
13 (bases 1 to 163908)
Chen,F., Hu,X., Budarf,M., Emanuel,B. and Roe,B.A.
Direct Submission
Submitted (31-MAY 2000) Department Of Chemistry And Biochemistry,
Submitted (31-MAY 2000) Department of Chemistry And Biochemistry,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
Submitted (19-OCT-1999) Department Of Chemistry And Biochemistry,
The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           nucleotide polymorphisms in the overlapping regions below. ACO04031(p_m11) 89227 145356 (0) overlaps ACO07050(bac32) 1 59304 (104604) ACO07050(bac32) 141234 13908 (0) overlaps ACO07308(pac408) 1 22675 (193113).
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On Nov 20, 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OK 73019, USA
10 (bases 1 to 163908)
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OR Apr 12, 1999 this sequence version replaced gi:4580479.

On Apr 12, 1999 this sequence version replaced gi:4580479.

Decause these overlapping clones came from different libraries account to the sequence of insertions, deletions, and single nucleotide polymorphisms in the overlapping regions below.

AC005500(p52f6) 113352 192592 (0) overlaps AC004033(p_m11) 1 78509 (66847) AC004033(p_m11) 89227 145356 (0) overlaps AC007050(bac32) 1
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Submitted (09-APR-1999) Department Of Chemistry And Biochemistry, The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (04-FEB-1999) Department Of Chemistry And Biochemistry, The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman
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Patent: WO 0.02568 A 1742 11-JAN-2001;
CHIRON CORPORATION (US); HYSEQ, INC. (US)
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147 aTTCAGCAGCCTCCGATGCAGCCACCAGCCTCCGAGCCTCTGCCCCAGCAG 88
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On Aug 18, 2001 this sequence version replaced gi:15208594.

* NOTE: This is a 'working draft' sequence. It currently

* NOTE: This is a 'working draft' sequence. It currently

* consists of 37 contigs. The true order of the pieces

* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence

* as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
Submitted (21-FEB-2001) Department Of Chemistry And Biochemistry,
The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 238442)
Jiang, X., Sonq, L. and Roe, B.A.
Mus musculus BAC Clone rp23-11f20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Jiang, X., Song, L. and Roe, B.A.
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                                                                     aggcggcgctacagcagcagcagcagcagcagcagcagcagttccaggctcagcaga 502
agcagcagcagcatctaattaaattgcatcatcaaaatcagcaacagatacagcagc 622
                              gtgccatgcagcagttccaagcagtagtgcagcagcagcagcagctccagcagcagc 562
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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="rp23-11f20"
/clone_lib="RPCI mouse BAC library 23"
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g of 8283 bp in length
g of 8283 bp in length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NEDO human cDNA sequencing project supported by Ministry of International Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology; cDNA library construction, 5'- & 3'-end one pass sequencing and clone selection: Kazusa DNA Research Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (14-FEB-2000) to the DDBJ/EMBL/GenBank databases. Osiohara, Kazusa DNA Research Institute, Department of Human Gene Research; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan (E-mail:cdnainfo@kazusa.or.jp, URL:http://www.kazusa.or.jp, Tel:81-438-52-3913, Fax:81-438-52-3914)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 4701)
Ohara,O., Kikuno,R., Nagase,T. and Okumura,K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ohara,O., Kikuno,R., Nagase,T. and Okumura,K. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Published Only in DataBase (2000) In press (bases 1 to 4701)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The nucleotide sequence of a long cDNA clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens adult spleen cDNA to mRNA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AK000003.1 GI:7209306 FLJ00003 protein; fis (full insert sequence).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AK000003 4701 bp mRNA
Homo sapiens mRNA for FLJ00003 protein,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            spleen
                                                                        /note-"For this clone, GeneMark analysis triggered an alert for spurious CDS split. The result of GeneMark analysis of the nucleotide sequence of this clone is accessible through http://www.kazusa.or.jp.
                                                        Start codon is not identified."
                                                                                                                                                                                                                      /tissue_type="spleen"
/note="vector: pBluescriptII
/product="FLJ00003 protein"
/protein_id="BAA92228.1"
                                                                                                                                                                     /gene="FLJ00003"
<3081. .3788
                                                                                                                                                                                                          3081. .3788
                                                                                                                                                   /gene="FLJ00003"
                                                                                                                                                                                                                                                                                    /clone="as00003"
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/db_xref="taxon:9606"
                                      /codon_start=:
                                                                                                                                                                                                                                                                /dev_stage="adult"
                                                                                                                                                                                                                                                                                                                                                        location/Qualifiers
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partial cds.
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POLYA_signal BASE COUNT ORIGIN
LOCUS AC091616 121330 bp DNA 10-MAY-2001
DEFINITION Rattus norvegicus clone RP31-153JB strain Brown Norway, WORKING
DRAFT SEQUENCE, 8 unordered pieces.
                                                                                             AC091616/c
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                                                                                                                                                                                                               1183 GAGCCTTCTGGACATICTGACAGACCCCTCGAAGCGGTGAGCTTTGCCCAC 1233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1503 gagcettetggacattetgacagaceetegaageggtgteeeetgaagae 1553
                                                                                                                                                                                                                                                                                                                                 1123 CCGCATGATCAACAAJATCGACAAGAACGAAGACAGAAAAAAGGACCTGAGTAAGATGAA 1182
                                                                                                                                                                                                                                                                                                                                                                                        1443 ccgcatgatcaacaayatcgacaagaacgaagacagaaaaaaggacctgagtaagatgaa 1502
                                                                                                                                                                                                                                                                                                                                                                                                                                                         1063 TGAGGAGCAGCAGTACCTGGACAAGCTGAAGCAGCTGTCGAAGTACATCGAGCCCCTGCG 1122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1383 tgaggagcagcagtacctggacaagctgaagcagctgtcgaagtacatcgagcccctgcg 1442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1200 ctccaacgt----- 1208
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1288 cygaccccacagaacttcagtgtcccctcacctggacctttaaacacacct----- 1338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 943 GAGCTCTGGGGCCCTCAGAGCTCAAGTTCCCCACCCGAGGGGTCGAGGGCTGTGGCCTCAC 1002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      883 GGCCTGAGGTGCTAAGGTCACCTCCTCACCTTTATGAGGCCTCAGCTCATACTGGGTGTGC 942
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               523 CCAGAGCAGCCTCCCCATGCTGTCCTCGCCGTCACCGGGCCAGCAGGTGCAGACCCCGCA 582
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LLNTWAQSVHQACLSAA"
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PGFTFGNLRVRETSSRLCHKLHQNLPGCGVLFQSRAVRQGRPGLVQVTDRAFCVADDK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM
                                                                                                                        source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      * NOTE: This is a 'working draft' sequence. It currently
consists of 8 contigs. The true order of the pieces
is not known and their order in this sequence record is
arbitrary. Gaps between the contigs are represented as
runs of N, but the exact sizes of the gaps are unknown.
This record will be updated with the finished sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (10-MAY-2001) NIH Intramural Sequencing Center, 8717 Grovemont Circle, Gaithersburg, MD 20877, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AC091616
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Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B., Blakesley, R.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AC091616.1 GI:14017488
HTG; HTGS_PHASE1; HTGS_DRAFT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Norway rat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequencing vector: plasmid: n/a; 100% of reads
Sequencing vector: plasmid: n/a; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 119082 bases at least Q40
Consensus quality: 119775 bases at least Q30
Consensus quality: 120163 bases at least Q20
Insert size: 142000; agarose-fp
Cuality coverage: 7.29x in Q20 bases; agarose-fp
Quality coverage: 8.58x in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   as soon as it is available and the accession number will be preserved.  
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4543
14617
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35424
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                                                                                                                                                                                                                                                                         69564
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Center: NIH Intramural Sequencing Center Center code: NISC
   /organism="Rattus norvegicus"
/strain=srown Norway"
/db_xref="taxon:10116"
/clone="RP31-153J8"
                                                                                                                 1. .121330
                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                     4442: contig of 4442 bp in length
4542: gap of unknown length
14516: contig of 10074 bp in length
14716: gap of unknown length
24162: contig of 9446 bp in length
24262: gap of unknown length
24262: gap of unknown length
35423: contig of 11161 bp in length
35523: gap of unknown length
47959: contig of 12436 bp in length
48059: gap of unknown length
69563: contig of 22669 bp in length
69563: gap of unknown length
69563: gap of unknown length
19232: contig of 23698 bp in length
92432: gap of unknown length
121330: contig of 28898 bp in length
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                                                                                                                                                                                                                                                                                                                                                                                                                               610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            370 cagacccagctgcagctccagcaggtggcgctgcagcagcagcagcagcagcagcagttc 429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         y Match 12.18;
Local Similarity 57.68;
                  gctccgatggtggtgcagcagccccagtgcagccccaggtgcagcagcagca 1022
                                                                                                                                                                                                              attcagcagccaccgatgcagcagccacagcctcccgccctcccaggctctgccccagcag 789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ctccagcagcagcagcagcagcagcatctaattaaattgcatcatcaaaatcagcaa 609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CAACAGCAGCAGCAACAACAACAACAGCAGCAGCATCAACAACAACAACAGCAGCAACAGCAA 66143
                                                                                                                                                         gttgctcagaaccaaccatcacaactcccgccacagtcgcagacccagcctttggtgtca 909
                                                                                                                                                                                             TAACAGCAGCAACAACAACAACAACAATAGCAGCAACAACAGCAGCATCAACAACAA 65843
                                                                                                                                                                                                                                                             caacagcagcagcagcagcagcagcagcagcagcaggctttggaggcccagccacca 729
                                                                                                                                                                                                                                                                                                                                                                                             cagatacagcagcagcagcagctgcagcgaatagcacagctgcagctccaacaacag 669
                                                                                                                                                                                                                                                                                                                                                                                                                                                              CAGCAGCAACAGCAACAACAGCAACAATAGCAGCCACAACAGCAGCATCAACAACAACAACAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 caggctcagcagagtgccatgcagcagcttccaagcagtagtgcagcagcagcagcag 549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cagcagcagcagcagcgcgctacagcagcagcagcagcagcagcagcagcagttc 489
                                                               CAGCAACAACAGCAGCATCAACAACAACAGCAGCAACAGCAACAACAACAACAACAA
                                                                                          caggogcaagototocotggacaaatgttgtatacccaaccaccactgaaatttgtocga 969
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/note="assembly_fragment"
a 28576 c 30426 g 31079 t
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4543. .14616
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         clone_end:T7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           48060.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="assembly_fragment
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="assembly_fragment"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .69563
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches 277;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 209.8; DB 2
Pred. No. 3.3e-23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 2;
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JOURNAL
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AUTHORS
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AUTHORS
TITLE
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AC087802/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACCESSION
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                                                                                                                                                                                                                    source
                    889
                                                                                                                                                                             769
                                                                                                                                                                                                                                                         709
                                                                                                                                                                                                                                                                                                                    Local
cagacccagcctttggtgtcacaggcgcaagctctccctggacaaatgttgta---tacc
                                                           ccacagccccagcagcctccagttgctcagaaccaaccatcacaactcccgccacagtcg 888
                                                                                                                                      TCTCAGGCCCTACCCCAGCAGCTGTCACAGCTGCATCATCCACAGCCATCACCAGCCACCA
                                                                                                                                                             ACU87802 187315 bp DNA HTG 23-APR-20 Mus musculus chromosome 16 clone rp23-472f15, WORKING DRAFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            On Apr 23, 2001 this sequence version replaced gi:12740049.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 4 contigs. Gaps between the contigs.
* are represented as runs of N. The order of the pieces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OK 73019, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (26-JAN-2001) Department Of Chemistry And Biochemistry, The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 (bases 1 to 187315)
Jiang, X., Song, L. and Roe, B.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus Chromosome 16 BAC Clone rp23-472f15
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Jiang, X., Song, L. and Roe, B.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus
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    provided by the submittor

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This sequence will be replaced

by the finished sequence as soon as it is available and
the accession number will be preserved.

1 7408 | 19308: contig of 7408 bp in length
7509 | 17332: contig of 9824 bp in length
17333 | 17432: gap of unknown length
17333 | 17432: gap of unknown length
17433 | 93194: contig of 75762 bp in length
17439 | 93294: gap of unknown length
17431 | 93195 | 93294: gap of unknown length
17431 | 93195 | 93294: gap of unknown length
17431 | 93295 | 187315: contig of 94021 bp in length
                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  49420
                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Mus musculus"
/db_xref="taxon:10090"
/chromosome="16"
/clone="rp23-472f15"
/clone_lib="rp23"
20 a 44136 c 42281 g 51159 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1. .187315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                              Score 209.6; DB 2
Pred. No. 3.3e-23;
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Db 72241 CAGAGCCAGCCTTTGGTGTCACAAGCACAAGCCCTTCCTGGACCGATGCTGTATGCTGCC 72182

Search completed: February 28, 2002, 19:26:56 Job time: 10749 sec